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109P1D4 SSH sequence of 192 nucleotides. (SEQ ID NO: 1).

1 GATCCTGGTT GCAGCTGTTG CTGGCACCAT AACTGTCGTT GTAGTTATTT TCATCACTGC
61 TGTAAGTAAGA TGTCGCCAGG CACACACCTT AAGGCTGCTC AGAAAAACAT GCAGAATTCT
121 GAATGGGGCTA CCCCAAACCC AGAAAACAGG CAGATGATAA AAAAAAAAAA AAAAAAAAAA
181 AAAAGCTTGA TC

(57) Abstract: A novel gene 109P1D4 and its encoded protein, and variants thereof, are described wherein 109P1D4 exhibits tis-
sue specific expression in normal adult tissue, and is aberrantly expressed in the cancers listed in Table i. Consequently, 109P1D4
provides a diagnostic, prognostic, prophylactic and/or therapeutic target for cancer. The 109P1D4 gene or fragment thereof, or its
encoded protein, or variants thereof, or a fragment thereof, can be used to elicit a humoral or cellular immune response; antibodies
or T cells reactive with 109P1D4 can be used in active or passive immunization.

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**NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED 109P1D4
USEFUL IN TREATMENT AND DETECTION OF CANCER**

STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH

Not applicable.

FIELD OF THE INVENTION

The invention described herein relates to genes and their encoded proteins, termed 109P1D4 and variants thereof, expressed in certain cancers, and to diagnostic and therapeutic methods and compositions useful in the management of cancers that express 109P1D4.

BACKGROUND OF THE INVENTION

Cancer is the second leading cause of human death next to coronary disease. Worldwide, millions of people die from cancer every year. In the United States alone, as reported by the American Cancer Society, cancer causes the death of well over a half-million people annually, with over 1.2 million new cases diagnosed per year. While deaths from heart disease have been declining significantly, those resulting from cancer generally are on the rise. In the early part of the next century, cancer is predicted to become the leading cause of death.

Worldwide, several cancers stand out as the leading killers. In particular, carcinomas of the lung, prostate, breast, colon, pancreas, and ovary represent the primary causes of cancer death. These and virtually all other carcinomas share a common lethal feature. With very few exceptions, metastatic disease from a carcinoma is fatal. Moreover, even for those cancer patients who initially survive their primary cancers, common experience has shown that their lives are dramatically altered. Many cancer patients experience strong anxieties driven by the awareness of the potential for recurrence or treatment failure. Many cancer patients experience physical debilitations following treatment. Furthermore, many cancer patients experience a recurrence.

Worldwide, prostate cancer is the fourth most prevalent cancer in men. In North America and Northern Europe, it is by far the most common cancer in males and is the second leading cause of cancer death in men. In the United States alone, well over 30,000 men die annually of this disease - second only to lung cancer. Despite the magnitude of these figures, there is still no effective treatment for metastatic prostate cancer. Surgical prostatectomy, radiation therapy, hormone ablation therapy, surgical castration and chemotherapy continue to be the main treatment modalities. Unfortunately, these treatments are ineffective for many and are often associated with undesirable consequences.

On the diagnostic front, the lack of a prostate tumor marker that can accurately detect early-stage, localized tumors remains a significant limitation in the diagnosis and management of this disease. Although the serum prostate specific antigen (PSA) assay has been a very useful tool, however its specificity and general utility is widely regarded as lacking in several important respects.

Progress in identifying additional specific markers for prostate cancer has been improved by the generation of prostate cancer xenografts that can recapitulate different stages of the disease in mice. The LAPC (Los Angeles Prostate Cancer) xenografts are prostate cancer xenografts that have survived passage in severe combined immune deficient (SCID) mice and have exhibited the capacity to mimic the transition from androgen dependence to androgen independence (Klein *et al.*, 1997, Nat. Med. 3:402). More recently identified prostate cancer markers include PCTA-1 (Su *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93: 7252), prostate-specific membrane (PSM) antigen (Pinto *et al.*, Clin Cancer Res 1996 Sep 2 (9): 1445-51), STEAP (Hubert, *et al.*, Proc Natl Acad Sci U S A. 1999 Dec 7; 96(25): 14523-8) and prostate stem cell antigen (PSCA) (Reiter *et al.*, 1998, Proc. Natl. Acad. Sci. USA 95: 1735).

While previously identified markers such as PSA, PSM, PCTA and PSCA have facilitated efforts to diagnose and treat prostate cancer, there is need for the identification of additional markers and therapeutic targets for prostate and related cancers in order to further improve diagnosis and therapy.

Renal cell carcinoma (RCC) accounts for approximately 3 percent of adult malignancies. Once adenomas reach a diameter of 2 to 3 cm, malignant potential exists. In the adult, the two principal malignant renal tumors are renal cell adenocarcinoma and transitional cell carcinoma of the renal pelvis or ureter. The incidence of renal cell adenocarcinoma is estimated at more than 29,000 cases in the United States, and more than 11,600 patients died of this disease in 1998. Transitional cell carcinoma is less frequent, with an incidence of approximately 500 cases per year in the United States.

Surgery has been the primary therapy for renal cell adenocarcinoma for many decades. Until recently, metastatic disease has been refractory to any systemic therapy. With recent developments in systemic therapies, particularly immunotherapies, metastatic renal cell carcinoma may be approached aggressively in appropriate patients with a possibility of durable responses. Nevertheless, there is a remaining need for effective therapies for these patients.

Of all new cases of cancer in the United States, bladder cancer represents approximately 5 percent in men (fifth most common neoplasm) and 3 percent in women (eighth most common neoplasm). The incidence is increasing slowly, concurrent with an increasing older population. In 1998, there was an estimated 54,500 cases, including 39,500 in men and 15,000 in women. The age-adjusted incidence in the United States is 32 per 100,000 for men and eight per 100,000 in women. The historic male/female ratio of 3:1 may be decreasing related to smoking patterns in women. There were an estimated 11,000 deaths from bladder cancer in 1998 (7,800 in men and 3,900 in women). Bladder cancer incidence and mortality strongly increase with age and will be an increasing problem as the population becomes more elderly.

Most bladder cancers recur in the bladder. Bladder cancer is managed with a combination of transurethral resection of the bladder (TUR) and intravesical chemotherapy or immunotherapy. The multifocal and recurrent nature of bladder cancer points out the limitations of TUR. Most muscle-invasive cancers are not cured by TUR alone. Radical cystectomy and urinary diversion is the most effective means to eliminate the cancer but carry an undeniable impact on urinary and sexual function. There continues to be a significant need for treatment modalities that are beneficial for bladder cancer patients.

An estimated 130,200 cases of colorectal cancer occurred in 2000 in the United States, including 93,800 cases of colon cancer and 36,400 of rectal cancer. Colorectal cancers are the third most common cancers in men and women. Incidence rates declined significantly during 1992-1996 (-2.1% per year). Research suggests that these declines have been due to increased screening and polyp removal, preventing progression of polyps to invasive cancers. There were an estimated 56,300 deaths (47,700 from colon cancer, 8,600 from rectal cancer) in 2000, accounting for about 11% of all U.S. cancer deaths.

At present, surgery is the most common form of therapy for colorectal cancer, and for cancers that have not spread, it is frequently curative. Chemotherapy, or chemotherapy plus radiation, is given before or after surgery to most

patients whose cancer has deeply perforated the bowel wall or has spread to the lymph nodes. A permanent colostomy (creation of an abdominal opening for elimination of body wastes) is occasionally needed for colon cancer and is infrequently required for rectal cancer. There continues to be a need for effective diagnostic and treatment modalities for colorectal cancer.

There were an estimated 164,100 new cases of lung and bronchial cancer in 2000, accounting for 14% of all U.S. cancer diagnoses. The incidence rate of lung and bronchial cancer is declining significantly in men, from a high of 86.5 per 100,000 in 1984 to 70.0 in 1996. In the 1990s, the rate of increase among women began to slow. In 1996, the incidence rate in women was 42.3 per 100,000.

Lung and bronchial cancer caused an estimated 156,900 deaths in 2000, accounting for 28% of all cancer deaths. During 1992–1996, mortality from lung cancer declined significantly among men (-1.7% per year) while rates for women were still significantly increasing (0.9% per year). Since 1987, more women have died each year of lung cancer than breast cancer, which, for over 40 years, was the major cause of cancer death in women. Decreasing lung cancer incidence and mortality rates most likely resulted from decreased smoking rates over the previous 30 years; however, decreasing smoking patterns among women lag behind those of men. Of concern, although the declines in adult tobacco use have slowed, tobacco use in youth is increasing again.

Treatment options for lung and bronchial cancer are determined by the type and stage of the cancer and include surgery, radiation therapy, and chemotherapy. For many localized cancers, surgery is usually the treatment of choice. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often needed in combination with surgery. Chemotherapy alone or combined with radiation is the treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which in some cases is long lasting. There is however, an ongoing need for effective treatment and diagnostic approaches for lung and bronchial cancers.

An estimated 182,800 new invasive cases of breast cancer were expected to occur among women in the United States during 2000. Additionally, about 1,400 new cases of breast cancer were expected to be diagnosed in men in 2000. After increasing about 4% per year in the 1980s, breast cancer incidence rates in women have leveled off in the 1990s to about 110.6 cases per 100,000.

In the U.S. alone, there were an estimated 41,200 deaths (40,800 women, 400 men) in 2000 due to breast cancer. Breast cancer ranks second among cancer deaths in women. According to the most recent data, mortality rates declined significantly during 1992–1996 with the largest decreases in younger women, both white and black. These decreases were probably the result of earlier detection and improved treatment.

Taking into account the medical circumstances and the patient's preferences, treatment of breast cancer may involve lumpectomy (local removal of the tumor) and removal of the lymph nodes under the arm; mastectomy (surgical removal of the breast) and removal of the lymph nodes under the arm; radiation therapy; chemotherapy; or hormone therapy. Often, two or more methods are used in combination. Numerous studies have shown that, for early stage disease, long-term survival rates after lumpectomy plus radiotherapy are similar to survival rates after modified radical mastectomy. Significant advances in reconstruction techniques provide several options for breast reconstruction after mastectomy. Recently, such reconstruction has been done at the same time as the mastectomy.

Local excision of ductal carcinoma *in situ* (DCIS) with adequate amounts of surrounding normal breast tissue may prevent the local recurrence of the DCIS. Radiation to the breast and/or tamoxifen may reduce the chance of DCIS occurring in the remaining breast tissue. This is important because DCIS, if left untreated, may develop into invasive breast cancer. Nevertheless, there are serious side effects or sequelae to these treatments. There is, therefore, a need for efficacious breast cancer treatments.

There were an estimated 23,100 new cases of ovarian cancer in the United States in 2000. It accounts for 4% of all cancers among women and ranks second among gynecologic cancers. During 1992–1996, ovarian cancer incidence rates were significantly declining. Consequent to ovarian cancer, there were an estimated 14,000 deaths in 2000. Ovarian cancer causes more deaths than any other cancer of the female reproductive system.

Surgery, radiation therapy, and chemotherapy are treatment options for ovarian cancer. Surgery usually includes the removal of one or both ovaries, the fallopian tubes (salpingo-oophorectomy), and the uterus (hysterectomy). In some very early tumors, only the involved ovary will be removed, especially in young women who wish to have children. In advanced disease, an attempt is made to remove all intra-abdominal disease to enhance the effect of chemotherapy. There continues to be an important need for effective treatment options for ovarian cancer.

There were an estimated 28,300 new cases of pancreatic cancer in the United States in 2000. Over the past 20 years, rates of pancreatic cancer have declined in men. Rates among women have remained approximately constant but may be beginning to decline. Pancreatic cancer caused an estimated 28,200 deaths in 2000 in the United States. Over the past 20 years, there has been a slight but significant decrease in mortality rates among men (about –0.9% per year) while rates have increased slightly among women.

Surgery, radiation therapy, and chemotherapy are treatment options for pancreatic cancer. These treatment options can extend survival and/or relieve symptoms in many patients but are not likely to produce a cure for most. There is a significant need for additional therapeutic and diagnostic options for pancreatic cancer.

SUMMARY OF THE INVENTION

The present invention relates to a gene, designated 109P1D4, that has now been found to be over-expressed in the cancer(s) listed in Table I. Northern blot expression analysis of 109P1D4 gene expression in normal tissues shows a restricted expression pattern in adult tissues. The nucleotide (Figure 2) and amino acid (Figure 2, and Figure 3) sequences of 109P1D4 are provided. The tissue-related profile of 109P1D4 in normal adult tissues, combined with the over-expression observed in the tissues listed in Table I, shows that 109P1D4 is aberrantly over-expressed in at least some cancers, and thus serves as a useful diagnostic, prophylactic, prognostic, and/or therapeutic target for cancers of the tissue(s) such as those listed in Table I.

The invention provides polynucleotides corresponding or complementary to all or part of the 109P1D4 genes, mRNAs, and/or coding sequences, preferably in isolated form, including polynucleotides encoding 109P1D4-related proteins and fragments of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 contiguous amino acids; at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100 or more than 100 contiguous amino acids of a 109P1D4-related protein, as well as the peptides/proteins themselves; DNA, RNA, DNA/RNA hybrids, and related molecules, polynucleotides or oligonucleotides complementary or having at least a 90% homology to the 109P1D4 genes or mRNA sequences or parts thereof, and polynucleotides or oligonucleotides that hybridize to the 109P1D4 genes, mRNAs, or to 109P1D4-encoding polynucleotides. Also provided are means for isolating cDNAs and the genes encoding 109P1D4. Recombinant DNA molecules containing 109P1D4 polynucleotides, cells transformed or transduced with such molecules, and host-vector systems for the expression of 109P1D4 gene products are also provided. The invention further provides antibodies that bind to 109P1D4 proteins and polypeptide fragments thereof, including polyclonal and monoclonal antibodies, murine and other mammalian antibodies, chimeric antibodies, humanized and fully human antibodies, and antibodies labeled with a detectable marker or therapeutic agent. In certain embodiments, there is a proviso that the entire nucleic acid sequence of Figure 2 is not encoded and/or the entire amino acid sequence of Figure 2 is not prepared. In certain embodiments, the entire nucleic acid sequence of Figure 2 is encoded and/or the entire amino acid sequence of Figure 2 is prepared, either of which are in respective human unit dose forms.

The invention further provides methods for detecting the presence and status of 109P1D4 polynucleotides and proteins in various biological samples, as well as methods for identifying cells that express 109P1D4. A typical embodiment of this invention provides methods for monitoring 109P1D4 gene products in a tissue or hematology sample having or suspected of having some form of growth dysregulation such as cancer.

The invention further provides various immunogenic or therapeutic compositions and strategies for treating cancers that express 109P1D4 such as cancers of tissues listed in Table I, including therapies aimed at inhibiting the transcription, translation, processing or function of 109P1D4 as well as cancer vaccines. In one aspect, the invention provides compositions, and methods comprising them, for treating a cancer that expresses 109P1D4 in a human subject wherein the composition comprises a carrier suitable for human use and a human unit dose of one or more than one agent that inhibits the production or function of 109P1D4. Preferably, the carrier is a uniquely human carrier. In another aspect of the invention, the agent is a moiety that is immunoreactive with 109P1D4 protein. Non-limiting examples of such moieties include, but are not limited to, antibodies (such as single chain, monoclonal, polyclonal, humanized, chimeric, or human antibodies), functional equivalents thereof (whether naturally occurring or synthetic), and combinations thereof. The antibodies can be conjugated to a diagnostic or therapeutic moiety. In another aspect, the agent is a small molecule as defined herein.

In another aspect, the agent comprises one or more than one peptide which comprises a cytotoxic T lymphocyte (CTL) epitope that binds an HLA class I molecule in a human to elicit a CTL response to 109P1D4 and/or one or more than one peptide which comprises a helper T lymphocyte (HTL) epitope which binds an HLA class II molecule in a human to elicit an HTL response. The peptides of the invention may be on the same or on one or more separate polypeptide molecules. In a further aspect of the invention, the agent comprises one or more than one nucleic acid molecule that expresses one or more than one of the CTL or HTL response stimulating peptides as described above. In yet another aspect of the invention, the one or more than one nucleic acid molecule may express a moiety that is immunologically reactive with 109P1D4 as described above. The one or more than one nucleic acid molecule may also be, or encode, a molecule that inhibits production of 109P1D4. Non-limiting examples of such molecules include, but are not limited to, those complementary to a nucleotide sequence essential for production of 109P1D4 (e.g. antisense sequences or molecules that form a triple helix with a nucleotide double helix essential for 109P1D4 production) or a ribozyme effective to lyse 109P1D4 mRNA.

Note that to determine the starting position of any peptide set forth in Tables VIII-XXI and XXII to XLIX (collectively HLA Peptide Tables) relative to its parental protein, e.g., variant 1, variant 2, etc., reference is made to three factors: the particular variant, the length of the peptide in an HLA Peptide Table, and the Search Peptides in Table VII. Generally, a unique Search Peptide is used to obtain HLA peptides of a particular for a particular variant. The position of each Search Peptide relative to its respective parent molecule is listed in Table VII. Accordingly, if a Search Peptide begins at position "X", one must add the value "X - 1" to each position in Tables VIII-XXI and XXII to XLIX to obtain the actual position of the HLA peptides in their parental molecule. For example, if a particular Search Peptide begins at position 150 of its parental molecule, one must add 150 - 1, i.e., 149 to each HLA peptide amino acid position to calculate the position of that amino acid in the parent molecule.

One embodiment of the invention comprises an HLA peptide, that occurs at least twice in Tables VIII-XXI and XXII to XLIX collectively, or an oligonucleotide that encodes the HLA peptide. Another embodiment of the invention comprises an HLA peptide that occurs at least once in Tables VIII-XXI and at least once in tables XXII to XLIX, or an oligonucleotide that encodes the HLA peptide.

Another embodiment of the invention is antibody epitopes, which comprise a peptide regions, or an oligonucleotide encoding the peptide region, that has one two, three, four, or five of the following characteristics:

- i) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Hydrophilicity profile of Figure 5;
- ii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or less than 0.5, 0.4, 0.3, 0.2, 0.1, or having a value equal to 0.0, in the Hydropathicity profile of Figure 6;
- iii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Percent Accessible Residues profile of Figure 7;
- iv) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Average Flexibility profile of Figure 8; or
- v) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Beta-turn profile of Figure 9.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. The 109P1D4 SSH sequence of 192 nucleotides.

Figure 2. A) The cDNA and amino acid sequence of 109P1D4 variant 1 (also called "109P1D4 v.1" or "109P1D4 variant 1") is shown in Figure 2A. The start methionine is underlined. The open reading frame extends from nucleic acid 846-3911 including the stop codon.

B) The cDNA and amino acid sequence of 109P1D4 variant 2 (also called "109P1D4 v.2") is shown in Figure 2B. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 503-3667 including the stop codon.

C) The cDNA and amino acid sequence of 109P1D4 variant 3 (also called "109P1D4 v.3") is shown in Figure 2C. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 846-4889 including the stop codon.

D) The cDNA and amino acid sequence of 109P1D4 variant 4 (also called "109P1D4 v.4") is shown in Figure 2D. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 846-4859 including the stop codon.

E) The cDNA and amino acid sequence of 109P1D4 variant 5 (also called "109P1D4 v.5") is shown in Figure 2E. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 846-4778 including the stop codon.

F) The cDNA and amino acid sequence of 109P1D4 variant 6 (also called "109P1D4 v.6") is shown in Figure 2F. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 614-3727 including the stop codon.

G) The cDNA and amino acid sequence of 109P1D4 variant 7 (also called "109P1D4 v.7") is shown in Figure 2G. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 735-3881 including the stop codon.

H) The cDNA and amino acid sequence of 109P1D4 variant 8 (also called "109P1D4 v.8") is shown in Figure 2H. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 735-4757 including the stop codon.

I) The cDNA and amino acid sequence of 109P1D4 variant 9 (also called "109P1D4 v.9") is shown in Figure 2I. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 514-3627 including the stop codon.

J) **109P1D4 v.1, v.2 and v.3 SNP variants.** Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above.

K) **109P1D4 v.6, v.7 and v.8 SNP variants.** Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above.

Figure 3.

A) The amino acid sequence of 109P1D4 v.1 is shown in Figure 3A; it has 1021 amino acids.

B) The amino acid sequence of 109P1D4 v.2 is shown in Figure 3B; it has 1054 amino acids.

C) The amino acid sequence of 109P1D4 v.3 is shown in Figure 3C; it has 1347 amino acids.

D) The amino acid sequence of 109P1D4 v.4 is shown in Figure 3D; it has 1337 amino acids.

E) The amino acid sequence of 109P1D4 v.5 is shown in Figure 3E; it has 1310 amino acids.

F) The amino acid sequence of 109P1D4 v.6 is shown in Figure 3F; it has 1037 amino acids.

G) The amino acid sequence of 109P1D4 v.7 is shown in Figure 3G; it has 1048 amino acids.

H) The amino acid sequence of 109P1D4 v.8 is shown in Figure 3H; it has 1340 amino acids.

I) The amino acid sequence of 109P1D4 v.9 is shown in Figure 3I; it has 1037 amino acids.

As used herein, a reference to 109P1D4 includes all variants thereof, including those shown in Figures 2, 3, 10, 11, and 12 unless the context clearly indicates otherwise.

Figure 4. Alignment of 109P1D4 v.1 Protein with protocadherin-11.

Figure 5. Hydrophilicity amino acid profile of 109P1D4 v.1-v.9 determined by computer algorithm sequence analysis using the method of Hopp and Woods (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828) accessed on the Protscale website located on the World Wide Web at (expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 6. Hydropathicity amino acid profile of 109P1D4 v.1-v.9 determined by computer algorithm sequence analysis using the method of Kyte and Doolittle (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132) accessed on the ProtScale website located on the World Wide Web at (expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 7. Percent accessible residues amino acid profile of 109P1D4 v.1-v.9 determined by computer algorithm sequence analysis using the method of Janin (Janin J., 1979 Nature 277:491-492) accessed on the ProtScale website located on the World Wide Web at (expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 8. Average flexibility amino acid profile of 109P1D4 v.1-v.9 determined by computer algorithm sequence analysis using the method of Bhaskaran and Ponnuswamy (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255) accessed on the ProtScale website located on the World Wide Web at (expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 9. Beta-turn amino acid profile of 109P1D4 v.1-v.9 determined by computer algorithm sequence analysis using the method of Deleage and Roux (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294) accessed on the ProtScale website located on the World Wide Web at (expasy.ch/cgi-bin/protscale.pl) through the ExPasy molecular biology server.

Figure 10. Structure of transcript variants of 109P1D4. Variants 109P1D4 v.2 through v.9 were transcript variants of v.1. Variant v.2 shared middle portion of v.1 sequence (the 3' portion of exon 1 and 5' portion of exon 2). Variant

v.6 was similar to v.2 but added an extra exon between exons 1 and 2 of v.2. V.3 shared exon 1 and 5' portion of exon 2 with v.1 with five additional exons downstream. Compared with v.3, v.4 deleted exon 4 of v.3 while v.5 deleted exons 3 and 4 of v.3. Variant v.5 lacked exons 3 and 4. This gene (called PCD11) is located in sex chromosomes X and Y. Ends of exons in the transcripts are marked above the boxes. Potential exons of this gene are shown in order as on the human genome. Poly A tails and single nucleotide differences are not shown in the figure. Lengths of introns and exons are not proportional.

Figure 11. Schematic alignment of protein variants of 109P1D4. Variants 109P1D4 v.2 through v.9 were proteins translated from the corresponding transcript variants. All these protein variants shared a common portion of the sequence, i.e., 3-1011 of v.1, except for a few amino acids different in this segment resulted from SNP in the transcripts. Variant v.6 and v.9 were the same except for two amino acids at 906 and 1001. Variant v.8 was almost the same as v.5, except for the N-terminal end, and a 2-aa deletion at 1117-8. Single amino acid difference was not shown. Numbers in parentheses corresponded to positions in variant v.3.

Figure 12. Intentionally Omitted.

Figure 13. Figures 13(a)-(i): Secondary structure and transmembrane domains prediction for 109P1D4 protein variants 1-9 (v.1 – (SEQ ID NO: 31); v.2 – (SEQ ID NO: 32); v.3 – (SEQ ID NO: 33); v.4 – (SEQ ID NO: 34); v.5 – (SEQ ID NO: 35); v.6 – (SEQ ID NO: 36); v.7 – (SEQ ID NO: 37); v.8 – (SEQ ID NO: 38); v.9 – (SEQ ID NO: 39)). The secondary structures of 109P1D4 protein variants were predicted using the HNN - Hierarchical Neural Network method (NPS@: Network Protein Sequence Analysis TIBS 2000 March Vol. 25, No 3 [291]:147-150 Combet C., Blanchet C., Geourjon C. and Deléage G., http://pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_nn.html), accessed from the ExPasy molecular biology server located on the World Wide Web at (.expasy.ch/tools/). This method predicts the presence and location of alpha helices, extended strands, and random coils from the primary protein sequence. The percent of the protein variant in a given secondary structure is also listed. **Figures 13(j)-(r) top panels:** Schematic representation of the probability of existence of transmembrane regions of 109P1D4 variants based on the TMPred algorithm of Hofmann and Stoffel which utilizes TMbase (K. Hofmann, W. Stoffel. TMbase - A database of membrane spanning protein segments Biol. Chem. Hoppe-Seyler 374:166, 1993). **Figures 13(j)-(r) bottom panels:** Schematic representation of the probability of the existence of transmembrane regions of 109P1D4 variants based on the TMHMM algorithm of Sonnhammer, von Heijne, and Krogh (Erik L.L. Sonnhammer, Gunnar von Heijne, and Anders Krogh: A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p 175-182 Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998). The TMPred and TMHMM algorithms are accessed from the ExPasy molecular biology server located on the World Wide Web at (.expasy.ch/tools/).

Figure 14. Expression of 109P1D4 in Lymphoma Cancer Patient Specimens. RNA was extracted from peripheral blood lymphocytes, cord blood isolated from normal individuals, and from lymphoma patient cancer specimens. Northern blots with 10µg of total RNA were probed with the 109P1D4 sequence. Size standards in kilobases are on the side. Results show expression of 109P1D4 in lymphoma patient specimens but not in the normal blood cells tested.

Figure 15. Expression of 109P1D4 by RT-PCR. First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), prostate cancer pool, bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, cancer metastasis pool, and pancreas cancer pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 109P1D4, was performed at 30 cycles of amplification. Results show strong expression of 109P1D4 in all cancer pools tested. Very low expression was detected in the vital pools.

Figure 16. Expression of 109P1D4 in normal tissues. Two multiple tissue northern blots (Clontech), both with 2 µg of mRNA/lane, were probed with the 109P1D4 SSH fragment. Size standards in kilobases (kb) are indicated on the side.

Results show expression of approximately 10 kb 109P1D4 transcript in ovary. Weak expression was also detected in placenta and brain, but not in the other normal tissues tested.

Figure 17. Expression of 109P1D4 in human cancer cell lines. RNA was extracted from a number of human prostate and bone cancer cell lines. Northern blots with 10 µg of total RNA/lane were probed with the 109P1D4 SSH fragment. Size standards in kilobases (kb) are indicated on the side. Results show expression of 109P1D4 in LAPC-9AD, LAPC-9AI, LNCaP prostate cancer cell lines, and in the bone cancer cell lines, SK-ES-1 and RD-ES.

Figure 18. Figure 18A: 109P1D4 Expression in Human Normal Tissues. An cDNA dot blot containing 76 different samples from human tissues was analyzed using a 109P1D4 SSH probe. Expression was only detected in multiple areas of the brain, placenta, ovary, and fetal brain, amongst all tissues tested. **Figure 18B: Expression of 109P1D4 in patient cancer specimens.** Expression of 109P1D4 was assayed in a panel of human cancers (T) and their respective matched normal tissues (N) on RNA dot blots. Upregulated expression of 109P1D4 in tumors compared to normal tissues was observed in uterus, lung and stomach. The expression detected in normal adjacent tissues (isolated from diseased tissues) but not in normal tissues (isolated from healthy donors) may indicate that these tissues are not fully normal and that 109P1D4 may be expressed in early stage tumors.

Figure 19. 109P1D4 Expression in Lung Cancer Patient Specimens. RNA was extracted from normal lung, prostate cancer xenograft LAPC-9AD, bone cancer cell line RD-ES, and lung cancer patient tumors. Northern blots with 10 µg of total RNA were probed with 109P1D4. Size standards in kilobases are on the side. Results show strong expression of 109P1D4 in lung tumor tissues as well as the RD-ES cell line, but not in normal lung.

Figure 20. Expression of soluble secreted Tag5 109P1D4 in 293T cells. 293T cells were transfected with either an empty vector or with the Tag5 secretion vector encoding the extracellular domain (ECD; amino acids 24-812) of 109P1D4 variant 1 fused to a Myc/His epitope Tag. 2 days later, cells and media harvested and analyzed for expression of the recombinant Tag5 109P1D4 protein by SDS-PAGE followed by anti-His epitope tag Western blotting. An arrow indicates the immunoreactive band corresponding to the 109P1D4 ECD present in the media and the lysate from Tag5 109P1D4 transfected cells.

Figure 21. Expression of 109P1D4 protein in 293T cells. 293T cells were transfected with either an empty vector or with pCDNA3.1 vector encoding the full length cDNA of 109P1D4 variant 1 fused to a Myc/His epitope Tag. 2 days later, cells were harvested and analyzed for expression of 109P1D4 variant 1 protein by SDS-PAGE followed by anti-His epitope tag Western blotting. An arrow indicates the immunoreactive band corresponding to the full length 109P1D4 variant 1 protein expressed in cells transfected with the 109P1D4 vector but not in control cells.

Figure 22. Tyrosine phosphorylation of 109P1D4 after pervanadate treatment. 293T cells were transfected with the neomycin resistance gene alone or with 109P1D4 in pSRµ vector. Twenty four hours after transfection, the cells were either left in 10% serum or grown in 0.1% serum overnight. The cells were then left untreated or were treated with 200 µM pervanadate (1:1 mixture of Na₂VO₄ and H₂O₂) for 30 minutes. The cells were lysed in Triton X-100, and the 109P1D4 protein was immunoprecipitated with anti-His monoclonal antibody. The immunoprecipitates were run on SDS-PAGE and then Western blotted with either anti-phosphotyrosine (upper panel) or anti-His (lower panel). The 109P1D4 protein is phosphorylated on tyrosine in response to pervanadate treatment, and a large amount of the protein moves to the insoluble fraction following pervanadate-induced activation.

Figure 23. Effect of 109P1D4 RNAi on cell proliferation. LNCaP cells were transfected with Lipofectamine 2000 alone or with siRNA oligonucleotides. The siRNA oligonucleotides included a negative control, Luc4, specific for Luciferase, a positive control, Eg5, specific for the mitotic spindle protein Eg5, or three siRNAs specific for the 109P1D4 protein, 109P1D4.a, 109P1D4.c and 109P1D4.d at 20 nM concentration. Twenty four hours after transfection, the cells were pulsed

with ^3H -thymidine and incorporation was measured after 72 hours. All three siRNAs to 109P1D4 inhibited the proliferation of LNCaP cells, indicating that 109P1D4 expression is important for the cell growth pathway of these cancer cells.

DETAILED DESCRIPTION OF THE INVENTION

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I.) Definitions:

Unless otherwise defined, all terms of art, notations and other scientific terms or terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. Many of the techniques and procedures described or referenced herein are well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

The terms "advanced prostate cancer", "locally advanced prostate cancer", "advanced disease" and "locally advanced disease" mean prostate cancers that have extended through the prostate capsule, and are meant to include stage C disease under the American Urological Association (AUA) system, stage C1 - C2 disease under the Whitmore-Jewett system, and stage T3 - T4 and N+ disease under the TNM (tumor, node, metastasis) system. In general, surgery is not recommended for patients with locally advanced disease, and these patients have substantially less favorable outcomes compared to patients having clinically localized (organ-confined) prostate cancer. Locally advanced disease is clinically identified by palpable evidence of induration beyond the lateral border of the prostate, or asymmetry or induration above the prostate base. Locally advanced prostate cancer is presently diagnosed pathologically following radical prostatectomy if the tumor invades or penetrates the prostatic capsule, extends into the surgical margin, or invades the seminal vesicles.

"Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence 109P1D4 (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence 109P1D4. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

The term "analog" refers to a molecule which is structurally similar or shares similar or corresponding attributes with another molecule (e.g. a 109P1D4-related protein). For example, an analog of a 109P1D4 protein can be specifically bound by an antibody or T cell that specifically binds to 109P1D4.

The term "antibody" is used in the broadest sense. Therefore, an "antibody" can be naturally occurring or man-made such as monoclonal antibodies produced by conventional hybridoma technology. Anti-109P1D4 antibodies comprise monoclonal and polyclonal antibodies as well as fragments containing the antigen-binding domain and/or one or more complementarity determining regions of these antibodies.

An "antibody fragment" is defined as at least a portion of the variable region of the immunoglobulin molecule that binds to its target, i.e., the antigen-binding region. In one embodiment it specifically covers single anti-109P1D4 antibodies and clones thereof (including agonist, antagonist and neutralizing antibodies) and anti-109P1D4 antibody compositions with polypeptidic specificity.

The term "codon optimized sequences" refers to nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage frequency of less than about 20%. Nucleotide sequences that have been optimized for expression in a given host species by elimination of spurious polyadenylation sequences, elimination of exon/intron splicing signals, elimination of transposon-like repeats and/or optimization of GC content in addition to codon

optimization are referred to herein as an "expression enhanced sequences."

A "combinatorial library" is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Numerous chemical compounds are synthesized through such combinatorial mixing of chemical building blocks (Gallop et al., *J. Med. Chem.* 37(9): 1233-1251 (1994)).

Preparation and screening of combinatorial libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton et al., *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio- oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs et al., *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara et al., *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidic peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann et al., *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen et al., *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, et al., *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell et al., *J. Org. Chem.* 59:658 (1994)). See, generally, Gordon et al., *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn et al., *Nature Biotechnology* 14(3): 309-314 (1996), and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al., *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 NIPS, 390 NIPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A, Applied Biosystems, Foster City, CA; 9050, Plus, Millipore, Bedford, MA). A number of well-known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations such as the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate H, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The term "cytotoxic agent" refers to a substance that inhibits or prevents the expression activity of cells, function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof. Examples of cytotoxic agents include, but are not limited to auristatins, auromycins, maytansinoids, yttrium, bismuth, ricin, ricin A-chain, combrestatin, duocarmycins, dolostatins, doxorubicin, daunorubicin, taxol, cisplatin, cc1065, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, *Pseudomonas* exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain,

alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crocin, calicheamicin, *Saponaia officinalis* inhibitor, and glucocorticoid and other chemotherapeutic agents, as well as radioisotopes such as At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹² or ²¹³, P³² and radioactive isotopes of Lu including Lu¹⁷⁷. Antibodies may also be conjugated to an anti-cancer pro-drug activating enzyme capable of converting the pro-drug to its active form.

The "gene product" is sometimes referred to herein as a protein or mRNA. For example, a "gene product of the invention" is sometimes referred to herein as a "cancer amino acid sequence", "cancer protein", "protein of a cancer listed in Table I", a "cancer mRNA", "mRNA of a cancer listed in Table I", etc. In one embodiment, the cancer protein is encoded by a nucleic acid of Figure 2. The cancer protein can be a fragment, or alternatively, be the full-length protein to the fragment encoded by the nucleic acids of Figure 2. In one embodiment, a cancer amino acid sequence is used to determine sequence identity or similarity. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Figure 2. In another embodiment, the sequences are sequence variants as further described herein.

"High throughput screening" assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins; U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays); while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Amersham Biosciences, Piscataway, NJ; Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

The term "homolog" refers to a molecule which exhibits homology to another molecule, by for example, having sequences of chemical residues that are the same or similar at corresponding positions.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (see, e.g., Stites, *et al.*, IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994).

The terms "hybridize", "hybridizing", "hybridizes" and the like, used in the context of polynucleotides, are meant to refer to conventional hybridization conditions, preferably such as hybridization in 50% formamide/6XSSC/0.1% SDS/100 µg/ml ssDNA, in which temperatures for hybridization are above 37 degrees C and temperatures for washing in 0.1XSSC/0.1% SDS are above 55 degrees C.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. For example, a polynucleotide is said to be "isolated" when it is substantially separated from contaminant polynucleotides that correspond or are complementary to genes other than the 109P1D4 genes or that encode polypeptides other than 109P1D4 gene product or fragments thereof. A skilled artisan can readily employ nucleic acid isolation procedures to obtain an isolated 109P1D4 polynucleotide. A protein is said to be "isolated," for example, when physical, mechanical or chemical methods are employed to remove the 109P1D4 proteins from cellular constituents that are normally associated with the protein. A skilled artisan can readily

employ standard purification methods to obtain an isolated 109P1D4 protein. Alternatively, an isolated protein can be prepared by chemical means.

The term "mammal" refers to any organism classified as a mammal, including mice, rats, rabbits, dogs, cats, cows, horses and humans. In one embodiment of the invention, the mammal is a mouse. In another embodiment of the invention, the mammal is a human.

The terms "metastatic prostate cancer" and "metastatic disease" mean prostate cancers that have spread to regional lymph nodes or to distant sites, and are meant to include stage D disease under the AUA system and stage TxNxM+ under the TNM system. As is the case with locally advanced prostate cancer, surgery is generally not indicated for patients with metastatic disease, and hormonal (androgen ablation) therapy is a preferred treatment modality. Patients with metastatic prostate cancer eventually develop an androgen-refractory state within 12 to 18 months of treatment initiation. Approximately half of these androgen-refractory patients die within 6 months after developing that status. The most common site for prostate cancer metastasis is bone. Prostate cancer bone metastases are often osteoblastic rather than osteolytic (i.e., resulting in net bone formation). Bone metastases are found most frequently in the spine, followed by the femur, pelvis, rib cage, skull and humerus. Other common sites for metastasis include lymph nodes, lung, liver and brain. Metastatic prostate cancer is typically diagnosed by open or laparoscopic pelvic lymphadenectomy, whole body radionuclide scans, skeletal radiography, and/or bone lesion biopsy.

The term "modulator" or "test compound" or "drug candidate" or grammatical equivalents as used herein describe any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequences, or effects of cancer sequences (e.g., signaling, gene expression, protein interaction, etc.) In one aspect, a modulator will neutralize the effect of a cancer protein of the invention. By "neutralize" is meant that an activity of a protein is inhibited or blocked, along with the consequent effect on the cell. In another aspect, a modulator will neutralize the effect of a gene, and its corresponding protein, of the invention by normalizing levels of said protein. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein, or downstream effector pathways. In one embodiment, the modulator suppresses a cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures is run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Modulators, drug candidates or test compounds encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 Daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Modulators also comprise biomolecules such as peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides. One class of modulators are peptides, for example of from about five to about 35 amino acids, with from about five to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. Preferably, the cancer modulatory protein is soluble, includes a non-transmembrane region, and/or, has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, i.e., to cysteine. In one embodiment, a cancer protein of the invention is conjugated to an

immunogenic agent as discussed herein. In one embodiment, the cancer protein is conjugated to BSA. The peptides of the invention, e.g., of preferred lengths, can be linked to each other or to other amino acids to create a longer peptide/protein. The modulatory peptides can be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. In a preferred embodiment, peptide/protein-based modulators are antibodies, and fragments thereof, as defined herein.

Modulators of cancer can also be nucleic acids. Nucleic acid modulating agents can be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes can be used in an approach analogous to that outlined above for proteins.

The term "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the antibodies comprising the population are identical except for possible naturally occurring mutations that are present in minor amounts.

A "motif", as in biological motif of a 109P1D4-related protein, refers to any pattern of amino acids forming part of the primary sequence of a protein, that is associated with a particular function (e.g. protein-protein interaction, protein-DNA interaction, etc) or modification (e.g. that is phosphorylated, glycosylated or amidated), or localization (e.g. secretory sequence, nuclear localization sequence, etc.) or a sequence that is correlated with being immunogenic, either humorally or cellularly. A motif can be either contiguous or capable of being aligned to certain positions that are generally correlated with a certain function or property. In the context of HLA motifs, "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs for HLA binding are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "pharmaceutical excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservative, and the like.

"Pharmaceutically acceptable" refers to a non-toxic, inert, and/or composition that is physiologically compatible with humans or other mammals.

The term "polynucleotide" means a polymeric form of nucleotides of at least 10 bases or base pairs in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide, and is meant to include single and double stranded forms of DNA and/or RNA. In the art, this term is often used interchangeably with "oligonucleotide". A polynucleotide can comprise a nucleotide sequence disclosed herein wherein thymidine (T), as shown for example in Figure 2, can also be uracil (U); this definition pertains to the differences between the chemical structures of DNA and RNA, in particular the observation that one of the four major bases in RNA is uracil (U) instead of thymidine (T).

The term "polypeptide" means a polymer of at least about 4, 5, 6, 7, or 8 amino acids. Throughout the specification, standard three letter or single letter designations for amino acids are used. In the art, this term is often used interchangeably with "peptide" or "protein".

An HLA "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding groove of an HLA molecule, with their side chains buried in specific pockets of the binding groove. In one embodiment, for example, the primary anchor residues for an HLA class I molecule are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 8, 9, 10, 11, or 12 residue peptide epitope in accordance with the invention. Alternatively, in another embodiment, the primary anchor

residues of a peptide binds an HLA class II molecule are spaced relative to each other, rather than to the termini of a peptide, where the peptide is generally of at least 9 amino acids in length. The primary anchor positions for each motif and supermotif are set forth in Table IV. For example, analog peptides can be created by altering the presence or absence of particular residues in the primary and/or secondary anchor positions shown in Table IV. Such analogs are used to modulate the binding affinity and/or population coverage of a peptide comprising a particular HLA motif or supermotif.

"Radioisotopes" include, but are not limited to the following (non-limiting exemplary uses are also set forth):

Examples of Medical Isotopes:

Isotope	Description of use
Actinium-225 (Ac-225)	See Thorium-229 (Th-229)
Actinium-227 (Ac-227)	Parent of Radium-223 (Ra-223) which is an alpha emitter used to treat metastases in the skeleton resulting from cancer (i.e., breast and prostate cancers), and cancer radioimmunotherapy
Bismuth-212 (Bi-212)	See Thorium-228 (Th-228)
Bismuth-213 (Bi-213)	See Thorium-229 (Th-229)
Cadmium-109 (Cd-109)	Cancer detection
Cobalt-60 (Co-60)	Radiation source for radiotherapy of cancer, for food irradiators, and for sterilization of medical supplies
Copper-64 (Cu-64)	A positron emitter used for cancer therapy and SPECT imaging
Copper-67 (Cu-67)	Beta/gamma emitter used in cancer radioimmunotherapy and diagnostic studies (i.e., breast and colon cancers, and lymphoma)
Dysprosium-166 (Dy-166)	Cancer radioimmunotherapy
Erbium-169 (Er-169)	Rheumatoid arthritis treatment, particularly for the small joints associated with fingers and toes
Europium-152 (Eu-152)	Radiation source for food irradiation and for sterilization of medical supplies
Europium-154 (Eu-154)	Radiation source for food irradiation and for sterilization of medical supplies
Gadolinium-153 (Gd-153)	Osteoporosis detection and nuclear medical quality assurance devices
Gold-198 (Au-198)	Implant and intracavity therapy of ovarian, prostate, and brain cancers
Holmium-166 (Ho-166)	Multiple myeloma treatment in targeted skeletal therapy, cancer radioimmunotherapy, bone marrow ablation, and rheumatoid arthritis treatment
Iodine-125 (I-125)	Osteoporosis detection, diagnostic imaging, tracer drugs, brain cancer treatment, radiolabeling, tumor imaging, mapping of receptors in the brain, interstitial radiation therapy, brachytherapy for treatment of prostate cancer, determination of glomerular filtration rate (GFR), determination of plasma volume, detection of deep vein thrombosis of the legs
Iodine-131 (I-131)	Thyroid function evaluation, thyroid disease detection, treatment of thyroid cancer as well as other non-malignant thyroid diseases (i.e., Graves disease, goiters, and hyperthyroidism), treatment of leukemia, lymphoma, and other forms of cancer (e.g., breast cancer) using radioimmunotherapy
Iridium-192 (Ir-192)	Brachytherapy, brain and spinal cord tumor treatment, treatment of blocked arteries (i.e., arteriosclerosis and restenosis), and implants for breast and prostate tumors
Lutetium-177 (Lu-177)	Cancer radioimmunotherapy and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Molybdenum-99 (Mo-99)	Parent of Technetium-99m (Tc-99m) which is used for imaging the brain, liver, lungs, heart, and other organs. Currently, Tc-99m is the most widely used radioisotope used for diagnostic imaging of various cancers and diseases involving the brain, heart, liver, lungs; also used in detection of deep vein thrombosis of the legs
Osmium-194 (Os-194)	Cancer radioimmunotherapy

Palladium-103 (Pd-103)	Prostate cancer treatment
Platinum-195m (Pt-195m)	Studies on biodistribution and metabolism of cisplatin, a chemotherapeutic drug
Phosphorus-32 (P-32)	Polycythemia rubra vera (blood cell disease) and leukemia treatment, bone cancer diagnosis/treatment; colon, pancreatic, and liver cancer treatment; radiolabeling nucleic acids for in vitro research, diagnosis of superficial tumors, treatment of blocked arteries (i.e., arteriosclerosis and restenosis), and intracavity therapy
Phosphorus-33 (P-33)	Leukemia treatment, bone disease diagnosis/treatment, radiolabeling, and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Radium-223 (Ra-223)	See Actinium-227 (Ac-227)
Rhenium-186 (Re-186)	Bone cancer pain relief, rheumatoid arthritis treatment, and diagnosis and treatment of lymphoma and bone, breast, colon, and liver cancers using radioimmunotherapy
Rhenium-188 (Re-188)	Cancer diagnosis and treatment using radioimmunotherapy, bone cancer pain relief, treatment of rheumatoid arthritis, and treatment of prostate cancer
Rhodium-105 (Rh-105)	Cancer radioimmunotherapy
Samarium-145 (Sm-145)	Ocular cancer treatment
Samarium-153 (Sm-153)	Cancer radioimmunotherapy and bone cancer pain relief
Scandium-47 (Sc-47)	Cancer radioimmunotherapy and bone cancer pain relief
Selenium-75 (Se-75)	Radiotracer used in brain studies, imaging of adrenal cortex by gamma-scintigraphy, lateral locations of steroid secreting tumors, pancreatic scanning, detection of hyperactive parathyroid glands, measure rate of bile acid loss from the endogenous pool
Strontium-85 (Sr-85)	Bone cancer detection and brain scans
Strontium-89 (Sr-89)	Bone cancer pain relief, multiple myeloma treatment, and osteoblastic therapy
Technetium-99m (Tc-99m)	See Molybdenum-99 (Mo-99)
Thorium-228 (Th-228)	Parent of Bismuth-212 (Bi-212) which is an alpha emitter used in cancer radioimmunotherapy
Thorium-229 (Th-229)	Parent of Actinium-225 (Ac-225) and grandparent of Bismuth-213 (Bi-213) which are alpha emitters used in cancer radioimmunotherapy
Thulium-170 (Tm-170)	Gamma source for blood irradiators, energy source for implanted medical devices
Tin-117m (Sn-117m)	Cancer immunotherapy and bone cancer pain relief
Tungsten-188 (W-188)	Parent for Rhenium-188 (Re-188) which is used for cancer diagnostics/treatment, bone cancer pain relief, rheumatoid arthritis treatment, and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Xenon-127 (Xe-127)	Neuroimaging of brain disorders, high resolution SPECT studies, pulmonary function tests, and cerebral blood flow studies
Ytterbium-175 (Yb-175)	Cancer radioimmunotherapy
Yttrium-90 (Y-90)	Microseeds obtained from irradiating Yttrium-89 (Y-89) for liver cancer treatment
Yttrium-91 (Y-91)	A gamma-emitting label for Yttrium-90 (Y-90) which is used for cancer radioimmunotherapy (i.e., lymphoma, breast, colon, kidney, lung, ovarian, prostate, pancreatic, and inoperable liver cancers)

By "randomized" or grammatical equivalents as herein applied to nucleic acids and proteins is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. These random peptides (or nucleic acids, discussed herein) can incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, a library is "fully randomized," with no sequence preferences or constants at any position. In another embodiment, the library is a "biased random" library. That is, some positions within the sequence either are held constant, or are selected from a limited number of possibilities. For example, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

A "recombinant" DNA or RNA molecule is a DNA or RNA molecule that has been subjected to molecular manipulation *in vitro*.

Non-limiting examples of small molecules include compounds that bind or interact with 109P1D4, ligands including hormones, neuropeptides, chemokines, odorants, phospholipids, and functional equivalents thereof that bind and preferably inhibit 109P1D4 protein function. Such non-limiting small molecules preferably have a molecular weight of less than about 10 kDa, more preferably below about 9, about 8, about 7, about 6, about 5 or about 4 kDa. In certain embodiments, small molecules physically associate with, or bind, 109P1D4 protein; are not found in naturally occurring metabolic pathways; and/or are more soluble in aqueous than non-aqueous solutions

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured nucleic acid sequences to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature that can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, are identified by, but not limited to, those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42 °C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42 °C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55 °C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55 °C. "Moderately stringent conditions" are described by, but not limited to, those in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include

the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

An HLA "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Overall phenotypic frequencies of HLA-supertypes in different ethnic populations are set forth in Table IV (F). The non-limiting constituents of various supertypes are as follows:

A2: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*6802, A*6901, A*0207

A3: A3, A11, A31, A*3301, A*6801, A*0301, A*1101, A*3101

B7: B7, B*3501-03, B*51, B*5301, B*5401, B*5501, B*5502, B*5601, B*6701, B*7801, B*0702, B*5101, B*5602

B44: B*3701, B*4402, B*4403, B*60 (B*4001), B61 (B*4006)

A1: A*0102, A*2604, A*3601, A*4301, A*8001

A24: A*24, A*30, A*2403, A*2404, A*3002, A*3003

B27: B*1401-02, B*1503, B*1509, B*1510, B*1518, B*3801-02, B*3901, B*3902, B*3903-04, B*4801-02, B*7301, B*2701-08

B58: B*1516, B*1517, B*5701, B*5702, B58

B62: B*4601, B52, B*1501 (B62), B*1502 (B75), B*1513 (B77)

Calculated population coverage afforded by different HLA-supertype combinations are set forth in Table IV (G).

As used herein "to treat" or "therapeutic" and grammatically related terms, refer to any improvement of any consequence of disease, such as prolonged survival, less morbidity, and/or a lessening of side effects which are the byproducts of an alternative therapeutic modality; full eradication of disease is not required.

A "transgenic animal" (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A "transgene" is a DNA that is integrated into the genome of a cell from which a transgenic animal develops.

As used herein, an HLA or cellular immune response "vaccine" is a composition that contains or encodes one or more peptides of the invention. There are numerous embodiments of such vaccines, such as a cocktail of one or more individual peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such individual peptides or polypeptides, e.g., a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150 or more, e.g., at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I peptides of the invention can be admixed with, or linked to, HLA class II peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. HLA vaccines can also comprise peptide-pulsed antigen presenting cells, e.g., dendritic cells.

The term "variant" refers to a molecule that exhibits a variation from a described type or norm, such as a protein that has one or more different amino acid residues in the corresponding position(s) of a specifically described protein (e.g. the 109P1D4 protein shown in Figure 2 or Figure 3. An analog is an example of a variant protein. Splice isoforms and single nucleotide polymorphisms (SNPs) are further examples of variants.

The "109P1D4-related proteins" of the invention include those specifically identified herein, as well as allelic variants, conservative substitution variants, analogs and homologs that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art. Fusion proteins that combine parts of different 109P1D4 proteins or fragments thereof, as well as fusion proteins of a 109P1D4 protein and a heterologous polypeptide are also included. Such 109P1D4 proteins are collectively referred to as the 109P1D4-related proteins, the proteins of the invention, or 109P1D4. The term "109P1D4-related protein" refers to a polypeptide fragment or a 109P1D4 protein sequence of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 amino acids; or, at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, or 576 or more amino acids.

II.) 109P1D4 Polynucleotides

One aspect of the invention provides polynucleotides corresponding or complementary to all or part of a 109P1D4 gene, mRNA, and/or coding sequence, preferably in isolated form, including polynucleotides encoding a 109P1D4-related protein and fragments thereof, DNA, RNA, DNA/RNA hybrid, and related molecules, polynucleotides or oligonucleotides complementary to a 109P1D4 gene or mRNA sequence or a part thereof, and polynucleotides or oligonucleotides that hybridize to a 109P1D4 gene, mRNA, or to a 109P1D4 encoding polynucleotide (collectively, "109P1D4 polynucleotides"). In all instances when referred to in this section, T can also be U in Figure 2.

Embodiments of a 109P1D4 polynucleotide include: a 109P1D4 polynucleotide having the sequence shown in Figure 2, the nucleotide sequence of 109P1D4 as shown in Figure 2 wherein T is U; at least 10 contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2; or, at least 10 contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2 where T is U. For example, embodiments of 109P1D4 nucleotides comprise, without limitation:

- (I) a polynucleotide comprising, consisting essentially of, or consisting of a sequence as shown in Figure 2, wherein T can also be U;
- (II) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2A, from nucleotide residue number 846 through nucleotide residue number 3911, including the stop codon, wherein T can also be U;
- (III) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2B, from nucleotide residue number 503 through nucleotide residue number 3667, including the stop codon, wherein T can also be U;
- (IV) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2C, from nucleotide residue number 846 through nucleotide residue number 4889, including the a stop codon, wherein T can also be U;
- (V) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2D, from nucleotide residue number 846 through nucleotide residue number 4859, including the stop codon, wherein T can also be U;
- (VI) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2E, from nucleotide residue number 846 through nucleotide residue number 4778, including the stop codon, wherein T can also be U;

- (VII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2F, from nucleotide residue number 614 through nucleotide residue number 3727, including the stop codon, wherein T can also be U;
- (VIII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2G, from nucleotide residue number 735 through nucleotide residue number 3881, including the stop codon, wherein T can also be U;
- (IX) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2H, from nucleotide residue number 735 through nucleotide residue number 4757, including the stop codon, wherein T can also be U;
- (X) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2I, from nucleotide residue number 514 through nucleotide residue number 3627, including the stop codon, wherein T can also be U;
- (XI) a polynucleotide that encodes a 109P1D4-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homologous to an entire amino acid sequence shown in Figure 2A-I;
- (XII) a polynucleotide that encodes a 109P1D4-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identical to an entire amino acid sequence shown in Figure 2A-I;
- (XIII) a polynucleotide that encodes at least one peptide set forth in Tables VIII-XXI and XXII-XLIX;
- (XIV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figures 3A in any whole number increment up to 1021 that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;
- (XV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A in any whole number increment up to 1021 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;
- (XVI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A in any whole number increment up to 1021 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;
- (XVII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A in any whole number increment up to 1021 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;
- (XVIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,

18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A in any whole number increment up to 1021 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XIX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3B, 3C, and/or 3D in any whole number increment up to 1054, 1347, and/or 1337 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3B, 3C, and/or 3D in any whole number increment up to 1054, 1347, and/or 1337 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3B, 3C, and/or 3D in any whole number increment up to 1054, 1347, and/or 1337 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3B, 3C, and/or 3D in any whole number increment up to 1054, 1347, and/or 1337 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3B, 3C, and/or 3D in any whole number increment up to 1054, 1347, and/or 1337 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXIV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3E, 3F, 3G, 3H and/or 3I in any whole number increment up to 1310, 1037, 1048, 1340, and/or 1037 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3E, 3F, 3G, 3H and/or 3I in any whole number increment up to 1310, 1037, 1048, 1340, and/or 1037 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXVI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3E, 3F, 3G, 3H and/or 3I in any whole number increment up to 1310, 1037, 1048, 1340, and/or 1037 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXVII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3E, 3F, 3G, 3H and/or 3I in any whole number increment up to 1310, 1037, 1048, 1340, and/or 1037 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXVIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3E, 3F, 3G, 3H, and/or 3I in any whole number increment up to 1310, 1037, 1048, 1340, and/or 1037 respectively that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXIX) a polynucleotide that is fully complementary to a polynucleotide of any one of (I)-(XXVIII);

(XXX) a polynucleotide that is fully complementary to a polynucleotide of any one of (I)-(XXIX);

(XXXI) a peptide that is encoded by any of (I) to (XXX); and;

(XXXII) a composition comprising a polynucleotide of any of (I)-(XXX) or peptide of (XXXI) together with a pharmaceutical excipient and/or in a human unit dose form;

(XXXIII) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to modulate a cell expressing 109P1D4;

(XXXIV) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 109P1D4;

(XXXV) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 109P1D4, said cell from a cancer of a tissue listed in Table I;

(XXXVI) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to diagnose, prophylax, prognose, or treat a cancer;

(XXXVII) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to diagnose, prophylax, prognose, or treat a cancer of a tissue listed in Table I; and;

(XXXVIII) a method of using a polynucleotide of any (I)-(XXX) or peptide of (XXXI) or a composition of (XXXII) in a method to identify or characterize a modulator of a cell expressing 109P1D4.

As used herein, a range is understood to disclose specifically all whole unit positions thereof.

Typical embodiments of the invention disclosed herein include 109P1D4 polynucleotides that encode specific portions of 109P1D4 mRNA sequences (and those which are complementary to such sequences) such as those that encode the proteins and/or fragments thereof, for example: .

(a) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875, 900, 925, 950, 975, 1000, 1010, 1020, and 1021 or more contiguous amino acids of 109P1D4 variant 1; the maximal lengths relevant for other variants are: variant 2, 1054 amino acids; variant 3, 1347 amino acids, variant 4, 1337 amino acids, variant 5, 1310 amino acids, variant 6; 1047 amino acids, variant 7; 1048 amino acids, variant 8; 1340 amino acids and variant 9; 1037 amino acids.

For example, representative embodiments of the invention disclosed herein include: polynucleotides and their encoded peptides themselves encoding about amino acid 1 to about amino acid 10 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 10 to about amino acid 20 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 20 to about amino acid 30 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 30 to about amino acid 40 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 40 to about amino acid 50 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 50 to about amino acid 60 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 60 to about amino acid 70 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 70 to about amino acid 80 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 80 to about amino acid 90 of the 109P1D4 protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 90 to about amino acid 100 of the 109P1D4 protein shown in Figure 2 or Figure 3, in increments of about 10 amino acids, ending at the carboxyl terminal amino acid set forth in Figure 2 or Figure 3. Accordingly, polynucleotides encoding portions of the amino acid sequence (of about 10 amino acids), of amino acids, 100 through the carboxyl terminal amino acid of the 109P1D4 protein are embodiments of the invention. Wherein it is understood that each particular amino acid position discloses that position plus or minus five amino acid residues.

Polynucleotides encoding relatively long portions of a 109P1D4 protein are also within the scope of the invention. For example, polynucleotides encoding from about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 30, or 40 or 50 etc.) of the 109P1D4 protein "or variant" shown in Figure 2 or Figure 3 can be generated by a variety of techniques well known in the art. These polynucleotide fragments can include any portion of the 109P1D4 sequence as shown in Figure 2.

Additional illustrative embodiments of the invention disclosed herein include 109P1D4 polynucleotide fragments encoding one or more of the biological motifs contained within a 109P1D4 protein "or variant" sequence, including one or more of the motif-bearing subsequences of a 109P1D4 protein "or variant" set forth in Tables VIII-XXI and XXII-XLIX. In another embodiment, typical polynucleotide fragments of the invention encode one or more of the regions of 109P1D4 protein or variant that exhibit homology to a known molecule. In another embodiment of the invention, typical polynucleotide fragments can encode one or more of the 109P1D4 protein or variant N-glycosylation sites, cAMP and cGMP-dependent protein kinase phosphorylation sites, casein kinase II phosphorylation sites or N-myristoylation site and amidation sites.

Note that to determine the starting position of any peptide set forth in Tables VIII-XXI and Tables XXII to XLIX (collectively HLA Peptide Tables) respective to its parental protein, e.g., variant 1, variant 2, etc., reference is made to three factors: the particular variant, the length of the peptide in an HLA Peptide Table, and the Search Peptides listed in Table VII. Generally, a unique Search Peptide is used to obtain HLA peptides for a particular variant. The position of each Search Peptide relative to its respective parent molecule is listed in Table VII. Accordingly, if a Search Peptide begins at position "X", one must add the value "X minus 1" to each position in Tables VIII-XXI and Tables XXII-IL to obtain the actual position of the HLA peptides in their parental molecule. For example if a particular Search Peptide begins at position 150 of its parental molecule, one must add 150 - 1, i.e., 149 to each HLA peptide amino acid position to calculate the position of that amino acid

in the parent molecule.

II.A.) Uses of 109P1D4 Polynucleotides

II.A.1.) Monitoring of Genetic Abnormalities

The polynucleotides of the preceding paragraphs have a number of different specific uses. The human 109P1D4 gene maps to the chromosomal location set forth in the Example entitled "Chromosomal Mapping of 109P1D4." For example, because the 109P1D4 gene maps to this chromosome, polynucleotides that encode different regions of the 109P1D4 proteins are used to characterize cytogenetic abnormalities of this chromosomal locale, such as abnormalities that are identified as being associated with various cancers. In certain genes, a variety of chromosomal abnormalities including rearrangements have been identified as frequent cytogenetic abnormalities in a number of different cancers (see e.g. Krajcinovic *et al.*, *Mutat. Res.* 382(3-4): 81-83 (1998); Johansson *et al.*, *Blood* 86(10): 3905-3914 (1995) and Finger *et al.*, *P.N.A.S.* 85(23): 9158-9162 (1988)). Thus, polynucleotides encoding specific regions of the 109P1D4 proteins provide new tools that can be used to delineate, with greater precision than previously possible, cytogenetic abnormalities in the chromosomal region that encodes 109P1D4 that may contribute to the malignant phenotype. In this context, these polynucleotides satisfy a need in the art for expanding the sensitivity of chromosomal screening in order to identify more subtle and less common chromosomal abnormalities (see e.g. Evans *et al.*, *Am. J. Obstet. Gynecol* 171(4): 1055-1057 (1994)).

Furthermore, as 109P1D4 was shown to be highly expressed in prostate and other cancers, 109P1D4 polynucleotides are used in methods assessing the status of 109P1D4 gene products in normal versus cancerous tissues. Typically, polynucleotides that encode specific regions of the 109P1D4 proteins are used to assess the presence of perturbations (such as deletions, insertions, point mutations, or alterations resulting in a loss of an antigen etc.) in specific regions of the 109P1D4 gene, such as regions containing one or more motifs. Exemplary assays include both RT-PCR assays as well as single-strand conformation polymorphism (SSCP) analysis (see, e.g., Marrogi *et al.*, *J. Cutan. Pathol.* 26(8): 369-378 (1999), both of which utilize polynucleotides encoding specific regions of a protein to examine these regions within the protein.

II.A.2.) Antisense Embodiments

Other specifically contemplated nucleic acid related embodiments of the invention disclosed herein are genomic DNA, cDNAs, ribozymes, and antisense molecules, as well as nucleic acid molecules based on an alternative backbone, or including alternative bases, whether derived from natural sources or synthesized, and include molecules capable of inhibiting the RNA or protein expression of 109P1D4. For example, antisense molecules can be RNAs or other molecules, including peptide nucleic acids (PNAs) or non-nucleic acid molecules such as phosphorothioate derivatives that specifically bind DNA or RNA in a base pair-dependent manner. A skilled artisan can readily obtain these classes of nucleic acid molecules using the 109P1D4 polynucleotides and polynucleotide sequences disclosed herein.

Antisense technology entails the administration of exogenous oligonucleotides that bind to a target polynucleotide located within the cells. The term "antisense" refers to the fact that such oligonucleotides are complementary to their intracellular targets, e.g., 109P1D4. See for example, Jack Cohen, *Oligodeoxynucleotides, Antisense Inhibitors of Gene Expression*, CRC Press, 1989; and Synthesis 1:1-5 (1988). The 109P1D4 antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, see, Jack Cohen, *supra*), which exhibit enhanced cancer cell growth inhibitory action. S-oligos (nucleoside phosphorothioates) are isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-oligos of the present invention can be prepared by treatment of the corresponding O-oligos with 3H-1,2-benzodithiol-3-one-1,1-dioxide, which is a sulfur transfer reagent. See, e.g., Iyer, R. P. *et al.*, *J. Org. Chem.* 55:4693-4698

(1990); and Iyer, R. P. *et al.*, J. Am. Chem. Soc. 112:1253-1254 (1990). Additional 109P1D4 antisense oligonucleotides of the present invention include morpholino antisense oligonucleotides known in the art (see, e.g., Partridge *et al.*, 1996, Antisense & Nucleic Acid Drug Development 6: 169-175).

The 109P1D4 antisense oligonucleotides of the present invention typically can be RNA or DNA that is complementary to and stably hybridizes with the first 100 5' codons or last 100 3' codons of a 109P1D4 genomic sequence or the corresponding mRNA. Absolute complementarity is not required, although high degrees of complementarity are preferred. Use of an oligonucleotide complementary to this region allows for the selective hybridization to 109P1D4 mRNA and not to mRNA specifying other regulatory subunits of protein kinase. In one embodiment, 109P1D4 antisense oligonucleotides of the present invention are 15 to 30-mer fragments of the antisense DNA molecule that have a sequence that hybridizes to 109P1D4 mRNA. Optionally, 109P1D4 antisense oligonucleotide is a 30-mer oligonucleotide that is complementary to a region in the first 10 5' codons or last 10 3' codons of 109P1D4. Alternatively, the antisense molecules are modified to employ ribozymes in the inhibition of 109P1D4 expression, see, e.g., L. A. Couture & D. T. Stinchcomb; *Trends Genet* 12: 510-515 (1996).

II.A.3.) Primers and Primer Pairs

Further specific embodiments of these nucleotides of the invention include primers and primer pairs, which allow the specific amplification of polynucleotides of the invention or of any specific parts thereof, and probes that selectively or specifically hybridize to nucleic acid molecules of the invention or to any part thereof. Probes can be labeled with a detectable marker, such as, for example, a radioisotope, fluorescent compound, bioluminescent compound, a chemiluminescent compound, metal chelator or enzyme. Such probes and primers are used to detect the presence of a 109P1D4 polynucleotide in a sample and as a means for detecting a cell expressing a 109P1D4 protein.

Examples of such probes include polypeptides comprising all or part of the human 109P1D4 cDNA sequence shown in Figure 2. Examples of primer pairs capable of specifically amplifying 109P1D4 mRNAs are also described in the Examples. As will be understood by the skilled artisan, a great many different primers and probes can be prepared based on the sequences provided herein and used effectively to amplify and/or detect a 109P1D4 mRNA.

The 109P1D4 polynucleotides of the invention are useful for a variety of purposes, including but not limited to their use as probes and primers for the amplification and/or detection of the 109P1D4 gene(s), mRNA(s), or fragments thereof; as reagents for the diagnosis and/or prognosis of prostate cancer and other cancers; as coding sequences capable of directing the expression of 109P1D4 polypeptides; as tools for modulating or inhibiting the expression of the 109P1D4 gene(s) and/or translation of the 109P1D4 transcript(s); and as therapeutic agents.

The present invention includes the use of any probe as described herein to identify and isolate a 109P1D4 or 109P1D4 related nucleic acid sequence from a naturally occurring source, such as humans or other mammals, as well as the isolated nucleic acid sequence *per se*, which would comprise all or most of the sequences found in the probe used.

II.A.4.) Isolation of 109P1D4-Encoding Nucleic Acid Molecules

The 109P1D4 cDNA sequences described herein enable the isolation of other polynucleotides encoding 109P1D4 gene product(s), as well as the isolation of polynucleotides encoding 109P1D4 gene product homologs, alternatively spliced isoforms, allelic variants, and mutant forms of a 109P1D4 gene product as well as polynucleotides that encode analogs of 109P1D4-related proteins. Various molecular cloning methods that can be employed to isolate full length cDNAs encoding a 109P1D4 gene are well known (see, for example, Sambrook, J. *et al.*, Molecular Cloning: A Laboratory Manual, 2d edition, Cold Spring Harbor Press, New York, 1989; Current Protocols in Molecular Biology. Ausubel *et al.*, Eds., Wiley and Sons, 1995). For example, lambda phage cloning methodologies can be conveniently employed, using commercially available cloning systems (e.g., Lambda ZAP Express, Stratagene). Phage clones containing 109P1D4 gene cDNAs can be identified by probing with a labeled 109P1D4

cDNA or a fragment thereof. For example, in one embodiment, a 109P1D4 cDNA (e.g., Figure 2) or a portion thereof can be synthesized and used as a probe to retrieve overlapping and full-length cDNAs corresponding to a 109P1D4 gene. A 109P1D4 gene itself can be isolated by screening genomic DNA libraries, bacterial artificial chromosome libraries (BACs), yeast artificial chromosome libraries (YACs), and the like, with 109P1D4 DNA probes or primers.

II.A.5.) Recombinant Nucleic Acid Molecules and Host-Vector Systems

The invention also provides recombinant DNA or RNA molecules containing a 109P1D4 polynucleotide, a fragment, analog or homologue thereof, including but not limited to phages, plasmids, phagemids, cosmids, YACs, BACs, as well as various viral and non-viral vectors well known in the art, and cells transformed or transfected with such recombinant DNA or RNA molecules. Methods for generating such molecules are well known (see, for example, Sambrook *et al.*, 1989, *supra*).

The invention further provides a host-vector system comprising a recombinant DNA molecule containing a 109P1D4 polynucleotide, fragment, analog or homologue thereof within a suitable prokaryotic or eukaryotic host cell. Examples of suitable eukaryotic host cells include a yeast cell, a plant cell, or an animal cell, such as a mammalian cell or an insect cell (e.g., a baculovirus-infectible cell such as an Sf9 or HighFive cell). Examples of suitable mammalian cells include various prostate cancer cell lines such as DU145 and TsuPr1, other transfectable or transducible prostate cancer cell lines, primary cells (PrEC), as well as a number of mammalian cells routinely used for the expression of recombinant proteins (e.g., COS, CHO, 293, 293T cells). More particularly, a polynucleotide comprising the coding sequence of 109P1D4 or a fragment, analog or homolog thereof can be used to generate 109P1D4 proteins or fragments thereof using any number of host-vector systems routinely used and widely known in the art.

A wide range of host-vector systems suitable for the expression of 109P1D4 proteins or fragments thereof are available, see for example, Sambrook *et al.*, 1989, *supra*; Current Protocols in Molecular Biology, 1995, *supra*). Preferred vectors for mammalian expression include but are not limited to pcDNA 3.1 myc-His-tag (Invitrogen) and the retroviral vector pSR α kneo (Muller *et al.*, 1991, MCB 11:1785). Using these expression vectors, 109P1D4 can be expressed in several prostate cancer and non-prostate cell lines, including for example 293, 293T, rat-1, NIH 3T3 and TsuPr1. The host-vector systems of the invention are useful for the production of a 109P1D4 protein or fragment thereof. Such host-vector systems can be employed to study the functional properties of 109P1D4 and 109P1D4 mutations or analogs.

Recombinant human 109P1D4 protein or an analog or homolog or fragment thereof can be produced by mammalian cells transfected with a construct encoding a 109P1D4-related nucleotide. For example, 293T cells can be transfected with an expression plasmid encoding 109P1D4 or fragment, analog or homolog thereof, a 109P1D4-related protein is expressed in the 293T cells, and the recombinant 109P1D4 protein is isolated using standard purification methods (e.g., affinity purification using anti-109P1D4 antibodies). In another embodiment, a 109P1D4 coding sequence is subcloned into the retroviral vector pSR α MSVikneo and used to infect various mammalian cell lines, such as NIH 3T3, TsuPr1, 293 and rat-1 in order to establish 109P1D4 expressing cell lines. Various other expression systems well known in the art can also be employed. Expression constructs encoding a leader peptide joined in frame to a 109P1D4 coding sequence can be used for the generation of a secreted form of recombinant 109P1D4 protein.

As discussed herein, redundancy in the genetic code permits variation in 109P1D4 gene sequences. In particular, it is known in the art that specific host species often have specific codon preferences, and thus one can adapt the disclosed sequence as preferred for a desired host. For example, preferred analog codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific species are calculated, for example, by utilizing codon usage tables available on the INTERNET such as at URL dna.affrc.go.jp/~nakamura/codon.html.

Additional sequence modifications are known to enhance protein expression in a cellular host. These include

elimination of sequences encoding spurious polyadenylation signals, exon/intron splice site signals, transposon-like repeats, and/or other such well-characterized sequences that are deleterious to gene expression. The GC content of the sequence is adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. Where possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures. Other useful modifications include the addition of a translational initiation consensus sequence at the start of the open reading frame, as described in Kozak, *Mol. Cell Biol.*, 9:5073-5080 (1989). Skilled artisans understand that the general rule that eukaryotic ribosomes initiate translation exclusively at the 5' proximal AUG codon is abrogated only under rare conditions (see, e.g., Kozak PNAS 92(7): 2662-2666, (1995) and Kozak NAR 15(20): 8125-8148 (1987)).

III.) 109P1D4-related Proteins

Another aspect of the present invention provides 109P1D4-related proteins. Specific embodiments of 109P1D4 proteins comprise a polypeptide having all or part of the amino acid sequence of human 109P1D4 as shown in Figure 2 or Figure 3. Alternatively, embodiments of 109P1D4 proteins comprise variant, homolog or analog polypeptides that have alterations in the amino acid sequence of 109P1D4 shown in Figure 2 or Figure 3.

Embodiments of a 109P1D4 polypeptide include: a 109P1D4 polypeptide having a sequence shown in Figure 2, a peptide sequence of a 109P1D4 as shown in Figure 2 wherein T is U; at least 10 contiguous nucleotides of a polypeptide having the sequence as shown in Figure 2; or, at least 10 contiguous peptides of a polypeptide having the sequence as shown in Figure 2 where T is U. For example, embodiments of 109P1D4 peptides comprise, without limitation:

- (I) a protein comprising, consisting essentially of, or consisting of an amino acid sequence as shown in Figure 2A-I or Figure 3A-I;
- (II) a 109P1D4-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homologous to an entire amino acid sequence shown in Figure 2A-I or 3A-I;
- (III) a 109P1D4-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identical to an entire amino acid sequence shown in Figure 2A-I or 3A-I;
- (IV) a protein that comprises at least one peptide set forth in Tables VIII to XLIX, optionally with a *proviso* that it is not an entire protein of Figure 2;
- (V) a protein that comprises at least one peptide set forth in Tables VIII-XXI, collectively, which peptide is also set forth in Tables XXII to XLIX, collectively, optionally with a *proviso* that it is not an entire protein of Figure 2;
- (VI) a protein that comprises at least two peptides selected from the peptides set forth in Tables VIII-XLIX, optionally with a *proviso* that it is not an entire protein of Figure 2;
- (VII) a protein that comprises at least two peptides selected from the peptides set forth in Tables VIII to XLIX collectively, with a *proviso* that the protein is not a contiguous sequence from an amino acid sequence of Figure 2;
- (VIII) a protein that comprises at least one peptide selected from the peptides set forth in Tables VIII-XXI; and at least one peptide selected from the peptides set forth in Tables XXII to XLIX, with a *proviso* that the protein is not a contiguous sequence from an amino acid sequence of Figure 2;
- (IX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A, 3B, 3C, 3D and/or 3E in any whole number increment up to 1021, 1054, 1347, 1337, and/or 1310 respectively that includes at least 1, 2, 3, 4, 5,

6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(X) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A, 3B, 3C, 3D, and/or 3E, in any whole number increment up to 1021, 1054, 1347, 1337, and/or 1310 respectively respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A, 3B, 3C, 3D, and/or 3E, in any whole number increment up to 1021, 1054, 1347, 1337, and/or 1310 respectively respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A, 3B, 3C, 3D, and/or 3E, in any whole number increment up to 1021, 1054, 1347, 1337, and/or 1310 respectively respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3A, 3B, 3C, 3D, and 3E in any whole number increment up to 1021, 1054, 1347, 1337, and/or 1310 respectively respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XIV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3F, 3G, 3H, and/or 3I, in any whole number increment up to 1037, 1048, 1340, and/or 1037 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3F, 3G, 3H, and/or 3I in any whole number increment up to 1037, 1048, 1340, and/or 1037 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XVI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3F, 3G, 3H, and/or 3I in any whole number increment up to 1037, 1048, 1340, and/or 1037 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XVII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24,

25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3F, 3G, 3H, and/or 3I in any whole number increment up to 1037, 1048, 1340, and/or 1037 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XVIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3F, 3G, 3H, and/or 3I in any whole number increment up to 1037, 1048, 1340, and/or 1037 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XIX) a peptide that occurs at least twice in Tables VIII-XXI and XXII to XLIX, collectively;

(XX) a peptide that occurs at least three times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXI) a peptide that occurs at least four times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXII) a peptide that occurs at least five times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXIII) a peptide that occurs at least once in Tables VIII-XXI, and at least once in tables XXII to XLIX;

(XXIV) a peptide that occurs at least once in Tables VIII-XXI, and at least twice in tables XXII to XLIX;

(XXV) a peptide that occurs at least twice in Tables VIII-XXI, and at least once in tables XXII to XLIX;

(XXVI) a peptide that occurs at least twice in Tables VIII-XXI, and at least twice in tables XXII to XLIX;

(XXVII) a peptide which comprises one two, three, four, or five of the following characteristics, or an oligonucleotide encoding such peptide:

i) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Hydrophilicity profile of Figure 5;

ii) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or less than 0.5, 0.4, 0.3, 0.2, 0.1, or having a value equal to 0.0, in the Hydrophobicity profile of Figure 6;

iii) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Percent Accessible Residues profile of Figure 7;

iv) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Average Flexibility profile of Figure 8; or,

v) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Beta-turn profile of Figure 9;;

(XXVIII) a composition comprising a peptide of (I)-(XXVII) or an antibody or binding region thereof together with a pharmaceutical excipient and/or in a human unit dose form.

(XXIX) a method of using a peptide of (I)-(XXVII), or an antibody or binding region thereof or a composition of (XXVIII) in a method to modulate a cell expressing 109P1D4,;

(XXX) a method of using a peptide of (I)-(XXVII) or an antibody or binding region thereof or a composition of (XXVIII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 109P1D4;

(XXXI) a method of using a peptide of (I)-(XXVII) or an antibody or binding region thereof or a composition (XXVIII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 109P1D4, said cell from a cancer of a tissue listed in Table I;

(XXXII) a method of using a peptide of (I)-(XXVII) or an antibody or binding region thereof or a composition of (XXVIII) in a method to diagnose, prophylax, prognose, or treat a cancer;

(XXXIII) a method of using a peptide of (I)-(XXVII) or an antibody or binding region thereof or a composition of (XXVIII) in a method to diagnose, prophylax, prognose, or treat a cancer of a tissue listed in Table I; and;

(XXXIV) a method of using a a peptide of (I)-(XXVII) or an antibody or binding region thereof or a composition (XXVIII) in a method to identify or characterize a modulator of a cell expressing 109P1D4

As used herein, a range is understood to specifically disclose all whole unit positions thereof.

Typical embodiments of the invention disclosed herein include 109P1D4 polynucleotides that encode specific portions of 109P1D4 mRNA sequences (and those which are complementary to such sequences) such as those that encode the proteins and/or fragments thereof, for example:

(a) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875, 900, 925, 950, 975, 1000, 1010, 1020, and 1021 or more contiguous amino acids of 109P1D4 variant 1; the maximal lengths relevant for other variants are: variant 2, 1054 amino acids; variant 3, 1347 amino acids, variant 4, 1337 amino acids, variant 5, 1310 amino acids, variant 6; 1037 amino acids, variant 7; 1048 amino acids, variant 8; 1340 amino acids, and variant 9; 1037 amino acids. .

In general, naturally occurring allelic variants of human 109P1D4 share a high degree of structural identity and homology (e.g., 90% or more homology). Typically, allelic variants of a 109P1D4 protein contain conservative amino acid substitutions within the 109P1D4 sequences described herein or contain a substitution of an amino acid from a corresponding position in a homologue of 109P1D4. One class of 109P1D4 allelic variants are proteins that share a high degree of homology with at least a small region of a particular 109P1D4 amino acid sequence, but further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. In comparisons of protein sequences, the terms, similarity, identity, and homology each have a distinct meaning as appreciated in the field of genetics. Moreover, orthology and paralogy can be important concepts describing the relationship of members of a given protein family in one organism to the members of the same family in other organisms.

Amino acid abbreviations are provided in Table II. Conservative amino acid substitutions can frequently be made in a protein without altering either the conformation or the function of the protein. Proteins of the invention can comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 conservative substitutions. Such changes include substituting any of isoleucine (I), valine (V), and leucine (L) for any other of these hydrophobic amino acids; aspartic acid (D) for glutamic acid (E) and vice versa; glutamine (Q) for asparagine (N) and vice versa; and serine (S) for threonine (T) and vice versa. Other substitutions

can also be considered conservative, depending on the environment of the particular amino acid and its role in the three-dimensional structure of the protein. For example, glycine (G) and alanine (A) can frequently be interchangeable, as can alanine (A) and valine (V). Methionine (M), which is relatively hydrophobic, can frequently be interchanged with leucine and isoleucine, and sometimes with valine. Lysine (K) and arginine (R) are frequently interchangeable in locations in which the significant feature of the amino acid residue is its charge and the differing pK's of these two amino acid residues are not significant. Still other changes can be considered "conservative" in particular environments (see, e.g. Table III herein; pages 13-15 "Biochemistry" 2nd ED. Lubert Stryer ed (Stanford University); Henikoff *et al.*, PNAS 1992 Vol 89 10915-10919; Lei *et al.*, J Biol Chem 1995 May 19; 270(20):11882-6).

Embodiments of the invention disclosed herein include a wide variety of art-accepted variants or analogs of 109P1D4 proteins such as polypeptides having amino acid insertions, deletions and substitutions. 109P1D4 variants can be made using methods known in the art such as site-directed mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter *et al.*, *Nucl. Acids Res.*, 13:4331 (1986); Zoller *et al.*, *Nucl. Acids Res.*, 10:6487 (1987)), cassette mutagenesis (Wells *et al.*, *Gene*, 34:315 (1985)), restriction selection mutagenesis (Wells *et al.*, *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)) or other known techniques can be performed on the cloned DNA to produce the 109P1D4 variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence that is involved in a specific biological activity such as a protein-protein interaction. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions (Creighton, *The Proteins*, (W.H. Freeman & Co., N.Y.); Choithia, *J. Mol. Biol.*, 150:1 (1976)). If alanine substitution does not yield adequate amounts of variant, an isosteric amino acid can be used.

As defined herein, 109P1D4 variants, analogs or homologs, have the distinguishing attribute of having at least one epitope that is "cross reactive" with a 109P1D4 protein having an amino acid sequence of Figure 3. As used in this sentence, "cross reactive" means that an antibody or T cell that specifically binds to a 109P1D4 variant also specifically binds to a 109P1D4 protein having an amino acid sequence set forth in Figure 3. A polypeptide ceases to be a variant of a protein shown in Figure 3, when it no longer contains any epitope capable of being recognized by an antibody or T cell that specifically binds to the starting 109P1D4 protein. Those skilled in the art understand that antibodies that recognize proteins bind to epitopes of varying size, and a grouping of the order of about four or five amino acids, contiguous or not, is regarded as a typical number of amino acids in a minimal epitope. See, e.g., Nair *et al.*, *J. Immunol* 2000 165(12): 6949-6955; Hebbes *et al.*, *Mol Immunol* (1989) 26(9):865-73; Schwartz *et al.*, *J Immunol* (1985) 135(4):2598-608.

Other classes of 109P1D4-related protein variants share 70%, 75%, 80%, 85% or 90% or more similarity with an amino acid sequence of Figure 3, or a fragment thereof. Another specific class of 109P1D4 protein variants or analogs comprises one or more of the 109P1D4 biological motifs described herein or presently known in the art. Thus, encompassed by the present invention are analogs of 109P1D4 fragments (nucleic or amino acid) that have altered functional (e.g. immunogenic) properties relative to the starting fragment. It is to be appreciated that motifs now or which become part of the art are to be applied to the nucleic or amino acid sequences of Figure 2 or Figure 3.

As discussed herein, embodiments of the claimed invention include polypeptides containing less than the full amino acid sequence of a 109P1D4 protein shown in Figure 2 or Figure 3. For example, representative embodiments of the invention comprise peptides/proteins having any 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous amino acids of a

109P1D4 protein shown in Figure 2 or Figure 3.

Moreover, representative embodiments of the invention disclosed herein include polypeptides consisting of about amino acid 1 to about amino acid 10 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 10 to about amino acid 20 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 20 to about amino acid 30 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 30 to about amino acid 40 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 40 to about amino acid 50 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 50 to about amino acid 60 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 60 to about amino acid 70 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 70 to about amino acid 80 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 80 to about amino acid 90 of a 109P1D4 protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 90 to about amino acid 100 of a 109P1D4 protein shown in Figure 2 or Figure 3, etc. throughout the entirety of a 109P1D4 amino acid sequence. Moreover, polypeptides consisting of about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 130, or 140 or 150 etc.) of a 109P1D4 protein shown in Figure 2 or Figure 3 are embodiments of the invention. It is to be appreciated that the starting and stopping positions in this paragraph refer to the specified position as well as that position plus or minus 5 residues.

109P1D4-related proteins are generated using standard peptide synthesis technology or using chemical cleavage methods well known in the art. Alternatively, recombinant methods can be used to generate nucleic acid molecules that encode a 109P1D4-related protein. In one embodiment, nucleic acid molecules provide a means to generate defined fragments of a 109P1D4 protein (or variants, homologs or analogs thereof).

III.A.) Motif-bearing Protein Embodiments

Additional illustrative embodiments of the invention disclosed herein include 109P1D4 polypeptides comprising the amino acid residues of one or more of the biological motifs contained within a 109P1D4 polypeptide sequence set forth in Figure 2 or Figure 3. Various motifs are known in the art, and a protein can be evaluated for the presence of such motifs by a number of publicly available Internet sites (see, e.g., URL addresses: pfam.wustl.edu/; searchlauncher.bcm.tmc.edu/seq-search/struc-predict.html; psort.ims.u-tokyo.ac.jp/; cbs.dtu.dk/; ebi.ac.uk/interpro/scan.html; expasy.ch/tools/scnpsit1.html; Epimatrix™ and Epimer™, Brown University, brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, bimas.dcrf.nih.gov/).

Motif bearing subsequences of all 109P1D4 variant proteins are set forth and identified in Tables VIII-XXI and XXII-XLIX.

Table V sets forth several frequently occurring motifs based on pfam searches (see URL address pfam.wustl.edu/). The columns of Table V list (1) motif name abbreviation, (2) percent identity found amongst the different member of the motif family, (3) motif name or description and (4) most common function; location information is included if the motif is relevant for location.

Polypeptides comprising one or more of the 109P1D4 motifs discussed above are useful in elucidating the specific characteristics of a malignant phenotype in view of the observation that the 109P1D4 motifs discussed above are associated with growth dysregulation and because 109P1D4 is overexpressed in certain cancers (See, e.g., Table I). Casein kinase II, cAMP and camp-dependent protein kinase, and Protein Kinase C, for example, are enzymes known to be associated with the development of the malignant phenotype (see e.g. Chen *et al.*, *Lab Invest.*, 78(2): 165-174 (1998); Gaiddon *et al.*, *Endocrinology* 136(10): 4331-4338 (1995); Hall *et al.*, *Nucleic Acids Research* 24(6): 1119-1126 (1996); Peterziel *et al.*, *Oncogene* 18(46): 6322-6329 (1999) and O'Brian, *Oncol. Rep.* 5(2): 305-309 (1998)). Moreover, both glycosylation and

myristoylation are protein modifications also associated with cancer and cancer progression (see e.g. Dennis *et al.*, *Biochem. Biophys. Acta* 1473(1):21-34 (1999); Raju *et al.*, *Exp. Cell Res.* 235(1): 145-154 (1997)). Amidation is another protein modification also associated with cancer and cancer progression (see e.g. Treston *et al.*, *J. Natl. Cancer Inst. Monogr.* (13): 169-175 (1992)).

In another embodiment, proteins of the invention comprise one or more of the immunoreactive epitopes identified in accordance with art-accepted methods, such as the peptides set forth in Tables VIII-XXI and XXII-XLIX. CTL epitopes can be determined using specific algorithms to identify peptides within a 109P1D4 protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV; Epimatrix™ and Epimer™, Brown University, URL brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, URL bimas.dort.nih.gov/). Moreover, processes for identifying peptides that have sufficient binding affinity for HLA molecules and which are correlated with being immunogenic epitopes, are well known in the art, and are carried out without undue experimentation. In addition, processes for identifying peptides that are immunogenic epitopes, are well known in the art, and are carried out without undue experimentation either *in vitro* or *in vivo*.

Also known in the art are principles for creating analogs of such epitopes in order to modulate immunogenicity. For example, one begins with an epitope that bears a CTL or HTL motif (see, e.g., the HLA Class I and HLA Class II motifs/supermotifs of Table IV). The epitope is analoged by substituting out an amino acid at one of the specified positions, and replacing it with another amino acid specified for that position. For example, on the basis of residues defined in Table IV, one can substitute out a deleterious residue in favor of any other residue, such as a preferred residue; substitute a less-preferred residue with a preferred residue; or substitute an originally-occurring preferred residue with another preferred residue. Substitutions can occur at primary anchor positions or at other positions in a peptide; see, e.g., Table IV.

A variety of references reflect the art regarding the identification and generation of epitopes in a protein of interest as well as analogs thereof. See, for example, WO 97/33602 to Chesnut *et al.*; Sette, *Immunogenetics* 1999 50(3-4): 201-212; Sette *et al.*, *J. Immunol.* 2001 166(2): 1389-1397; Sidney *et al.*, *Hum. Immunol.* 1997 58(1): 12-20; Kondo *et al.*, *Immunogenetics* 1997 45(4): 249-258; Sidney *et al.*, *J. Immunol.* 1996 157(8): 3480-90; and Falk *et al.*, *Nature* 351: 290-6 (1991); Hunt *et al.*, *Science* 255:1261-3 (1992); Parker *et al.*, *J. Immunol.* 149:3580-7 (1992); Parker *et al.*, *J. Immunol.* 152:163-75 (1994); Kast *et al.*, 1994 152(8): 3904-12; Borrás-Cuesta *et al.*, *Hum. Immunol.* 2000 61(3): 266-278; Alexander *et al.*, *J. Immunol.* 2000 164(3): 164(3): 1625-1633; Alexander *et al.*, PMID: 7895164, UI: 95202582; O'Sullivan *et al.*, *J. Immunol.* 1991 147(8): 2663-2669; Alexander *et al.*, *Immunity* 1994 1(9): 751-761 and Alexander *et al.*, *Immunol. Res.* 1998 18(2): 79-92.

Related embodiments of the invention include polypeptides comprising combinations of the different motifs set forth in Table VI, and/or, one or more of the predicted CTL epitopes of Tables VIII-XXI and XXII-XLIX, and/or, one or more of the predicted HTL epitopes of Tables XLVI-XLIX, and/or, one or more of the T cell binding motifs known in the art. Preferred embodiments contain no insertions, deletions or substitutions either within the motifs or within the intervening sequences of the polypeptides. In addition, embodiments which include a number of either N-terminal and/or C-terminal amino acid residues on either side of these motifs may be desirable (to, for example, include a greater portion of the polypeptide architecture in which the motif is located). Typically, the number of N-terminal and/or C-terminal amino acid residues on either side of a motif is between about 1 to about 100 amino acid residues, preferably 5 to about 50 amino acid residues.

109P1D4-related proteins are embodied in many forms, preferably in isolated form. A purified 109P1D4 protein molecule will be substantially free of other proteins or molecules that impair the binding of 109P1D4 to antibody, T cell or other ligand. The nature and degree of isolation and purification will depend on the intended use. Embodiments of a 109P1D4-related proteins include purified 109P1D4-related proteins and functional, soluble 109P1D4-related proteins. In one embodiment, a functional, soluble 109P1D4 protein or fragment thereof retains the ability to be bound by antibody, T cell or

other ligand.

The invention also provides 109P1D4 proteins comprising biologically active fragments of a 109P1D4 amino acid sequence shown in Figure 2 or Figure 3. Such proteins exhibit properties of the starting 109P1D4 protein, such as the ability to elicit the generation of antibodies that specifically bind an epitope associated with the starting 109P1D4 protein; to be bound by such antibodies; to elicit the activation of HTL or CTL; and/or, to be recognized by HTL or CTL that also specifically bind to the starting protein.

109P1D4-related polypeptides that contain particularly interesting structures can be predicted and/or identified using various analytical techniques well known in the art, including, for example, the methods of Chou-Fasman, Gamier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis, or based on immunogenicity. Fragments that contain such structures are particularly useful in generating subunit-specific anti-109P1D4 antibodies or T cells or in identifying cellular factors that bind to 109P1D4. For example, hydrophilicity profiles can be generated, and immunogenic peptide fragments identified, using the method of Hopp, T.P. and Woods, K.R., 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:3824-3828. Hydrophaticity profiles can be generated, and immunogenic peptide fragments identified, using the method of Kyte, J. and Doolittle, R.F., 1982, *J. Mol. Biol.* 157:105-132. Percent (%) Accessible Residues profiles can be generated, and immunogenic peptide fragments identified, using the method of Janin J., 1979, *Nature* 277:491-492. Average Flexibility profiles can be generated, and immunogenic peptide fragments identified, using the method of Bhaskaran R., Ponnuswamy P.K., 1988, *Int. J. Pept. Protein Res.* 32:242-255. Beta-turn profiles can be generated, and immunogenic peptide fragments identified, using the method of Deleage, G., Roux B., 1987, *Protein Engineering* 1:289-294.

CTL epitopes can be determined using specific algorithms to identify peptides within a 109P1D4 protein that are capable of optimally binding to specified HLA alleles (e.g., by using the SYFPEITHI site at World Wide Web URL syfpeithi.bmi-heidelberg.com/; the listings in Table IV(A)-(E); Epimatrix™ and Epimer™, Brown University, URL (brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html); and BIMAS, URL bimas.dcrf.nih.gov/). Illustrating this, peptide epitopes from 109P1D4 that are presented in the context of human MHC Class I molecules, e.g., HLA-A1, A2, A3, A11, A24, B7 and B35 were predicted (see, e.g., Tables VIII-XXI, XXII-XLIX). Specifically, the complete amino acid sequence of the 109P1D4 protein and relevant portions of other variants, i.e., for HLA Class I predictions 9 flanking residues on either side of a point mutation or exon junction, and for HLA Class II predictions 14 flanking residues on either side of a point mutation or exon junction corresponding to that variant, were entered into the HLA Peptide Motif Search algorithm found in the Bioinformatics and Molecular Analysis Section (BIMAS) web site listed above; in addition to the site SYFPEITHI, at URL syfpeithi.bmi-heidelberg.com/.

The HLA peptide motif search algorithm was developed by Dr. Ken Parker based on binding of specific peptide sequences in the groove of HLA Class I molecules, in particular HLA-A2 (see, e.g., Falk *et al.*, *Nature* 351: 290-6 (1991); Hunt *et al.*, *Science* 255:1261-3 (1992); Parker *et al.*, *J. Immunol.* 149:3580-7 (1992); Parker *et al.*, *J. Immunol.* 152:163-75 (1994)). This algorithm allows location and ranking of 8-mer, 9-mer, and 10-mer peptides from a complete protein sequence for predicted binding to HLA-A2 as well as numerous other HLA Class I molecules. Many HLA class I binding peptides are 8-, 9-, 10 or 11-mers. For example, for Class I HLA-A2, the epitopes preferably contain a leucine (L) or methionine (M) at position 2 and a valine (V) or leucine (L) at the C-terminus (see, e.g., Parker *et al.*, *J. Immunol.* 149:3580-7 (1992)). Selected results of 109P1D4 predicted binding peptides are shown in Tables VIII-XXI and XXII-XLIX herein. In Tables VIII-XXI and XXII-XLVII, selected candidates, 9-mers and 10-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. In Tables XLVI-XLIX, selected candidates, 15-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. The binding score corresponds to the estimated half time of dissociation of

complexes containing the peptide at 37°C at pH 6.5. Peptides with the highest binding score are predicted to be the most tightly bound to HLA Class I on the cell surface for the greatest period of time and thus represent the best immunogenic targets for T-cell recognition.

Actual binding of peptides to an HLA allele can be evaluated by stabilization of HLA expression on the antigen-processing defective cell line T2 (see, e.g., Xue *et al.*, Prostate 30:73-8 (1997) and Peshwa *et al.*, Prostate 36:129-38 (1998)). Immunogenicity of specific peptides can be evaluated *in vitro* by stimulation of CD8+ cytotoxic T lymphocytes (CTL) in the presence of antigen presenting cells such as dendritic cells.

It is to be appreciated that every epitope predicted by the BIMAS site, Epimer™ and Epimatrix™ sites, or specified by the HLA class I or class II motifs available in the art or which become part of the art such as set forth in Table IV (or determined using World Wide Web site URL syfpeithi.bmi-heidelberg.com/, or BIMAS, bimas.dcrt.nih.gov/) are to be "applied" to a 109P1D4 protein in accordance with the invention. As used in this context "applied" means that a 109P1D4 protein is evaluated, e.g., visually or by computer-based patterns finding methods, as appreciated by those of skill in the relevant art. Every subsequence of a 109P1D4 protein of 8, 9, 10, or 11 amino acid residues that bears an HLA Class I motif, or a subsequence of 9 or more amino acid residues that bear an HLA Class II motif are within the scope of the invention.

III.B.) Expression of 109P1D4-related Proteins

In an embodiment described in the examples that follow, 109P1D4 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 109P1D4 with a C-terminal 6XHis and MYC tag (pcDNA3.1/mycHis, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 109P1D4 protein in transfected cells. The secreted HIS-tagged 109P1D4 in the culture media can be purified, e.g., using a nickel column using standard techniques.

III.C.) Modifications of 109P1D4-related Proteins

Modifications of 109P1D4-related proteins such as covalent modifications are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a 109P1D4 polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of a 109P1D4 protein. Another type of covalent modification of a 109P1D4 polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of a protein of the invention. Another type of covalent modification of 109P1D4 comprises linking a 109P1D4 polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The 109P1D4-related proteins of the present invention can also be modified to form a chimeric molecule comprising 109P1D4 fused to another, heterologous polypeptide or amino acid sequence. Such a chimeric molecule can be synthesized chemically or recombinantly. A chimeric molecule can have a protein of the invention fused to another tumor-associated antigen or fragment thereof. Alternatively, a protein in accordance with the invention can comprise a fusion of fragments of a 109P1D4 sequence (amino or nucleic acid) such that a molecule is created that is not, through its length, directly homologous to the amino or nucleic acid sequences shown in Figure 2 or Figure 3. Such a chimeric molecule can comprise multiples of the same subsequence of 109P1D4. A chimeric molecule can comprise a fusion of a 109P1D4-related protein with a polyhistidine epitope tag, which provides an epitope to which immobilized nickel can selectively bind, with cytokines or with growth factors. The epitope tag is generally placed at the amino- or carboxyl- terminus of a 109P1D4

protein. In an alternative embodiment, the chimeric molecule can comprise a fusion of a 109P1D4-related protein with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a 109P1D4 polypeptide in place of at least one variable region within an Ig molecule. In a preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG molecule. For the production of immunoglobulin fusions see, e.g., U.S. Patent No. 5,428,130 issued June 27, 1995.

III.D.) Uses of 109P1D4-related Proteins

The proteins of the invention have a number of different specific uses. As 109P1D4 is highly expressed in prostate and other cancers, 109P1D4-related proteins are used in methods that assess the status of 109P1D4 gene products in normal versus cancerous tissues, thereby elucidating the malignant phenotype. Typically, polypeptides from specific regions of a 109P1D4 protein are used to assess the presence of perturbations (such as deletions, insertions, point mutations etc.) in those regions (such as regions containing one or more motifs). Exemplary assays utilize antibodies or T cells targeting 109P1D4-related proteins comprising the amino acid residues of one or more of the biological motifs contained within a 109P1D4 polypeptide sequence in order to evaluate the characteristics of this region in normal versus cancerous tissues or to elicit an immune response to the epitope. Alternatively, 109P1D4-related proteins that contain the amino acid residues of one or more of the biological motifs in a 109P1D4 protein are used to screen for factors that interact with that region of 109P1D4.

109P1D4 protein fragments/subsequences are particularly useful in generating and characterizing domain-specific antibodies (e.g., antibodies recognizing an extracellular or intracellular epitope of a 109P1D4 protein), for identifying agents or cellular factors that bind to 109P1D4 or a particular structural domain thereof, and in various therapeutic and diagnostic contexts, including but not limited to diagnostic assays, cancer vaccines and methods of preparing such vaccines.

Proteins encoded by the 109P1D4 genes, or by analogs, homologs or fragments thereof, have a variety of uses, including but not limited to generating antibodies and in methods for identifying ligands and other agents and cellular constituents that bind to a 109P1D4 gene product. Antibodies raised against a 109P1D4 protein or fragment thereof are useful in diagnostic and prognostic assays, and imaging methodologies in the management of human cancers characterized by expression of 109P1D4 protein, such as those listed in Table I. Such antibodies can be expressed intracellularly and used in methods of treating patients with such cancers. 109P1D4-related nucleic acids or proteins are also used in generating HTL or CTL responses.

Various immunological assays useful for the detection of 109P1D4 proteins are used, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), immunocytochemical methods, and the like. Antibodies can be labeled and used as immunological imaging reagents capable of detecting 109P1D4-expressing cells (e.g., in radioscintigraphic imaging methods). 109P1D4 proteins are also particularly useful in generating cancer vaccines, as further described herein.

IV.) 109P1D4 Antibodies

Another aspect of the invention provides antibodies that bind to 109P1D4-related proteins. Preferred antibodies specifically bind to a 109P1D4-related protein and do not bind (or bind weakly) to peptides or proteins that are not 109P1D4-related proteins under physiological conditions. In this context, examples of physiological conditions include: 1) phosphate buffered saline; 2) Tris-buffered saline containing 25mM Tris and 150 mM NaCl; or normal saline (0.9% NaCl); 4) animal serum

such as human serum; or, 5) a combination of any of 1) through 4); these reactions preferably taking place at pH 7.5, alternatively in a range of pH 7.0 to 8.0, or alternatively in a range of pH 6.5 to 8.5; also, these reactions taking place at a temperature between 4°C to 37°C. For example, antibodies that bind 109P1D4 can bind 109P1D4-related proteins such as the homologs or analogs thereof.

109P1D4 antibodies of the invention are particularly useful in cancer (see, e.g., Table I) diagnostic and prognostic assays, and imaging methodologies. Similarly, such antibodies are useful in the treatment, diagnosis, and/or prognosis of other cancers, to the extent 109P1D4 is also expressed or overexpressed in these other cancers. Moreover, intracellularly expressed antibodies (e.g., single chain antibodies) are therapeutically useful in treating cancers in which the expression of 109P1D4 is involved, such as advanced or metastatic prostate cancers.

The invention also provides various immunological assays useful for the detection and quantification of 109P1D4 and mutant 109P1D4-related proteins. Such assays can comprise one or more 109P1D4 antibodies capable of recognizing and binding a 109P1D4-related protein, as appropriate. These assays are performed within various immunological assay formats well known in the art, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), and the like.

Immunological non-antibody assays of the invention also comprise T cell Immunogenicity assays (inhibitory or stimulatory) as well as major histocompatibility complex (MHC) binding assays.

In addition, immunological imaging methods capable of detecting prostate cancer and other cancers expressing 109P1D4 are also provided by the invention, including but not limited to radioscintigraphic imaging methods using labeled 109P1D4 antibodies. Such assays are clinically useful in the detection, monitoring, and prognosis of 109P1D4 expressing cancers such as prostate cancer.

109P1D4 antibodies are also used in methods for purifying a 109P1D4-related protein and for isolating 109P1D4 homologues and related molecules. For example, a method of purifying a 109P1D4-related protein comprises incubating a 109P1D4 antibody, which has been coupled to a solid matrix, with a lysate or other solution containing a 109P1D4-related protein under conditions that permit the 109P1D4 antibody to bind to the 109P1D4-related protein; washing the solid matrix to eliminate impurities; and eluting the 109P1D4-related protein from the coupled antibody. Other uses of 109P1D4 antibodies in accordance with the invention include generating anti-idiotypic antibodies that mimic a 109P1D4 protein.

Various methods for the preparation of antibodies are well known in the art. For example, antibodies can be prepared by immunizing a suitable mammalian host using a 109P1D4-related protein, peptide, or fragment, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of 109P1D4 can also be used, such as a 109P1D4 GST-fusion protein. In a particular embodiment, a GST fusion protein comprising all or most of the amino acid sequence of Figure 2 or Figure 3 is produced, then used as an immunogen to generate appropriate antibodies. In another embodiment, a 109P1D4-related protein is synthesized and used as an immunogen.

In addition, naked DNA immunization techniques known in the art are used (with or without purified 109P1D4-related protein or 109P1D4 expressing cells) to generate an immune response to the encoded immunogen (for review, see Donnelly *et al.*, 1997, *Ann. Rev. Immunol.* 15: 617-648).

The amino acid sequence of a 109P1D4 protein as shown in Figure 2 or Figure 3 can be analyzed to select specific regions of the 109P1D4 protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of a 109P1D4 amino acid sequence are used to identify hydrophilic regions in the 109P1D4 structure. Regions of a 109P1D4 protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Hydrophilicity

profiles can be generated using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydrophaticity profiles can be generated using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294. Thus, each region identified by any of these programs or methods is within the scope of the present invention. Methods for the generation of 109P1D4 antibodies are further illustrated by way of the examples provided herein. Methods for preparing a protein or polypeptide for use as an immunogen are well known in the art. Also well known in the art are methods for preparing immunogenic conjugates of a protein with a carrier, such as BSA, KLH or other carrier protein. In some circumstances, direct conjugation using, for example, carbodiimide reagents are used; in other instances linking reagents such as those supplied by Pierce Chemical Co., Rockford, IL, are effective. Administration of a 109P1D4 immunogen is often conducted by injection over a suitable time period and with use of a suitable adjuvant, as is understood in the art. During the immunization schedule, titers of antibodies can be taken to determine adequacy of antibody formation.

109P1D4 monoclonal antibodies can be produced by various means well known in the art. For example, immortalized cell lines that secrete a desired monoclonal antibody are prepared using the standard hybridoma technology of Kohler and Milstein or modifications that immortalize antibody-producing B cells, as is generally known. Immortalized cell lines that secrete the desired antibodies are screened by immunoassay in which the antigen is a 109P1D4-related protein. When the appropriate immortalized cell culture is identified, the cells can be expanded and antibodies produced either from *in vitro* cultures or from ascites fluid.

The antibodies or fragments of the invention can also be produced, by recombinant means. Regions that bind specifically to the desired regions of a 109P1D4 protein can also be produced in the context of chimeric or complementarity-determining region (CDR) grafted antibodies of multiple species origin. Humanized or human 109P1D4 antibodies can also be produced, and are preferred for use in therapeutic contexts. Methods for humanizing murine and other non-human antibodies, by substituting one or more of the non-human antibody CDRs for corresponding human antibody sequences, are well known (see for example, Jones *et al.*, 1986, Nature 321: 522-525; Riechmann *et al.*, 1988, Nature 332: 323-327; Verhoeven *et al.*, 1988, Science 239: 1534-1536). See also, Carter *et al.*, 1993, Proc. Natl. Acad. Sci. USA 89: 4285 and Sims *et al.*, 1993, J. Immunol. 151: 2296.

Methods for producing fully human monoclonal antibodies include phage display and transgenic methods (for review, see Vaughan *et al.*, 1998, Nature Biotechnology 16: 535-539). Fully human 109P1D4 monoclonal antibodies can be generated using cloning technologies employing large human Ig gene combinatorial libraries (i.e., phage display) (Griffiths and Hoogenboom, Building an *in vitro* immune system: human antibodies from phage display libraries. In: Protein Engineering of Antibody Molecules for Prophylactic and Therapeutic Applications in Man, Clark, M. (Ed.), Nottingham Academic, pp 45-64 (1993); Burton and Barbas, Human Antibodies from combinatorial libraries. *Id.*, pp 65-82). Fully human 109P1D4 monoclonal antibodies can also be produced using transgenic mice engineered to contain human immunoglobulin gene loci as described in PCT Patent Application WO98/24893, Kucherlapati and Jakobovits *et al.*, published December 3, 1997 (see also, Jakobovits, 1998, Exp. Opin. Invest. Drugs 7(4): 607-614; U.S. patents 6,162,963 issued 19 December 2000; 6,150,584 issued 12 November 2000; and, 6,114,598 issued 5 September 2000). This method avoids the *in vitro* manipulation required with phage display technology and efficiently produces high affinity authentic human antibodies.

Reactivity of 109P1D4 antibodies with a 109P1D4-related protein can be established by a number of well known means, including Western blot, immunoprecipitation, ELISA, and FACS analyses using, as appropriate, 109P1D4-related proteins, 109P1D4-expressing cells or extracts thereof. A 109P1D4 antibody or fragment thereof can be labeled with a detectable marker or conjugated to a second molecule. Suitable detectable markers include, but are not limited to, a

radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme. Further, bi-specific antibodies specific for two or more 109P1D4 epitopes are generated using methods generally known in the art. Homodimeric antibodies can also be generated by cross-linking techniques known in the art (e.g., Wolff *et al.*, *Cancer Res.* 53: 2560-2565).

V.) 109P1D4 Cellular Immune Responses

The mechanism by which T cells recognize antigens has been delineated. Efficacious peptide epitope vaccine compositions of the invention induce a therapeutic or prophylactic immune responses in very broad segments of the world-wide population. For an understanding of the value and efficacy of compositions of the invention that induce cellular immune responses, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are set forth in Table IV (see also, e.g., Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via World Wide Web at URL (134.2.96.221/scripts.hlaserver.dll/home.htm); Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics* 1999 Nov; 50(3-4):201-12, Review).

Furthermore, x-ray crystallographic analyses of HLA-peptide complexes have revealed pockets within the peptide binding cleft/groove of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (See, e.g., Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that are correlated with binding to particular HLA antigen(s).

Thus, by a process of HLA motif identification, candidates for epitope-based vaccines have been identified; such candidates can be further evaluated by HLA-peptide binding assays to determine binding affinity and/or the time period of association of the epitope and its corresponding HLA molecule. Additional confirmatory work can be performed to select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, and/or immunogenicity.

Various strategies can be utilized to evaluate cellular immunogenicity, including:

- 1) Evaluation of primary T cell cultures from normal individuals (see, e.g., Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998). This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several

weeks. T cells specific for the peptide become activated during this time and are detected using, e.g., a lymphokine- or ^{51}Cr -release assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (see, e.g., Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997). For example, in such methods peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, e.g., a ^{51}Cr -release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from immune individuals who have been either effectively vaccinated and/or from chronically ill patients (see, e.g., Rehmann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997). Accordingly, recall responses are detected by culturing PBL from subjects that have been exposed to the antigen due to disease and thus have generated an immune response "naturally", or from patients who were vaccinated against the antigen. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

VI.) 109P1D4 Transgenic Animals

Nucleic acids that encode a 109P1D4-related protein can also be used to generate either transgenic animals or "knock out" animals that, in turn, are useful in the development and screening of therapeutically useful reagents. In accordance with established techniques, cDNA encoding 109P1D4 can be used to clone genomic DNA that encodes 109P1D4. The cloned genomic sequences can then be used to generate transgenic animals containing cells that express DNA that encode 109P1D4. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 issued 12 April 1988, and 4,870,009 issued 26 September 1989. Typically, particular cells would be targeted for 109P1D4 transgene incorporation with tissue-specific enhancers.

Transgenic animals that include a copy of a transgene encoding 109P1D4 can be used to examine the effect of increased expression of DNA that encodes 109P1D4. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this aspect of the invention, an animal is treated with a reagent and a reduced incidence of a pathological condition, compared to untreated animals that bear the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of 109P1D4 can be used to construct a 109P1D4 "knock out" animal that has a defective or altered gene encoding 109P1D4 as a result of homologous recombination between the endogenous gene encoding 109P1D4 and altered genomic DNA encoding 109P1D4 introduced into an embryonic cell of the animal. For example, cDNA that encodes 109P1D4 can be used to clone genomic DNA encoding 109P1D4 in accordance with established techniques. A portion of the genomic DNA encoding 109P1D4 can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA

are selected (see, e.g., Li *et al.*, *Cell*, 69:915 (1992)). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras (see, e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal, and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock out animals can be characterized, for example, for their ability to defend against certain pathological conditions or for their development of pathological conditions due to absence of a 109P1D4 polypeptide.

VII.) Methods for the Detection of 109P1D4

Another aspect of the present invention relates to methods for detecting 109P1D4 polynucleotides and 109P1D4-related proteins, as well as methods for identifying a cell that expresses 109P1D4. The expression profile of 109P1D4 makes it a diagnostic marker for metastasized disease. Accordingly, the status of 109P1D4 gene products provides information useful for predicting a variety of factors including susceptibility to advanced stage disease, rate of progression, and/or tumor aggressiveness. As discussed in detail herein, the status of 109P1D4 gene products in patient samples can be analyzed by a variety of protocols that are well known in the art including immunohistochemical analysis, the variety of Northern blotting techniques including *in situ* hybridization, RT-PCR analysis (for example on laser capture micro-dissected samples), Western blot analysis and tissue array analysis.

More particularly, the invention provides assays for the detection of 109P1D4 polynucleotides in a biological sample, such as serum, bone, prostate, and other tissues, urine, semen, cell preparations, and the like. Detectable 109P1D4 polynucleotides include, for example, a 109P1D4 gene or fragment thereof, 109P1D4 mRNA, alternative splice variant 109P1D4 mRNAs, and recombinant DNA or RNA molecules that contain a 109P1D4 polynucleotide. A number of methods for amplifying and/or detecting the presence of 109P1D4 polynucleotides are well known in the art and can be employed in the practice of this aspect of the invention.

In one embodiment, a method for detecting a 109P1D4 mRNA in a biological sample comprises producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced using a 109P1D4 polynucleotides as sense and antisense primers to amplify 109P1D4 cDNAs therein; and detecting the presence of the amplified 109P1D4 cDNA. Optionally, the sequence of the amplified 109P1D4 cDNA can be determined.

In another embodiment, a method of detecting a 109P1D4 gene in a biological sample comprises first isolating genomic DNA from the sample; amplifying the isolated genomic DNA using 109P1D4 polynucleotides as sense and antisense primers; and detecting the presence of the amplified 109P1D4 gene. Any number of appropriate sense and antisense probe combinations can be designed from a 109P1D4 nucleotide sequence (see, e.g., Figure 2) and used for this purpose.

The invention also provides assays for detecting the presence of a 109P1D4 protein in a tissue or other biological sample such as serum, semen, bone, prostate, urine, cell preparations, and the like. Methods for detecting a 109P1D4-related protein are also well known and include, for example, immunoprecipitation, immunohistochemical analysis, Western blot analysis, molecular binding assays, ELISA, ELIFA and the like. For example, a method of detecting the presence of a 109P1D4-related protein in a biological sample comprises first contacting the sample with a 109P1D4 antibody, a 109P1D4-reactive fragment thereof, or a recombinant protein containing an antigen-binding region of a 109P1D4 antibody; and then detecting the binding of 109P1D4-related protein in the sample.

Methods for identifying a cell that expresses 109P1D4 are also within the scope of the invention. In one embodiment,

an assay for identifying a cell that expresses a 109P1D4 gene comprises detecting the presence of 109P1D4 mRNA in the cell. Methods for the detection of particular mRNAs in cells are well known and include, for example, hybridization assays using complementary DNA probes (such as *in situ* hybridization using labeled 109P1D4 riboprobes, Northern blot and related techniques) and various nucleic acid amplification assays (such as RT-PCR using complementary primers specific for 109P1D4, and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like). Alternatively, an assay for identifying a cell that expresses a 109P1D4 gene comprises detecting the presence of 109P1D4-related protein in the cell or secreted by the cell. Various methods for the detection of proteins are well known in the art and are employed for the detection of 109P1D4-related proteins and cells that express 109P1D4-related proteins.

109P1D4 expression analysis is also useful as a tool for identifying and evaluating agents that modulate 109P1D4 gene expression. For example, 109P1D4 expression is significantly upregulated in prostate cancer, and is expressed in cancers of the tissues listed in Table I. Identification of a molecule or biological agent that inhibits 109P1D4 expression or over-expression in cancer cells is of therapeutic value. For example, such an agent can be identified by using a screen that quantifies 109P1D4 expression by RT-PCR, nucleic acid hybridization or antibody binding.

VIII.) Methods for Monitoring the Status of 109P1D4-related Genes and Their Products

Oncogenesis is known to be a multistep process where cellular growth becomes progressively dysregulated and cells progress from a normal physiological state to precancerous and then cancerous states (see, e.g., Alers *et al.*, Lab Invest. 77(5): 437-438 (1997) and Isaacs *et al.*, Cancer Surv. 23: 19-32 (1995)). In this context, examining a biological sample for evidence of dysregulated cell growth (such as aberrant 109P1D4 expression in cancers) allows for early detection of such aberrant physiology, before a pathologic state such as cancer has progressed to a stage that therapeutic options are more limited and/or the prognosis is worse. In such examinations, the status of 109P1D4 in a biological sample of interest can be compared, for example, to the status of 109P1D4 in a corresponding normal sample (e.g. a sample from that individual or alternatively another individual that is not affected by a pathology). An alteration in the status of 109P1D4 in the biological sample (as compared to the normal sample) provides evidence of dysregulated cellular growth. In addition to using a biological sample that is not affected by a pathology as a normal sample, one can also use a predetermined normative value such as a predetermined normal level of mRNA expression (see, e.g., Grever *et al.*, J. Comp. Neurol. 1996 Dec 9; 376(2): 306-14 and U.S. Patent No. 5,837,501) to compare 109P1D4 status in a sample.

The term "status" in this context is used according to its art accepted meaning and refers to the condition or state of a gene and its products. Typically, skilled artisans use a number of parameters to evaluate the condition or state of a gene and its products. These include, but are not limited to the location of expressed gene products (including the location of 109P1D4 expressing cells) as well as the level, and biological activity of expressed gene products (such as 109P1D4 mRNA, polynucleotides and polypeptides). Typically, an alteration in the status of 109P1D4 comprises a change in the location of 109P1D4 and/or 109P1D4 expressing cells and/or an increase in 109P1D4 mRNA and/or protein expression.

109P1D4 status in a sample can be analyzed by a number of means well known in the art, including without limitation, immunohistochemical analysis, *in situ* hybridization, RT-PCR analysis on laser capture micro-dissected samples, Western blot analysis, and tissue array analysis. Typical protocols for evaluating the status of a 109P1D4 gene and gene products are found, for example in Ausubel *et al.* eds., 1995, Current Protocols In Molecular Biology, Units 2 (Northern Blotting), 4 (Southern Blotting), 15 (Immunoblotting) and 18 (PCR Analysis). Thus, the status of 109P1D4 in a biological sample is evaluated by various methods utilized by skilled artisans including, but not limited to genomic Southern analysis (to examine, for example perturbations in a 109P1D4 gene), Northern analysis and/or PCR analysis of 109P1D4 mRNA (to examine, for example alterations in the polynucleotide sequences or expression levels of 109P1D4 mRNAs), and, Western and/or

immunohistochemical analysis (to examine, for example alterations in polypeptide sequences, alterations in polypeptide localization within a sample, alterations in expression levels of 109P1D4 proteins and/or associations of 109P1D4 proteins with polypeptide binding partners). Detectable 109P1D4 polynucleotides include, for example, a 109P1D4 gene or fragment thereof, 109P1D4 mRNA, alternative splice variants, 109P1D4 mRNAs, and recombinant DNA or RNA molecules containing a 109P1D4 polynucleotide.

The expression profile of 109P1D4 makes it a diagnostic marker for local and/or metastasized disease, and provides information on the growth or oncogenic potential of a biological sample. In particular, the status of 109P1D4 provides information useful for predicting susceptibility to particular disease stages, progression, and/or tumor aggressiveness. The invention provides methods and assays for determining 109P1D4 status and diagnosing cancers that express 109P1D4, such as cancers of the tissues listed in Table I. For example, because 109P1D4 mRNA is so highly expressed in prostate and other cancers relative to normal prostate tissue, assays that evaluate the levels of 109P1D4 mRNA transcripts or proteins in a biological sample can be used to diagnose a disease associated with 109P1D4 dysregulation, and can provide prognostic information useful in defining appropriate therapeutic options.

The expression status of 109P1D4 provides information including the presence, stage and location of dysplastic, precancerous and cancerous cells, predicting susceptibility to various stages of disease, and/or for gauging tumor aggressiveness. Moreover, the expression profile makes it useful as an imaging reagent for metastasized disease. Consequently, an aspect of the invention is directed to the various molecular prognostic and diagnostic methods for examining the status of 109P1D4 in biological samples such as those from individuals suffering from, or suspected of suffering from a pathology characterized by dysregulated cellular growth, such as cancer.

As described above, the status of 109P1D4 in a biological sample can be examined by a number of well-known procedures in the art. For example, the status of 109P1D4 in a biological sample taken from a specific location in the body can be examined by evaluating the sample for the presence or absence of 109P1D4 expressing cells (e.g. those that express 109P1D4 mRNAs or proteins). This examination can provide evidence of dysregulated cellular growth, for example, when 109P1D4-expressing cells are found in a biological sample that does not normally contain such cells (such as a lymph node), because such alterations in the status of 109P1D4 in a biological sample are often associated with dysregulated cellular growth. Specifically, one indicator of dysregulated cellular growth is the metastases of cancer cells from an organ of origin (such as the prostate) to a different area of the body (such as a lymph node). In this context, evidence of dysregulated cellular growth is important for example because occult lymph node metastases can be detected in a substantial proportion of patients with prostate cancer, and such metastases are associated with known predictors of disease progression (see, e.g., Murphy *et al.*, Prostate 42(4): 315-317 (2000); Su *et al.*, Semin. Surg. Oncol. 18(1): 17-28 (2000) and Freeman *et al.*, J Urol 1995 Aug 154(2 Pt 1):474-8).

In one aspect, the invention provides methods for monitoring 109P1D4 gene products by determining the status of 109P1D4 gene products expressed by cells from an individual suspected of having a disease associated with dysregulated cell growth (such as hyperplasia or cancer) and then comparing the status so determined to the status of 109P1D4 gene products in a corresponding normal sample. The presence of aberrant 109P1D4 gene products in the test sample relative to the normal sample provides an indication of the presence of dysregulated cell growth within the cells of the individual.

In another aspect, the invention provides assays useful in determining the presence of cancer in an individual, comprising detecting a significant increase in 109P1D4 mRNA or protein expression in a test cell or tissue sample relative to expression levels in the corresponding normal cell or tissue. The presence of 109P1D4 mRNA can, for example, be evaluated in tissues including but not limited to those listed in Table I. The presence of significant 109P1D4 expression in any of these tissues is useful to indicate the emergence, presence and/or severity of a cancer, since the corresponding

normal tissues do not express 109P1D4 mRNA or express it at lower levels.

In a related embodiment, 109P1D4 status is determined at the protein level rather than at the nucleic acid level. For example, such a method comprises determining the level of 109P1D4 protein expressed by cells in a test tissue sample and comparing the level so determined to the level of 109P1D4 expressed in a corresponding normal sample. In one embodiment, the presence of 109P1D4 protein is evaluated, for example, using immunohistochemical methods. 109P1D4 antibodies or binding partners capable of detecting 109P1D4 protein expression are used in a variety of assay formats well known in the art for this purpose.

In a further embodiment, one can evaluate the status of 109P1D4 nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules. These perturbations can include insertions, deletions, substitutions and the like. Such evaluations are useful because perturbations in the nucleotide and amino acid sequences are observed in a large number of proteins associated with a growth dysregulated phenotype (see, e.g., Marrogi *et al.*, 1999, J. Cutan. Pathol. 26(8):369-378). For example, a mutation in the sequence of 109P1D4 may be indicative of the presence or promotion of a tumor. Such assays therefore have diagnostic and predictive value where a mutation in 109P1D4 indicates a potential loss of function or increase in tumor growth.

A wide variety of assays for observing perturbations in nucleotide and amino acid sequences are well known in the art. For example, the size and structure of nucleic acid or amino acid sequences of 109P1D4 gene products are observed by the Northern, Southern, Western, PCR and DNA sequencing protocols discussed herein. In addition, other methods for observing perturbations in nucleotide and amino acid sequences such as single strand conformation polymorphism analysis are well known in the art (see, e.g., U.S. Patent Nos. 5,382,510 issued 7 September 1999, and 5,952,170 issued 17 January 1995).

Additionally, one can examine the methylation status of a 109P1D4 gene in a biological sample. Aberrant demethylation and/or hypermethylation of CpG islands in gene 5' regulatory regions frequently occurs in immortalized and transformed cells, and can result in altered expression of various genes. For example, promoter hypermethylation of the pi-class glutathione S-transferase (a protein expressed in normal prostate but not expressed in >90% of prostate carcinomas) appears to permanently silence transcription of this gene and is the most frequently detected genomic alteration in prostate carcinomas (De Marzo *et al.*, Am. J. Pathol. 155(6): 1985-1992 (1999)). In addition, this alteration is present in at least 70% of cases of high-grade prostatic intraepithelial neoplasia (PIN) (Brooks *et al.*, Cancer Epidemiol. Biomarkers Prev., 1998, 7:531-536). In another example, expression of the LAGE-I tumor specific gene (which is not expressed in normal prostate but is expressed in 25-50% of prostate cancers) is induced by deoxy-azacytidine in lymphoblastoid cells, suggesting that tumoral expression is due to demethylation (Lethe *et al.*, Int. J. Cancer 76(6): 903-908 (1998)). A variety of assays for examining methylation status of a gene are well known in the art. For example, one can utilize, in Southern hybridization approaches, methylation-sensitive restriction enzymes that cannot cleave sequences that contain methylated CpG sites to assess the methylation status of CpG islands. In addition, MSP (methylation specific PCR) can rapidly profile the methylation status of all the CpG sites present in a CpG island of a given gene. This procedure involves initial modification of DNA by sodium bisulfite (which will convert all unmethylated cytosines to uracil) followed by amplification using primers specific for methylated versus unmethylated DNA. Protocols involving methylation interference can also be found for example in Current Protocols In Molecular Biology, Unit 12, Frederick M. Ausubel *et al.* eds., 1995.

Gene amplification is an additional method for assessing the status of 109P1D4. Gene amplification is measured in a sample directly, for example, by conventional Southern blotting or Northern blotting to quantitate the transcription of mRNA (Thomas, 1980, Proc. Natl. Acad. Sci. USA, 77:5201-5205), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies are employed that recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein

duplexes. The antibodies in turn are labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Biopsied tissue or peripheral blood can be conveniently assayed for the presence of cancer cells using for example, Northern, dot blot or RT-PCR analysis to detect 109P1D4 expression. The presence of RT-PCR amplifiable 109P1D4 mRNA provides an indication of the presence of cancer. RT-PCR assays are well known in the art. RT-PCR detection assays for tumor cells in peripheral blood are currently being evaluated for use in the diagnosis and management of a number of human solid tumors. In the prostate cancer field, these include RT-PCR assays for the detection of cells expressing PSA and PSM (Verkaik *et al.*, 1997, *Urol. Res.* 25:373-384; Ghossein *et al.*, 1995, *J. Clin. Oncol.* 13:1195-2000; Heston *et al.*, 1995, *Clin. Chem.* 41:1687-1688).

A further aspect of the invention is an assessment of the susceptibility that an individual has for developing cancer. In one embodiment, a method for predicting susceptibility to cancer comprises detecting 109P1D4 mRNA or 109P1D4 protein in a tissue sample, its presence indicating susceptibility to cancer, wherein the degree of 109P1D4 mRNA expression correlates to the degree of susceptibility. In a specific embodiment, the presence of 109P1D4 in prostate or other tissue is examined, with the presence of 109P1D4 in the sample providing an indication of prostate cancer susceptibility (or the emergence or existence of a prostate tumor). Similarly, one can evaluate the integrity 109P1D4 nucleotide and amino acid sequences in a biological sample, in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations in 109P1D4 gene products in the sample is an indication of cancer susceptibility (or the emergence or existence of a tumor).

The invention also comprises methods for gauging tumor aggressiveness. In one embodiment, a method for gauging aggressiveness of a tumor comprises determining the level of 109P1D4 mRNA or 109P1D4 protein expressed by tumor cells, comparing the level so determined to the level of 109P1D4 mRNA or 109P1D4 protein expressed in a corresponding normal tissue taken from the same individual or a normal tissue reference sample, wherein the degree of 109P1D4 mRNA or 109P1D4 protein expression in the tumor sample relative to the normal sample indicates the degree of aggressiveness. In a specific embodiment, aggressiveness of a tumor is evaluated by determining the extent to which 109P1D4 is expressed in the tumor cells, with higher expression levels indicating more aggressive tumors. Another embodiment is the evaluation of the integrity of 109P1D4 nucleotide and amino acid sequences in a biological sample, in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations indicates more aggressive tumors.

Another embodiment of the invention is directed to methods for observing the progression of a malignancy in an individual over time. In one embodiment, methods for observing the progression of a malignancy in an individual over time comprise determining the level of 109P1D4 mRNA or 109P1D4 protein expressed by cells in a sample of the tumor, comparing the level so determined to the level of 109P1D4 mRNA or 109P1D4 protein expressed in an equivalent tissue sample taken from the same individual at a different time, wherein the degree of 109P1D4 mRNA or 109P1D4 protein expression in the tumor sample over time provides information on the progression of the cancer. In a specific embodiment, the progression of a cancer is evaluated by determining 109P1D4 expression in the tumor cells over time, where increased expression over time indicates a progression of the cancer. Also, one can evaluate the integrity 109P1D4 nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like, where the presence of one or more perturbations indicates a progression of the cancer.

The above diagnostic approaches can be combined with any one of a wide variety of prognostic and diagnostic protocols known in the art. For example, another embodiment of the invention is directed to methods for observing a coincidence between the expression of 109P1D4 gene and 109P1D4 gene products (or perturbations in 109P1D4 gene and 109P1D4 gene

products) and a factor that is associated with malignancy, as a means for diagnosing and prognosticating the status of a tissue sample. A wide variety of factors associated with malignancy can be utilized, such as the expression of genes associated with malignancy (e.g. PSA, PSCA and PSM expression for prostate cancer etc.) as well as gross cytological observations (see, e.g., Bocking *et al.*, 1984, *Anal. Quant. Cytol.* 6(2):74-88; Epstein, 1995, *Hum. Pathol.* 26(2):223-9; Thorson *et al.*, 1998, *Mod. Pathol.* 11(6):543-51; Baisden *et al.*, 1999, *Am. J. Surg. Pathol.* 23(8):918-24). Methods for observing a coincidence between the expression of 109P1D4 gene and 109P1D4 gene products (or perturbations in 109P1D4 gene and 109P1D4 gene products) and another factor that is associated with malignancy are useful, for example, because the presence of a set of specific factors that coincide with disease provides information crucial for diagnosing and prognosticating the status of a tissue sample.

In one embodiment, methods for observing a coincidence between the expression of 109P1D4 gene and 109P1D4 gene products (or perturbations in 109P1D4 gene and 109P1D4 gene products) and another factor associated with malignancy entails detecting the overexpression of 109P1D4 mRNA or protein in a tissue sample, detecting the overexpression of PSA mRNA or protein in a tissue sample (or PSCA or PSM expression), and observing a coincidence of 109P1D4 mRNA or protein and PSA mRNA or protein overexpression (or PSCA or PSM expression). In a specific embodiment, the expression of 109P1D4 and PSA mRNA in prostate tissue is examined, where the coincidence of 109P1D4 and PSA mRNA overexpression in the sample indicates the existence of prostate cancer, prostate cancer susceptibility or the emergence or status of a prostate tumor.

Methods for detecting and quantifying the expression of 109P1D4 mRNA or protein are described herein, and standard nucleic acid and protein detection and quantification technologies are well known in the art. Standard methods for the detection and quantification of 109P1D4 mRNA include *in situ* hybridization using labeled 109P1D4 riboprobes, Northern blot and related techniques using 109P1D4 polynucleotide probes, RT-PCR analysis using primers specific for 109P1D4, and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like. In a specific embodiment, semi-quantitative RT-PCR is used to detect and quantify 109P1D4 mRNA expression. Any number of primers capable of amplifying 109P1D4 can be used for this purpose, including but not limited to the various primer sets specifically described herein. In a specific embodiment, polyclonal or monoclonal antibodies specifically reactive with the wild-type 109P1D4 protein can be used in an immunohistochemical assay of biopsied tissue.

IX.) Identification of Molecules That Interact With 109P1D4

The 109P1D4 protein and nucleic acid sequences disclosed herein allow a skilled artisan to identify proteins, small molecules and other agents that interact with 109P1D4, as well as pathways activated by 109P1D4 via any one of a variety of art accepted protocols. For example, one can utilize one of the so-called interaction trap systems (also referred to as the "two-hybrid assay"). In such systems, molecules interact and reconstitute a transcription factor which directs expression of a reporter gene, whereupon the expression of the reporter gene is assayed. Other systems identify protein-protein interactions *in vivo* through reconstitution of a eukaryotic transcriptional activator, see, e.g., U.S. Patent Nos. 5,955,280 issued 21 September 1999, 5,925,523 issued 20 July 1999, 5,846,722 issued 8 December 1998 and 6,004,746 issued 21 December 1999. Algorithms are also available in the art for genome-based predictions of protein function (see, e.g., Marcotte, *et al.*, *Nature* 402: 4 November 1999, 83-86).

Alternatively one can screen peptide libraries to identify molecules that interact with 109P1D4 protein sequences. In such methods, peptides that bind to 109P1D4 are identified by screening libraries that encode a random or controlled collection of amino acids. Peptides encoded by the libraries are expressed as fusion proteins of bacteriophage coat proteins, the bacteriophage particles are then screened against the 109P1D4 protein(s).

Accordingly, peptides having a wide variety of uses, such as therapeutic, prognostic or diagnostic reagents, are thus identified without any prior information on the structure of the expected ligand or receptor molecule. Typical peptide

libraries and screening methods that can be used to identify molecules that interact with 109P1D4 protein sequences are disclosed for example in U.S. Patent Nos. 5,723,286 issued 3 March 1998 and 5,733,731 issued 31 March 1998.

Alternatively, cell lines that express 109P1D4 are used to identify protein-protein interactions mediated by 109P1D4. Such interactions can be examined using immunoprecipitation techniques (see, e.g., Hamilton B.J., *et al.* Biochem. Biophys. Res. Commun. 1999, 261:646-51). 109P1D4 protein can be immunoprecipitated from 109P1D4-expressing cell lines using anti-109P1D4 antibodies. Alternatively, antibodies against His-tag can be used in a cell line engineered to express fusions of 109P1D4 and a His-tag (vectors mentioned above). The immunoprecipitated complex can be examined for protein association by procedures such as Western blotting, ³⁵S-methionine labeling of proteins, protein microsequencing, silver staining and two-dimensional gel electrophoresis.

Small molecules and ligands that interact with 109P1D4 can be identified through related embodiments of such screening assays. For example, small molecules can be identified that interfere with protein function, including molecules that interfere with 109P1D4's ability to mediate phosphorylation and de-phosphorylation, interaction with DNA or RNA molecules as an indication of regulation of cell cycles, second messenger signaling or tumorigenesis. Similarly, small molecules that modulate 109P1D4-related ion channel, protein pump, or cell communication functions are identified and used to treat patients that have a cancer that expresses 109P1D4 (see, e.g., Hille, B., *Ionic Channels of Excitable Membranes 2nd Ed.*, Sinauer Assoc., Sunderland, MA, 1992). Moreover, ligands that regulate 109P1D4 function can be identified based on their ability to bind 109P1D4 and activate a reporter construct. Typical methods are discussed for example in U.S. Patent No. 5,928,868 issued 27 July 1999, and include methods for forming hybrid ligands in which at least one ligand is a small molecule. In an illustrative embodiment, cells engineered to express a fusion protein of 109P1D4 and a DNA-binding protein are used to co-express a fusion protein of a hybrid ligand/small molecule and a cDNA library transcriptional activator protein. The cells further contain a reporter gene, the expression of which is conditioned on the proximity of the first and second fusion proteins to each other, an event that occurs only if the hybrid ligand binds to target sites on both hybrid proteins. Those cells that express the reporter gene are selected and the unknown small molecule or the unknown ligand is identified. This method provides a means of identifying modulators, which activate or inhibit 109P1D4.

An embodiment of this invention comprises a method of screening for a molecule that interacts with a 109P1D4 amino acid sequence shown in Figure 2 or Figure 3, comprising the steps of contacting a population of molecules with a 109P1D4 amino acid sequence, allowing the population of molecules and the 109P1D4 amino acid sequence to interact under conditions that facilitate an interaction, determining the presence of a molecule that interacts with the 109P1D4 amino acid sequence, and then separating molecules that do not interact with the 109P1D4 amino acid sequence from molecules that do. In a specific embodiment, the method further comprises purifying, characterizing and identifying a molecule that interacts with the 109P1D4 amino acid sequence. The identified molecule can be used to modulate a function performed by 109P1D4. In a preferred embodiment, the 109P1D4 amino acid sequence is contacted with a library of peptides.

X.) Therapeutic Methods and Compositions

The identification of 109P1D4 as a protein that is normally expressed in a restricted set of tissues, but which is also expressed in cancers such as those listed in Table I, opens a number of therapeutic approaches to the treatment of such cancers.

Of note, targeted antitumor therapies have been useful even when the targeted protein is expressed on normal tissues, even vital normal organ tissues. A vital organ is one that is necessary to sustain life, such as the heart or colon. A non-vital organ is one that can be removed whereupon the individual is still able to survive. Examples of non-vital organs are ovary, breast, and prostate.

For example, Herceptin® is an FDA approved pharmaceutical that has as its active ingredient an antibody which is immunoreactive with the protein variously known as HER2, HER2/neu, and erb-b-2. It is marketed by Genentech and has been a commercially successful antitumor agent. Herceptin sales reached almost \$400 million in 2002. Herceptin is a treatment for HER2 positive metastatic breast cancer. However, the expression of HER2 is not limited to such tumors. The same protein is expressed in a number of normal tissues. In particular, it is known that HER2/neu is present in normal kidney and heart, thus these tissues are present in all human recipients of Herceptin. The presence of HER2/neu in normal kidney is also confirmed by Latif, Z., et al., *B.J.U. International* (2002) 89:5-9. As shown in this article (which evaluated whether renal cell carcinoma should be a preferred indication for anti-HER2 antibodies such as Herceptin) both protein and mRNA are produced in benign renal tissues. Notably, HER2/neu protein was strongly overexpressed in benign renal tissue. Despite the fact that HER2/neu is expressed in such vital tissues as heart and kidney, Herceptin is a very useful, FDA approved, and commercially successful drug. The effect of Herceptin on cardiac tissue, i.e., "cardiotoxicity," has merely been a side effect to treatment. When patients were treated with Herceptin alone, significant cardiotoxicity occurred in a very low percentage of patients.

Of particular note, although kidney tissue is indicated to exhibit normal expression, possibly even higher expression than cardiac tissue, kidney has no appreciable Herceptin side effect whatsoever. Moreover, of the diverse array of normal tissues in which HER2 is expressed, there is very little occurrence of any side effect. Only cardiac tissue has manifested any appreciable side effect at all. A tissue such as kidney, where HER2/neu expression is especially notable, has not been the basis for any side effect.

Furthermore, favorable therapeutic effects have been found for antitumor therapies that target epidermal growth factor receptor (EGFR). EGFR is also expressed in numerous normal tissues. There have been very limited side effects in normal tissues following use of anti-EGFR therapeutics.

Thus, expression of a target protein in normal tissue, even vital normal tissue, does not defeat the utility of a targeting agent for the protein as a therapeutic for certain tumors in which the protein is also overexpressed.

Accordingly, therapeutic approaches that inhibit the activity of a 109P1D4 protein are useful for patients suffering from a cancer that expresses 109P1D4. These therapeutic approaches generally fall into two classes. One class comprises various methods for inhibiting the binding or association of a 109P1D4 protein with its binding partner or with other proteins. Another class comprises a variety of methods for inhibiting the transcription of a 109P1D4 gene or translation of 109P1D4 mRNA.

X.A.) Anti-Cancer Vaccines

The invention provides cancer vaccines comprising a 109P1D4-related protein or 109P1D4-related nucleic acid. In view of the expression of 109P1D4, cancer vaccines prevent and/or treat 109P1D4-expressing cancers with minimal or no effects on non-target tissues. The use of a tumor antigen in a vaccine that generates humoral and/or cell-mediated immune responses as anti-cancer therapy is well known in the art and has been employed in prostate cancer using human PSMA and rodent PAP immunogens (Hodge *et al.*, 1995, *Int. J. Cancer* 63:231-237; Fong *et al.*, 1997, *J. Immunol.* 159:3113-3117).

Such methods can be readily practiced by employing a 109P1D4-related protein, or a 109P1D4-encoding nucleic acid molecule and recombinant vectors capable of expressing and presenting the 109P1D4 immunogen (which typically comprises a number of antibody or T cell epitopes). Skilled artisans understand that a wide variety of vaccine systems for delivery of immunoreactive epitopes are known in the art (see, e.g., Herylin *et al.*, *Ann Med* 1999 Feb 31(1):66-78; Maruyama *et al.*, *Cancer Immunol Immunother* 2000 Jun 49(3):123-32). Briefly, such methods of generating an immune response (e.g. humoral and/or cell-mediated) in a mammal, comprise the steps of: exposing the mammal's immune system to an

immunoreactive epitope (e.g. an epitope present in a 109P1D4 protein shown in Figure 3 or analog or homolog thereof) so that the mammal generates an immune response that is specific for that epitope (e.g. generates antibodies that specifically recognize that epitope). In a preferred method, a 109P1D4 immunogen contains a biological motif, see e.g., Tables VIII-XXI and XXII-XLIX, or a peptide of a size range from 109P1D4 indicated in Figure 5, Figure 6, Figure 7, Figure 8, and Figure 9.

The entire 109P1D4 protein, immunogenic regions or epitopes thereof can be combined and delivered by various means. Such vaccine compositions can include, for example, lipopeptides (e.g., Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J. P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, in: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (e.g., Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, in: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

In patients with 109P1D4-associated cancer, the vaccine compositions of the invention can also be used in conjunction with other treatments used for cancer, e.g., surgery, chemotherapy, drug therapies, radiation therapies, *etc.* including use in combination with immune adjuvants such as IL-2, IL-12, GM-CSF, and the like.

Cellular Vaccines:

CTL epitopes can be determined using specific algorithms to identify peptides within 109P1D4 protein that bind corresponding HLA alleles (see e.g., Table IV; Epimer™ and Epimatrix™, Brown University (URL brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html); and, BiMAS, (URL bimas.dcrt.nih.gov/; SYFPEITHI at URL syfpeithi.bmi-heidelberg.com/). In a preferred embodiment, a 109P1D4 immunogen contains one or more amino acid sequences identified using techniques well known in the art, such as the sequences shown in Tables VIII-XXI and XXII-XLIX or a peptide of 8, 9, 10 or 11 amino acids specified by an HLA Class I motif/supermotif (e.g., Table IV (A), Table IV (D), or Table IV (E)) and/or a peptide of at least 9 amino acids that comprises an HLA Class II motif/supermotif (e.g., Table IV (B) or Table IV (C)). As is appreciated in the art, the HLA Class I binding groove is essentially closed ended so that peptides of only a particular size range can fit into the groove and be bound, generally HLA Class I epitopes are 8, 9, 10, or 11 amino acids long. In contrast, the HLA Class II binding groove is essentially open ended; therefore a peptide of about 9 or more amino acids can be bound by an HLA Class II molecule. Due to the binding groove differences between HLA Class I and II, HLA Class I motifs are length specific, i.e., position two of a Class I motif is the second amino acid in an amino to carboxyl direction of the peptide. The amino acid positions in a Class II motif are relative only to each other, not the overall peptide, i.e., additional amino acids can be attached to the amino and/or carboxyl termini of a motif-bearing sequence. HLA Class II epitopes are often 9, 10, 11, 12, 13,

14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids long, or longer than 25 amino acids.

Antibody-based Vaccines

A wide variety of methods for generating an immune response in a mammal are known in the art (for example as the first step in the generation of hybridomas). Methods of generating an immune response in a mammal comprise exposing the mammal's immune system to an immunogenic epitope on a protein (e.g. a 109P1D4 protein) so that an immune response is generated. A typical embodiment consists of a method for generating an immune response to 109P1D4 in a host, by contacting the host with a sufficient amount of at least one 109P1D4 B cell or cytotoxic T-cell epitope or analog thereof; and at least one periodic interval thereafter re-contacting the host with the 109P1D4 B cell or cytotoxic T-cell epitope or analog thereof. A specific embodiment consists of a method of generating an immune response against a 109P1D4-related protein or a man-made multi-epitopic peptide comprising: administering 109P1D4 immunogen (e.g. a 109P1D4 protein or a peptide fragment thereof, a 109P1D4 fusion protein or analog etc.) in a vaccine preparation to a human or another mammal. Typically, such vaccine preparations further contain a suitable adjuvant (see, e.g., U.S. Patent No. 6,146,635) or a universal helper epitope such as a PADRE™ peptide (Epimmune Inc., San Diego, CA; see, e.g., Alexander *et al.*, J. Immunol. 2000 164(3): 1625-1633; Alexander *et al.*, Immunity 1994 1(9): 751-761 and Alexander *et al.*, Immunol. Res. 1998 18(2): 79-92). An alternative method comprises generating an immune response in an individual against a 109P1D4 immunogen by: administering *in vivo* to muscle or skin of the individual's body a DNA molecule that comprises a DNA sequence that encodes a 109P1D4 immunogen, the DNA sequence operatively linked to regulatory sequences which control the expression of the DNA sequence; wherein the DNA molecule is taken up by cells, the DNA sequence is expressed in the cells and an immune response is generated against the immunogen (see, e.g., U.S. Patent No. 5,962,428). Optionally a genetic vaccine facilitator such as anionic lipids; saponins; lectins; estrogenic compounds; hydroxylated lower alkyls; dimethyl sulfoxide; and urea is also administered. In addition, an anti-idiotypic antibody can be administered that mimics 109P1D4, in order to generate a response to the target antigen.

Nucleic Acid Vaccines:

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA that encode protein(s) of the invention can be administered to a patient. Genetic immunization methods can be employed to generate prophylactic or therapeutic humoral and cellular immune responses directed against cancer cells expressing 109P1D4. Constructs comprising DNA encoding a 109P1D4-related protein/immunogen and appropriate regulatory sequences can be injected directly into muscle or skin of an individual, such that the cells of the muscle or skin take-up the construct and express the encoded 109P1D4 protein/immunogen. Alternatively, a vaccine comprises a 109P1D4-related protein. Expression of the 109P1D4-related protein immunogen results in the generation of prophylactic or therapeutic humoral and cellular immunity against cells that bear a 109P1D4 protein. Various prophylactic and therapeutic genetic immunization techniques known in the art can be used (for review, see information and references published at Internet address genweb.com). Nucleic acid-based delivery is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, proteins of the invention can be expressed via viral or bacterial vectors. Various viral gene delivery systems that can be used in the practice of the invention include, but are not limited to, vaccinia, fowlpox, canarypox, adenovirus, influenza, poliovirus, adeno-associated virus, lentivirus, and sindbis virus (see, e.g., Restifo, 1996, *Curr. Opin. Immunol.* 8:658-663; Tsang *et al.* *J. Natl. Cancer Inst.* 87:982-990 (1995)). Non-viral delivery systems can also be employed by introducing naked DNA encoding a 109P1D4-related protein into the patient (e.g., intramuscularly or

intradermally) to induce an anti-tumor response.

Vaccinia virus is used, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into a host, the recombinant vaccinia virus expresses the protein immunogenic peptide, and thereby elicits a host immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g. adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Thus, gene delivery systems are used to deliver a 109P1D4-related nucleic acid molecule. In one embodiment, the full-length human 109P1D4 cDNA is employed. In another embodiment, 109P1D4 nucleic acid molecules encoding specific cytotoxic T lymphocyte (CTL) and/or antibody epitopes are employed.

Ex Vivo Vaccines

Various *ex vivo* strategies can also be employed to generate an immune response. One approach involves the use of antigen presenting cells (APCs) such as dendritic cells (DC) to present 109P1D4 antigen to a patient's immune system. Dendritic cells express MHC class I and II molecules, B7 co-stimulator, and IL-12, and are thus highly specialized antigen presenting cells. In prostate cancer, autologous dendritic cells pulsed with peptides of the prostate-specific membrane antigen (PSMA) are being used in a Phase I clinical trial to stimulate prostate cancer patients' immune systems (Tjota *et al.*, 1996, *Prostate* 28:65-69; Murphy *et al.*, 1996, *Prostate* 29:371-380). Thus, dendritic cells can be used to present 109P1D4 peptides to T cells in the context of MHC class I or II molecules. In one embodiment, autologous dendritic cells are pulsed with 109P1D4 peptides capable of binding to MHC class I and/or class II molecules. In another embodiment, dendritic cells are pulsed with the complete 109P1D4 protein. Yet another embodiment involves engineering the overexpression of a 109P1D4 gene in dendritic cells using various implementing vectors known in the art, such as adenovirus (Arthur *et al.*, 1997, *Cancer Gene Ther.* 4:17-25), retrovirus (Henderson *et al.*, 1996, *Cancer Res.* 56:3763-3770), lentivirus, adeno-associated virus, DNA transfection (Ribas *et al.*, 1997, *Cancer Res.* 57:2865-2869), or tumor-derived RNA transfection (Ashley *et al.*, 1997, *J. Exp. Med.* 186:1177-1182). Cells that express 109P1D4 can also be engineered to express immune modulators, such as GM-CSF, and used as immunizing agents.

X.B.) 109P1D4 as a Target for Antibody-based Therapy

109P1D4 is an attractive target for antibody-based therapeutic strategies. A number of antibody strategies are known in the art for targeting both extracellular and intracellular molecules (see, e.g., complement and ADCC mediated killing as well as the use of intrabodies). Because 109P1D4 is expressed by cancer cells of various lineages relative to corresponding normal cells, systemic administration of 109P1D4-immunoreactive compositions are prepared that exhibit excellent sensitivity without toxic, non-specific and/or non-target effects caused by binding of the immunoreactive composition to non-target organs and tissues. Antibodies specifically reactive with domains of 109P1D4 are useful to treat 109P1D4-expressing cancers systemically, either as conjugates with a toxin or therapeutic agent, or as naked antibodies capable of inhibiting cell proliferation or function.

109P1D4 antibodies can be introduced into a patient such that the antibody binds to 109P1D4 and modulates a function, such as an interaction with a binding partner, and consequently mediates destruction of the tumor cells and/or inhibits the growth of the tumor cells. Mechanisms by which such antibodies exert a therapeutic effect can include complement-mediated cytotoxicity, antibody-dependent cellular cytotoxicity, modulation of the physiological function of 109P1D4, inhibition of ligand binding or signal transduction pathways, modulation of tumor cell differentiation, alteration of

tumor angiogenesis factor profiles, and/or apoptosis.

Those skilled in the art understand that antibodies can be used to specifically target and bind immunogenic molecules such as an immunogenic region of a 109P1D4 sequence shown in Figure 2 or Figure 3. In addition, skilled artisans understand that it is routine to conjugate antibodies to cytotoxic agents (see, e.g., Slevers *et al.* Blood 93:11 3678-3684 (June 1, 1999)). When cytotoxic and/or therapeutic agents are delivered directly to cells, such as by conjugating them to antibodies specific for a molecule expressed by that cell (e.g. 109P1D4), the cytotoxic agent will exert its known biological effect (i.e. cytotoxicity) on those cells.

A wide variety of compositions and methods for using antibody-cytotoxic agent conjugates to kill cells are known in the art. In the context of cancers, typical methods entail administering to an animal having a tumor a biologically effective amount of a conjugate comprising a selected cytotoxic and/or therapeutic agent linked to a targeting agent (e.g. an anti-109P1D4 antibody) that binds to a marker (e.g. 109P1D4) expressed, accessible to binding or localized on the cell surfaces. A typical embodiment is a method of delivering a cytotoxic and/or therapeutic agent to a cell expressing 109P1D4, comprising conjugating the cytotoxic agent to an antibody that immunospecifically binds to a 109P1D4 epitope, and, exposing the cell to the antibody-agent conjugate. Another illustrative embodiment is a method of treating an individual suspected of suffering from metastasized cancer, comprising a step of administering parenterally to said individual a pharmaceutical composition comprising a therapeutically effective amount of an antibody conjugated to a cytotoxic and/or therapeutic agent.

Cancer immunotherapy using anti-109P1D4 antibodies can be done in accordance with various approaches that have been successfully employed in the treatment of other types of cancer, including but not limited to colon cancer (Arlen *et al.*, 1998, Crit. Rev. Immunol. 18:133-138), multiple myeloma (Ozaki *et al.*, 1997, Blood 90:3179-3186, Tsunenari *et al.*, 1997, Blood 90:2437-2444), gastric cancer (Kasprzyk *et al.*, 1992, Cancer Res. 52:2771-2776), B-cell lymphoma (Funakoshi *et al.*, 1996, J. Immunother. Emphasis Tumor Immunol. 19:93-101), leukemia (Zhong *et al.*, 1996, Leuk. Res. 20:581-589), colorectal cancer (Moun *et al.*, 1994, Cancer Res. 54:6160-6166; Velders *et al.*, 1995, Cancer Res. 55:4398-4403), and breast cancer (Shepard *et al.*, 1991, J. Clin. Immunol. 11:117-127). Some therapeutic approaches involve conjugation of naked antibody to a toxin or radioisotope, such as the conjugation of Y⁹¹ or I¹³¹ to anti-CD20 antibodies (e.g., Zevalin™, IDEC Pharmaceuticals Corp. or Bexxar™, Coulter Pharmaceuticals), while others involve co-administration of antibodies and other therapeutic agents, such as Herceptin™ (trastuzumab) with paclitaxel (Genentech, Inc.). The antibodies can be conjugated to a therapeutic agent. To treat prostate cancer, for example, 109P1D4 antibodies can be administered in conjunction with radiation, chemotherapy or hormone ablation. Also, antibodies can be conjugated to a toxin such as calicheamicin (e.g., Mylotarg™, Wyeth-Ayerst, Madison, NJ, a recombinant humanized IgG₄ kappa antibody conjugated to antitumor antibiotic calicheamicin) or a maytansinoid (e.g., taxane-based Tumor-Activated Prodrug, TAP, platform, ImmunoGen, Cambridge, MA, also see e.g., US Patent 5,416,064).

Although 109P1D4 antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well. Fan *et al.* (Cancer Res. 53:4637-4642, 1993), Prewett *et al.* (International J. of Onco. 9:217-224, 1996), and Hancock *et al.* (Cancer Res. 51:4575-4580, 1991) describe the use of various antibodies together with chemotherapeutic agents.

Although 109P1D4 antibody therapy is useful for all stages of cancer, antibody therapy can be particularly

appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well.

Cancer patients can be evaluated for the presence and level of 109P1D4 expression, preferably using immunohistochemical assessments of tumor tissue, quantitative 109P1D4 imaging, or other techniques that reliably indicate the presence and degree of 109P1D4 expression. Immunohistochemical analysis of tumor biopsies or surgical specimens is preferred for this purpose. Methods for immunohistochemical analysis of tumor tissues are well known in the art.

Anti-109P1D4 monoclonal antibodies that treat prostate and other cancers include those that initiate a potent immune response against the tumor or those that are directly cytotoxic. In this regard, anti-109P1D4 monoclonal antibodies (mAbs) can elicit tumor cell lysis by either complement-mediated or antibody-dependent cell cytotoxicity (ADCC) mechanisms, both of which require an intact Fc portion of the immunoglobulin molecule for interaction with effector cell Fc receptor sites on complement proteins. In addition, anti-109P1D4 mAbs that exert a direct biological effect on tumor growth are useful to treat cancers that express 109P1D4. Mechanisms by which directly cytotoxic mAbs act include: inhibition of cell growth, modulation of cellular differentiation, modulation of tumor angiogenesis factor profiles, and the induction of apoptosis. The mechanism(s) by which a particular anti-109P1D4 mAb exerts an anti-tumor effect is evaluated using any number of *in vitro* assays that evaluate cell death such as ADCC, ADMMC, complement-mediated cell lysis, and so forth, as is generally known in the art.

In some patients, the use of murine or other non-human monoclonal antibodies, or human/mouse chimeric mAbs can induce moderate to strong immune responses against the non-human antibody. This can result in clearance of the antibody from circulation and reduced efficacy. In the most severe cases, such an immune response can lead to the extensive formation of immune complexes which, potentially, can cause renal failure. Accordingly, preferred monoclonal antibodies used in the therapeutic methods of the invention are those that are either fully human or humanized and that bind specifically to the target 109P1D4 antigen with high affinity but exhibit low or no antigenicity in the patient.

Therapeutic methods of the invention contemplate the administration of single anti-109P1D4 mAbs as well as combinations, or cocktails, of different mAbs. Such mAb cocktails can have certain advantages inasmuch as they contain mAbs that target different epitopes, exploit different effector mechanisms or combine directly cytotoxic mAbs with mAbs that rely on immune effector functionality. Such mAbs in combination can exhibit synergistic therapeutic effects. In addition, anti-109P1D4 mAbs can be administered concomitantly with other therapeutic modalities, including but not limited to various chemotherapeutic agents, androgen-blockers, immune modulators (e.g., IL-2, GM-CSF), surgery or radiation. The anti-109P1D4 mAbs are administered in their "naked" or unconjugated form, or can have a therapeutic agent(s) conjugated to them.

Anti-109P1D4 antibody formulations are administered via any route capable of delivering the antibodies to a tumor cell. Routes of administration include, but are not limited to, intravenous, intraperitoneal, intramuscular, intratumor, intradermal, and the like. Treatment generally involves repeated administration of the anti-109P1D4 antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1, .2, .3, .4, .5, .6, .7, .8, .9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 mg/kg body weight. In general, doses in the range of 10-1000 mg mAb per week are effective and well tolerated.

Based on clinical experience with the Herceptin™ mAb in the treatment of metastatic breast cancer, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti-

109P1D4 mAb preparation represents an acceptable dosing regimen. Preferably, the initial loading dose is administered as a 90-minute or longer infusion. The periodic maintenance dose is administered as a 30 minute or longer infusion, provided the initial dose was well tolerated. As appreciated by those of skill in the art, various factors can influence the ideal dose regimen in a particular case. Such factors include, for example, the binding affinity and half life of the Ab or mAbs used, the degree of 109P1D4 expression in the patient, the extent of circulating shed 109P1D4 antigen, the desired steady-state antibody concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient.

Optionally, patients should be evaluated for the levels of 109P1D4 in a given sample (e.g. the levels of circulating 109P1D4 antigen and/or 109P1D4 expressing cells) in order to assist in the determination of the most effective dosing regimen, etc. Such evaluations are also used for monitoring purposes throughout therapy, and are useful to gauge therapeutic success in combination with the evaluation of other parameters (for example, urine cytology and/or ImmunoCyt levels in bladder cancer therapy, or by analogy, serum PSA levels in prostate cancer therapy).

Anti-idiotypic anti-109P1D4 antibodies can also be used in anti-cancer therapy as a vaccine for inducing an immune response to cells expressing a 109P1D4-related protein. In particular, the generation of anti-idiotypic antibodies is well known in the art; this methodology can readily be adapted to generate anti-idiotypic anti-109P1D4 antibodies that mimic an epitope on a 109P1D4-related protein (see, for example, Wagner *et al.*, 1997, *Hybridoma* 16: 33-40; Foon *et al.*, 1995, *J. Clin. Invest.* 96:334-342; Herlyn *et al.*, 1996, *Cancer Immunol. Immunother.* 43:65-76). Such an anti-idiotypic antibody can be used in cancer vaccine strategies.

X.C.) 109P1D4 as a Target for Cellular Immune Responses

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more HLA-binding peptides as described herein are further embodiments of the invention. Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, e.g., recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS). Moreover, an adjuvant such as a synthetic cytosine-phosphorothiolated-guanine-containing (CpG) oligonucleotides has been found to increase CTL responses 10- to 100-fold. (see, e.g. Davila and Celis, *J. Immunol.* 165:539-547 (2000))

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes

at least partially immune to later development of cells that express or overexpress 109P1D4 antigen, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and/or helper T cell responses directed to the target antigen. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a cross reactive HTL epitope such as PADRE™ (Epimmune, San Diego, CA) molecule (described e.g., in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, e.g., with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*. Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polypeptidic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. It is preferred that each of the following principles be balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with tumor clearance. For HLA Class I this includes 3-4 epitopes that come from at least one tumor associated antigen (TAA). For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one TAA (see, e.g., Rosenberg *et al.*, *Science* 278:1447-1450). Epitopes from one TAA may be used in combination with epitopes from one or more additional TAAs to produce a vaccine that targets tumors with varying expression patterns of frequently-expressed TAAs.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC₅₀ of 500 nM or less, often 200 nM or less; and for Class II an IC₅₀ of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise B cell, HLA class I and/or HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polypeptidic protein is created, or when creating a minigene, an objective is to generate the smallest

peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

7.) Where the sequences of multiple variants of the same target protein are present, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

X.C.1. Minigene Vaccines

A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding supermotif- and/or motif-bearing epitopes derived 109P1D4, the PADRE® universal helper T cell epitope or multiple HTL epitopes from 109P1D4 (see e.g., Tables VIII-XXI and XXII to XLIX), and an endoplasmic reticulum-translocating signal sequence can be engineered. A vaccine may also comprise epitopes that are derived from other TAAs.

The immunogenicity of a multi-epitopic minigene can be confirmed in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested. Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, antibody epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified

and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, e.g., U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (e.g., IL-2, IL-12, GM-CSF), cytokine-inducing molecules (e.g., LelF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well-known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, e.g., as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7):

682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (⁵¹Cr) labeled and used as target cells for epitope-specific CTL lines; cytotoxicity, detected by ⁵¹Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g., IM for DNA in PBS, intraperitoneal (i.p.) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytotoxicity of peptide-loaded, ⁵¹Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is confirmed in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

Minigenes can also be delivered using other bacterial or viral delivery systems well known in the art, e.g., an expression construct encoding epitopes of the invention can be incorporated into a viral vector such as vaccinia.

X.C.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising CTL peptides of the invention can be modified, e.g., analoged, to provide desired attributes, such as improved serum half life, broadened population coverage or enhanced immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a

genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as *tetanus toxoid* at positions 830-843 QYIKANSKFIGITE; (SEQ ID NO: 40), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 DIEKKIAKMEKASSVFNVNS; (SEQ ID NO: 41), and *Streptococcus* 18kD protein at positions 116-131 GAVDSILGGVATYGAA; (SEQ ID NO: 42). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (see, e.g., PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (e.g., PADRE™, Epimmune, Inc., San Diego, CA) are designed, most preferably, to bind most HLA-DR (human HLA class II) molecules. For instance, a *pan-DR-binding epitope* peptide having the formula: xXVAAWTLKAAx (SEQ ID NO: 43), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

X.C.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes B lymphocytes or T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo*. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, e.g., Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (see, e.g., Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to prime specifically an immune response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P₃CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

X.C.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Pharmacia-Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to 109P1D4.

Optionally, a helper T cell (HTL) peptide, such as a natural or artificial loosely restricted HLA Class II peptide, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention is used to treat a cancer which expresses or overexpresses 109P1D4.

X.D. Adoptive Immunotherapy

Antigenic 109P1D4-related peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (e.g., a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

X.E. Administration of Vaccines for Therapeutic or Prophylactic Purposes

Pharmaceutical and vaccine compositions of the invention are typically used to treat and/or prevent a cancer that expresses or overexpresses 109P1D4. In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective B cell, CTL and/or HTL response to the antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already bearing a tumor that expresses 109P1D4. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. Patients can be treated with the immunogenic peptides separately or in conjunction with other treatments, such as surgery, as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of 109P1D4-associated cancer. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polypeptidic polypeptides, minigenes, or TAA-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in a patient with a tumor that expresses 109P1D4, a vaccine comprising 109P1D4-specific CTL may be more efficacious in killing tumor cells in patient with advanced disease than alternative embodiments.

It is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to stimulate effectively a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months may be administered depending

upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood. Administration should continue until at least clinical symptoms or laboratory tests indicate that the neoplasia, has been eliminated or reduced and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

In certain embodiments, the peptides and compositions of the present invention are employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine can be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, nasal, intrathecal, or local (e.g. as a cream or topical ointment) administration. Preferably, the pharmaceutical compositions are administered parentally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier.

A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well-known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

A human unit dose form of a composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, in one embodiment an aqueous carrier, and is administered in a volume/quantity that is known by those of skill in the art to be used for administration of such compositions to humans (see, e.g., Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985). For example a peptide dose for initial immunization can be from about 1 to about 50,000 μg , generally 100-5,000 μg , for a 70 kg patient. For example, for nucleic acids an initial immunization may be performed using an expression vector in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu.

For antibodies, a treatment generally involves repeated administration of the anti-109P1D4 antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1 to about 10 mg/kg body weight. In general, doses in the range of 10-500 mg mAb per week are effective and well tolerated. Moreover, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti- 109P1D4 mAb preparation represents an acceptable dosing regimen. As appreciated by those of skill in the art, various factors can influence the ideal dose in a particular case. Such factors include, for example, half life of a composition, the binding affinity of an Ab, the immunogenicity of a substance, the degree of 109P1D4 expression in the patient, the extent of circulating shed 109P1D4 antigen, the desired steady-state concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient. Non-limiting preferred human unit doses are, for example, 500 μ g - 1mg, 1mg - 50mg, 50mg - 100mg, 100mg - 200mg, 200mg - 300mg, 400mg - 500mg, 500mg - 600mg, 600mg - 700mg, 700mg - 800mg, 800mg - 900mg, 900mg - 1g, or 1mg - 700mg. In certain embodiments, the dose is in a range of 2-5 mg/kg body weight, e.g., with follow on weekly doses of 1-3 mg/kg; 0.5mg, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10mg/kg body weight followed, e.g., in two, three or four weeks by weekly doses; 0.5 - 10mg/kg body weight, e.g., followed in two, three or four weeks by weekly doses; 225, 250, 275, 300, 325, 350, 375, 400mg m² of body area weekly; 1-600mg m² of body area weekly; 225-400mg m² of body area weekly; these doses can be followed by weekly doses for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more weeks.

In one embodiment, human unit dose forms of polynucleotides comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art a therapeutic effect depends on a number of factors, including the sequence of the polynucleotide, molecular weight of the polynucleotide and route of administration. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. Generally, for a polynucleotide of about 20 bases, a dosage range may be selected from, for example, an independently selected lower limit such as about 0.1, 0.25, 0.5, 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400 or 500 mg/kg up to an independently selected upper limit, greater than the lower limit, of about 60, 80, 100, 200, 300, 400, 500, 750, 1000, 1500, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000 or 10,000 mg/kg. For example, a dose may be about any of the following: 0.1 to 100 mg/kg, 0.1 to 50 mg/kg, 0.1 to 25 mg/kg, 0.1 to 10 mg/kg, 1 to 500 mg/kg, 100 to 400 mg/kg, 200 to 300 mg/kg, 1 to 100 mg/kg, 100 to 200 mg/kg, 300 to 400 mg/kg, 400 to 500 mg/kg, 500 to 1000 mg/kg, 500 to 5000 mg/kg, or 500 to 10,000 mg/kg. Generally, parenteral routes of administration may require higher doses of polynucleotide compared to more direct application to the nucleotide to diseased tissue, as do polynucleotides of increasing length.

In one embodiment, human unit dose forms of T-cells comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art, a therapeutic effect depends on a number of factors. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. A dose may be about 10⁴ cells to about 10⁸ cells, about 10⁶ cells to about 10⁸ cells, about 10⁸ to about 10¹¹ cells, or about 10⁸ to about 5 x 10¹⁰ cells. A dose may also about 10⁶ cells/m² to about 10¹⁰ cells/m², or about 10⁶ cells/m² to about 10⁸ cells/m².

Proteins(s) of the invention, and/or nucleic acids encoding the protein(s), can also be administered via liposomes, which may also serve to: 1) target the proteins(s) to a particular tissue, such as lymphoid tissue; 2) to target selectively to diseased cells; or, 3) to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other

therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are about 0.01%-20% by weight, preferably about 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from about 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute about 0.1%-20% by weight of the composition, preferably about 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal delivery.

XI.) Diagnostic and Prognostic Embodiments of 109P1D4.

As disclosed herein, 109P1D4 polynucleotides, polypeptides, reactive cytotoxic T cells (CTL), reactive helper T cells (HTL) and anti-polypeptide antibodies are used in well known diagnostic, prognostic and therapeutic assays that examine conditions associated with dysregulated cell growth such as cancer, in particular the cancers listed in Table I (see, e.g., both its specific pattern of tissue expression as well as its overexpression in certain cancers as described for example in the Example entitled "Expression analysis of 109P1D4 in normal tissues, and patient specimens").

109P1D4 can be analogized to a prostate associated antigen PSA, the archetypal marker that has been used by medical practitioners for years to identify and monitor the presence of prostate cancer (see, e.g., Merrill *et al.*, *J. Urol.* 163(2): 503-5120 (2000); Polascik *et al.*, *J. Urol.* Aug; 162(2):293-306 (1999) and Fortier *et al.*, *J. Nat. Cancer Inst.* 91(19): 1635-1640(1999)). A variety of other diagnostic markers are also used in similar contexts including p53 and K-ras (see, e.g., Tulchinsky *et al.*, *Int J Mol Med* 1999 Jul 4(1):99-102 and Minimoto *et al.*, *Cancer Detect Prev* 2000;24(1):1-12). Therefore, this disclosure of 109P1D4 polynucleotides and polypeptides (as well as 109P1D4 polynucleotide probes and anti-109P1D4 antibodies used to identify the presence of these molecules) and their properties allows skilled artisans to utilize these molecules in methods that are analogous to those used, for example, in a variety of diagnostic assays directed to examining conditions associated with cancer.

Typical embodiments of diagnostic methods which utilize the 109P1D4 polynucleotides, polypeptides, reactive T

cells and antibodies are analogous to those methods from well-established diagnostic assays, which employ, e.g., PSA polynucleotides, polypeptides, reactive T cells and antibodies. For example, just as PSA polynucleotides are used as probes (for example in Northern analysis, see, e.g., Sharief *et al.*, *Biochem. Mol. Biol. Int.* 33(3):567-74(1994)) and primers (for example in PCR analysis, see, e.g., Okegawa *et al.*, *J. Urol.* 163(4): 1189-1190 (2000)) to observe the presence and/or the level of PSA mRNAs in methods of monitoring PSA overexpression or the metastasis of prostate cancers, the 109P1D4 polynucleotides described herein can be utilized in the same way to detect 109P1D4 overexpression or the metastasis of prostate and other cancers expressing this gene. Alternatively, just as PSA polypeptides are used to generate antibodies specific for PSA which can then be used to observe the presence and/or the level of PSA proteins in methods to monitor PSA protein overexpression (see, e.g., Stephan *et al.*, *Urology* 55(4):560-3 (2000)) or the metastasis of prostate cells (see, e.g., Alanen *et al.*, *Pathol. Res. Pract.* 192(3):233-7 (1996)), the 109P1D4 polypeptides described herein can be utilized to generate antibodies for use in detecting 109P1D4 overexpression or the metastasis of prostate cells and cells of other cancers expressing this gene.

Specifically, because metastases involves the movement of cancer cells from an organ of origin (such as the lung or prostate gland etc.) to a different area of the body (such as a lymph node), assays which examine a biological sample for the presence of cells expressing 109P1D4 polynucleotides and/or polypeptides can be used to provide evidence of metastasis. For example, when a biological sample from tissue that does not normally contain 109P1D4-expressing cells (lymph node) is found to contain 109P1D4-expressing cells such as the 109P1D4 expression seen in LAPC4 and LAPC9, xenografts isolated from lymph node and bone metastasis, respectively, this finding is indicative of metastasis.

Alternatively 109P1D4 polynucleotides and/or polypeptides can be used to provide evidence of cancer, for example, when cells in a biological sample that do not normally express 109P1D4 or express 109P1D4 at a different level are found to express 109P1D4 or have an increased expression of 109P1D4 (see, e.g., the 109P1D4 expression in the cancers listed in Table I and in patient samples etc. shown in the accompanying Figures). In such assays, artisans may further wish to generate supplementary evidence of metastasis by testing the biological sample for the presence of a second tissue restricted marker (in addition to 109P1D4) such as PSA, PSCA etc. (see, e.g., Alanen *et al.*, *Pathol. Res. Pract.* 192(3): 233-237 (1996)).

The use of immunohistochemistry to identify the presence of a 109P1D4 polypeptide within a tissue section can indicate an altered state of certain cells within that tissue. It is well understood in the art that the ability of an antibody to localize to a polypeptide that is expressed in cancer cells is a way of diagnosing presence of disease, disease stage, progression and/or tumor aggressiveness. Such an antibody can also detect an altered distribution of the polypeptide within the cancer cells, as compared to corresponding non-malignant tissue.

The 109P1D4 polypeptide and immunogenic compositions are also useful in view of the phenomena of altered subcellular protein localization in disease states. Alteration of cells from normal to diseased state causes changes in cellular morphology and is often associated with changes in subcellular protein localization/distribution. For example, cell membrane proteins that are expressed in a polarized manner in normal cells can be altered in disease, resulting in distribution of the protein in a non-polar manner over the whole cell surface.

The phenomenon of altered subcellular protein localization in a disease state has been demonstrated with MUC1 and Her2 protein expression by use of immunohistochemical means. Normal epithelial cells have a typical apical distribution of MUC1, in addition to some supranuclear localization of the glycoprotein, whereas malignant lesions often demonstrate an apolar staining pattern (Diaz *et al.*, *The Breast Journal*, 7: 40-45 (2001); Zhang *et al.*, *Clinical Cancer Research*, 4: 2669-2676 (1998); Cao, *et al.*, *The Journal of Histochemistry and Cytochemistry*, 45: 1547-1557 (1997)). In addition, normal breast epithelium is either negative for Her2 protein or exhibits only a basolateral distribution whereas malignant cells can express

the protein over the whole cell surface (De Potter, *et al*, International Journal of Cancer, 44: 969-974 (1989); McCormick, *et al*, 117: 935-943 (2002)). Alternatively, distribution of the protein may be altered from a surface only localization to include diffuse cytoplasmic expression in the diseased state. Such an example can be seen with MUC1 (Diaz, *et al*, The Breast Journal, 7: 40-45 (2001)).

Alteration in the localization/distribution of a protein in the cell, as detected by immunohistochemical methods, can also provide valuable information concerning the favorability of certain treatment modalities. This last point is illustrated by a situation where a protein may be intracellular in normal tissue, but cell surface in malignant cells; the cell surface location makes the cells favorably amenable to antibody-based diagnostic and treatment regimens. When such an alteration of protein localization occurs for 109P1D4, the 109P1D4 protein and immune responses related thereto are very useful. Accordingly, the ability to determine whether alteration of subcellular protein localization occurred for 24P4C12 make the 109P1D4 protein and immune responses related thereto very useful. Use of the 109P1D4 compositions allows those skilled in the art to make important diagnostic and therapeutic decisions.

Immunohistochemical reagents specific to 109P1D4 are also useful to detect metastases of tumors expressing 109P1D4 when the polypeptide appears in tissues where 109P1D4 is not normally produced.

Thus, 109P1D4 polypeptides and antibodies resulting from immune responses thereto are useful in a variety of important contexts such as diagnostic, prognostic, preventative and/or therapeutic purposes known to those skilled in the art.

Just as PSA polynucleotide fragments and polynucleotide variants are employed by skilled artisans for use in methods of monitoring PSA, 109P1D4 polynucleotide fragments and polynucleotide variants are used in an analogous manner. In particular, typical PSA polynucleotides used in methods of monitoring PSA are probes or primers which consist of fragments of the PSA cDNA sequence. Illustrating this, primers used to PCR amplify a PSA polynucleotide must include less than the whole PSA sequence to function in the polymerase chain reaction. In the context of such PCR reactions, skilled artisans generally create a variety of different polynucleotide fragments that can be used as primers in order to amplify different portions of a polynucleotide of interest or to optimize amplification reactions (see, e.g., Caetano-Anolles, G. Biotechniques 25(3): 472-476, 478-480 (1998); Robertson *et al.*, Methods Mol. Biol. 98:121-154 (1998)). An additional illustration of the use of such fragments is provided in the Example entitled "Expression analysis of 109P1D4 in normal tissues, and patient specimens," where a 109P1D4 polynucleotide fragment is used as a probe to show the expression of 109P1D4 RNAs in cancer cells. In addition, variant polynucleotide sequences are typically used as primers and probes for the corresponding mRNAs in PCR and Northern analyses (see, e.g., Sawai *et al.*, Fetal Diagn. Ther. 1996 Nov-Dec 11(6):407-13 and Current Protocols In Molecular Biology, Volume 2, Unit 2, Frederick M. Ausubel *et al.* eds., 1995)). Polynucleotide fragments and variants are useful in this context where they are capable of binding to a target polynucleotide sequence (e.g., a 109P1D4 polynucleotide shown in Figure 2 or variant thereof) under conditions of high stringency.

Furthermore, PSA polypeptides which contain an epitope that can be recognized by an antibody or T cell that specifically binds to that epitope are used in methods of monitoring PSA. 109P1D4 polypeptide fragments and polypeptide analogs or variants can also be used in an analogous manner. This practice of using polypeptide fragments or polypeptide variants to generate antibodies (such as anti-PSA antibodies or T cells) is typical in the art with a wide variety of systems such as fusion proteins being used by practitioners (see, e.g., Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubel *et al.* eds., 1995). In this context, each epitope(s) functions to provide the architecture with which an antibody or T cell is reactive. Typically, skilled artisans create a variety of different polypeptide fragments that can be used in order to generate immune responses specific for different portions of a polypeptide of interest (see, e.g., U.S. Patent No. 5,840,501 and U.S. Patent No. 5,939,533). For example it may be preferable to utilize a polypeptide comprising one of the 109P1D4 biological motifs discussed herein or a motif-bearing subsequence which is readily identified by one of skill in the

art based on motifs available in the art. Polypeptide fragments, variants or analogs are typically useful in this context as long as they comprise an epitope capable of generating an antibody or T cell specific for a target polypeptide sequence (e.g. a 109P1D4 polypeptide shown in Figure 3).

As shown herein, the 109P1D4 polynucleotides and polypeptides (as well as the 109P1D4 polynucleotide probes and anti-109P1D4 antibodies or T cells used to identify the presence of these molecules) exhibit specific properties that make them useful in diagnosing cancers such as those listed in Table I. Diagnostic assays that measure the presence of 109P1D4 gene products, in order to evaluate the presence or onset of a disease condition described herein, such as prostate cancer, are used to identify patients for preventive measures or further monitoring, as has been done so successfully with PSA. Moreover, these materials satisfy a need in the art for molecules having similar or complementary characteristics to PSA in situations where, for example, a definite diagnosis of metastasis of prostatic origin cannot be made on the basis of a test for PSA alone (see, e.g., Alanen *et al.*, *Pathol. Res. Pract.* 192(3): 233-237 (1996)), and consequently, materials such as 109P1D4 polynucleotides and polypeptides (as well as the 109P1D4 polynucleotide probes and anti-109P1D4 antibodies used to identify the presence of these molecules) need to be employed to confirm a metastases of prostatic origin.

Finally, in addition to their use in diagnostic assays, the 109P1D4 polynucleotides disclosed herein have a number of other utilities such as their use in the identification of oncogenetic associated chromosomal abnormalities in the chromosomal region to which the 109P1D4 gene maps (see the Example entitled "Chromosomal Mapping of 109P1D4" below). Moreover, in addition to their use in diagnostic assays, the 109P1D4-related proteins and polynucleotides disclosed herein have other utilities such as their use in the forensic analysis of tissues of unknown origin (see, e.g., Takahama K *Forensic Sci Int* 1996 Jun 28;80(1-2): 63-9).

Additionally, 109P1D4-related proteins or polynucleotides of the invention can be used to treat a pathologic condition characterized by the over-expression of 109P1D4. For example, the amino acid or nucleic acid sequence of Figure 2 or Figure 3, or fragments of either, can be used to generate an immune response to a 109P1D4 antigen. Antibodies or other molecules that react with 109P1D4 can be used to modulate the function of this molecule, and thereby provide a therapeutic benefit.

XII.) Inhibition of 109P1D4 Protein Function

The invention includes various methods and compositions for inhibiting the binding of 109P1D4 to its binding partner or its association with other protein(s) as well as methods for inhibiting 109P1D4 function.

XII.A.) Inhibition of 109P1D4 With Intracellular Antibodies

In one approach, a recombinant vector that encodes single chain antibodies that specifically bind to 109P1D4 are introduced into 109P1D4 expressing cells via gene transfer technologies. Accordingly, the encoded single chain anti-109P1D4 antibody is expressed intracellularly, binds to 109P1D4 protein, and thereby inhibits its function. Methods for engineering such intracellular single chain antibodies are well known. Such intracellular antibodies, also known as "intrabodies", are specifically targeted to a particular compartment within the cell, providing control over where the inhibitory activity of the treatment is focused. This technology has been successfully applied in the art (for review, see Richardson and Marasco, 1995, *TIBTECH* vol. 13). Intrabodies have been shown to virtually eliminate the expression of otherwise abundant cell surface receptors (see, e.g., Richardson *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92: 3137-3141; Beerli *et al.*, 1994, *J. Biol. Chem.* 269: 23931-23936; Deshane *et al.*, 1994, *Gene Ther.* 1: 332-337).

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker

polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to target precisely the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

In one embodiment, intrabodies are used to capture 109P1D4 in the nucleus, thereby preventing its activity within the nucleus. Nuclear targeting signals are engineered into such 109P1D4 intrabodies in order to achieve the desired targeting. Such 109P1D4 intrabodies are designed to bind specifically to a particular 109P1D4 domain. In another embodiment, cytosolic intrabodies that specifically bind to a 109P1D4 protein are used to prevent 109P1D4 from gaining access to the nucleus, thereby preventing it from exerting any biological activity within the nucleus (e.g., preventing 109P1D4 from forming transcription complexes with other factors).

In order to specifically direct the expression of such intrabodies to particular cells, the transcription of the intrabody is placed under the regulatory control of an appropriate tumor-specific promoter and/or enhancer. In order to target intrabody expression specifically to prostate, for example, the PSA promoter and/or promoter/enhancer can be utilized (See, for example, U.S. Patent No. 5,919,652 issued 6 July 1999).

XII.B.) Inhibition of 109P1D4 with Recombinant Proteins

In another approach, recombinant molecules bind to 109P1D4 and thereby inhibit 109P1D4 function. For example, these recombinant molecules prevent or inhibit 109P1D4 from accessing/binding to its binding partner(s) or associating with other protein(s). Such recombinant molecules can, for example, contain the reactive part(s) of a 109P1D4 specific antibody molecule. In a particular embodiment, the 109P1D4 binding domain of a 109P1D4 binding partner is engineered into a dimeric fusion protein, whereby the fusion protein comprises two 109P1D4 ligand binding domains linked to the Fc portion of a human IgG, such as human IgG1. Such IgG portion can contain, for example, the C_H2 and C_H3 domains and the hinge region, but not the C_H1 domain. Such dimeric fusion proteins are administered in soluble form to patients suffering from a cancer associated with the expression of 109P1D4, whereby the dimeric fusion protein specifically binds to 109P1D4 and blocks 109P1D4 interaction with a binding partner. Such dimeric fusion proteins are further combined into multimeric proteins using known antibody linking technologies.

XII.C.) Inhibition of 109P1D4 Transcription or Translation

The present invention also comprises various methods and compositions for inhibiting the transcription of the 109P1D4 gene. Similarly, the invention also provides methods and compositions for inhibiting the translation of 109P1D4 mRNA into protein.

In one approach, a method of inhibiting the transcription of the 109P1D4 gene comprises contacting the 109P1D4 gene with a 109P1D4 antisense polynucleotide. In another approach, a method of inhibiting 109P1D4 mRNA translation comprises contacting a 109P1D4 mRNA with an antisense polynucleotide. In another approach, a 109P1D4 specific ribozyme is used to cleave a 109P1D4 message, thereby inhibiting translation. Such antisense and ribozyme based methods can also be directed to the regulatory regions of the 109P1D4 gene, such as 109P1D4 promoter and/or enhancer

elements. Similarly, proteins capable of inhibiting a 109P1D4 gene transcription factor are used to inhibit 109P1D4 mRNA transcription. The various polynucleotides and compositions useful in the aforementioned methods have been described above. The use of antisense and ribozyme molecules to inhibit transcription and translation is well known in the art.

Other factors that inhibit the transcription of 109P1D4 by interfering with 109P1D4 transcriptional activation are also useful to treat cancers expressing 109P1D4. Similarly, factors that interfere with 109P1D4 processing are useful to treat cancers that express 109P1D4. Cancer treatment methods utilizing such factors are also within the scope of the invention.

XII.D.) General Considerations for Therapeutic Strategies

Gene transfer and gene therapy technologies can be used to deliver therapeutic polynucleotide molecules to tumor cells synthesizing 109P1D4 (i.e., antisense, ribozyme, polynucleotides encoding intrabodies and other 109P1D4 inhibitory molecules). A number of gene therapy approaches are known in the art. Recombinant vectors encoding 109P1D4 antisense polynucleotides, ribozymes, factors capable of interfering with 109P1D4 transcription, and so forth, can be delivered to target tumor cells using such gene therapy approaches.

The above therapeutic approaches can be combined with any one of a wide variety of surgical, chemotherapy or radiation therapy regimens. The therapeutic approaches of the invention can enable the use of reduced dosages of chemotherapy (or other therapies) and/or less frequent administration, an advantage for all patients and particularly for those that do not tolerate the toxicity of the chemotherapeutic agent well.

The anti-tumor activity of a particular composition (e.g., antisense, ribozyme, intrabody), or a combination of such compositions, can be evaluated using various *in vitro* and *in vivo* assay systems. *In vitro* assays that evaluate therapeutic activity include cell growth assays, soft agar assays and other assays indicative of tumor promoting activity, binding assays capable of determining the extent to which a therapeutic composition will inhibit the binding of 109P1D4 to a binding partner, etc.

In vivo, the effect of a 109P1D4 therapeutic composition can be evaluated in a suitable animal model. For example, xenogenic prostate cancer models can be used, wherein human prostate cancer explants or passaged xenograft tissues are introduced into immune compromised animals, such as nude or SCID mice (Klein *et al.*, 1997, Nature Medicine 3: 402-408). For example, PCT Patent Application WO98/16628 and U.S. Patent 6,107,540 describe various xenograft models of human prostate cancer capable of recapitulating the development of primary tumors, micrometastasis, and the formation of osteoblastic metastases characteristic of late stage disease. Efficacy can be predicted using assays that measure inhibition of tumor formation, tumor regression or metastasis, and the like.

In vivo assays that evaluate the promotion of apoptosis are useful in evaluating therapeutic compositions. In one embodiment, xenografts from tumor bearing mice treated with the therapeutic composition can be examined for the presence of apoptotic foci and compared to untreated control xenograft-bearing mice. The extent to which apoptotic foci are found in the tumors of the treated mice provides an indication of the therapeutic efficacy of the composition.

The therapeutic compositions used in the practice of the foregoing methods can be formulated into pharmaceutical compositions comprising a carrier suitable for the desired delivery method. Suitable carriers include any material that when combined with the therapeutic composition retains the anti-tumor function of the therapeutic composition and is generally non-reactive with the patient's immune system. Examples include, but are not limited to, any of a number of standard pharmaceutical carriers such as sterile phosphate buffered saline solutions, bacteriostatic water, and the like (see, generally, Remington's Pharmaceutical Sciences 16th Edition, A. Osal., Ed., 1980).

Therapeutic formulations can be solubilized and administered via any route capable of delivering the therapeutic composition to the tumor site. Potentially effective routes of administration include, but are not limited to, intravenous, parenteral, intraperitoneal, intramuscular, intratumor, intradermal, intraorgan, orthotopic, and the like. A preferred

formulation for intravenous injection comprises the therapeutic composition in a solution of preserved bacteriostatic water, sterile unpreserved water, and/or diluted in polyvinylchloride or polyethylene bags containing 0.9% sterile Sodium Chloride for Injection, USP. Therapeutic protein preparations can be lyophilized and stored as sterile powders, preferably under vacuum, and then reconstituted in bacteriostatic water (containing for example, benzyl alcohol preservative) or in sterile water prior to injection.

Dosages and administration protocols for the treatment of cancers using the foregoing methods will vary with the method and the target cancer, and will generally depend on a number of other factors appreciated in the art.

XIII.) Identification, Characterization and Use of Modulators of 109P1D4

Methods to Identify and Use Modulators

In one embodiment, screening is performed to identify modulators that induce or suppress a particular expression profile, suppress or induce specific pathways, preferably generating the associated phenotype thereby. In another embodiment, having identified differentially expressed genes important in a particular state; screens are performed to identify modulators that alter expression of individual genes, either increase or decrease. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens are done for genes that are induced in response to a candidate agent. After identifying a modulator (one that suppresses a cancer expression pattern leading to a normal expression pattern, or a modulator of a cancer gene that leads to expression of the gene as in normal tissue) a screen is performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent-treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue, and vice versa. These agent-specific sequences are identified and used by methods described herein for cancer genes or proteins. In particular these sequences and the proteins they encode are used in marking or identifying agent-treated cells. In addition, antibodies are raised against the agent-induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Modulator-related Identification and Screening Assays:

Gene Expression-related Assays

Proteins, nucleic acids, and antibodies of the invention are used in screening assays. The cancer-associated proteins, antibodies, nucleic acids, modified proteins and cells containing these sequences are used in screening assays, such as evaluating the effect of drug candidates on a "gene expression profile," expression profile of polypeptides or alteration of biological function. In one embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Davis, GF, et al, J Biol Screen 7:69 (2002); Zlokam, et al., Science 279:84-8 (1998); Heid, Genome Res 6:986-94,1996).

The cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins or genes are used in screening assays. That is, the present invention comprises methods for screening for compositions which modulate the cancer phenotype or a physiological function of a cancer protein of the invention. This is done on a gene itself or by evaluating the effect of drug candidates on a "gene expression profile" or biological function. In one embodiment, expression profiles are used, preferably in conjunction with high throughput screening techniques to allow

monitoring after treatment with a candidate agent, see Zlokamik, supra.

A variety of assays are executed directed to the genes and proteins of the invention. Assays are run on an individual nucleic acid or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds are screened for the ability to modulate gene expression or for binding to the cancer protein of the invention. "Modulation" in this context includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue a target value of a 10-fold increase in expression by the test compound is often desired. Modulators that exacerbate the type of gene expression seen in cancer are also useful, e.g., as an upregulated target in further analyses.

The amount of gene expression is monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, a gene product itself is monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques also allow for quantification of expression.

Expression Monitoring to Identify Compounds that Modify Gene Expression

In one embodiment, gene expression monitoring, i.e., an expression profile, is monitored simultaneously for a number of entities. Such profiles will typically involve one or more of the genes of Figure 2. In this embodiment, e.g., cancer nucleic acid probes are attached to biochips to detect and quantify cancer sequences in a particular cell. Alternatively, PCR can be used. Thus, a series, e.g., wells of a microtiter plate, can be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring is performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in Figure 2. Generally, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins of the invention, bind to a cancer protein of the invention, or interfere with the binding of a cancer protein of the invention and an antibody or other binding partner.

In one embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds," as compounds for screening, or as therapeutics.

In certain embodiments, combinatorial libraries of potential modulators are screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

As noted above, gene expression monitoring is conveniently used to test candidate modulators (e.g., protein, nucleic acid or small molecule). After the candidate agent has been added and the cells allowed to incubate for a period, the sample containing a target sequence to be analyzed is, e.g., added to a biochip.

If required, the target sequence is prepared using known techniques. For example, a sample is treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally,

the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

The target sequence can be labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that is detected. Alternatively, the label is a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5, 681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124, 246; and 5,681,697. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions are used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc. These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus, it can be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein can be accomplished in a variety of ways. Components of the reaction can be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, etc. which can be used to facilitate optimal hybridization and detection, and/or reduce nonspecific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target. The assay data are analyzed to determine the expression levels of individual genes, and changes in expression levels as between states, forming a gene expression profile.

Biological Activity-related Assays

The invention provides methods identify or screen for a compound that modulates the activity of a cancer-related gene or protein of the invention. The methods comprise adding a test compound, as defined above, to a cell comprising a cancer protein of the invention. The cells contain a recombinant nucleic acid that encodes a cancer protein of the invention. In another embodiment, a library of candidate agents is tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e., cell-cell contacts). In another example, the determinations are made at different stages of the cell cycle process. In this way, compounds that modulate genes or proteins of the invention are identified. Compounds with pharmacological activity are able to enhance or

interfere with the activity of the cancer protein of the invention. Once identified, similar structures are evaluated to identify critical structural features of the compound.

In one embodiment, a method of modulating (e.g., inhibiting) cancer cell division is provided; the method comprises administration of a cancer modulator. In another embodiment, a method of modulating (e.g., inhibiting) cancer is provided; the method comprises administration of a cancer modulator. In a further embodiment, methods of treating cells or individuals with cancer are provided; the method comprises administration of a cancer modulator.

In one embodiment, a method for modulating the status of a cell that expresses a gene of the invention is provided. As used herein status comprises such art-accepted parameters such as growth, proliferation, survival, function, apoptosis, senescence, location, enzymatic activity, signal transduction, etc. of a cell. In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule. A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described herein.

High Throughput Screening to Identify Modulators

The assays to identify suitable modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

In one embodiment, modulators evaluated in high throughput screening methods are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, are used. In this way, libraries of proteins are made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes, or ligands and receptors.

Use of Soft Agar Growth and Colony Formation to Identify and Characterize Modulators

Normal cells require a solid substrate to attach and grow. When cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, can regenerate normal phenotype and once again require a solid substrate to attach to and grow. Soft agar growth or colony formation in assays are used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A modulator reduces or eliminates the host cells' ability to grow suspended in solid or semisolid media, such as agar.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, Culture of Animal Cells a Manual of Basic Technique (3rd ed., 1994). See also, the methods section of Garkavtsev et al. (1996), *supra*.

Evaluation of Contact Inhibition and Growth Density Limitation to Identify and Characterize Modulators

Normal cells typically grow in a flat and organized pattern in cell culture until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. Transformed cells, however, are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, transformed cells grow to a higher saturation density than corresponding normal cells. This is detected morphologically by the formation of a disoriented monolayer of cells or cells in foci. Alternatively, labeling index with (³H)-thymidine at saturation density is used to measure density limitation of growth, similarly an MTT or Alamar blue assay will reveal proliferation capacity of cells and the ability of modulators to affect same. See Freshney (1994), *supra*. Transformed cells, when transfected with tumor suppressor genes, can regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with ^3H -thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with ^3H -thymidine is determined by incorporated cpm.

Contact independent growth is used to identify modulators of cancer sequences, which had led to abnormal cellular proliferation and transformation. A modulator reduces or eliminates contact independent growth, and returns the cells to a normal phenotype.

Evaluation of Growth Factor or Serum Dependence to Identify and Characterize Modulators

Transformed cells have lower serum dependence than their normal counterparts (see, e.g., Temin, J. Natl. Cancer Inst. 37:167-175 (1966); Eagle et al., J. Exp. Med 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. The degree of growth factor or serum dependence of transformed host cells can be compared with that of control. For example, growth factor or serum dependence of a cell is monitored in methods to identify and characterize compounds that modulate cancer-associated sequences of the invention.

Use of Tumor-specific Marker Levels to Identify and Characterize Modulators

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, Angiogenesis, Tumor Vascularization, and Potential Interference with Tumor Growth, in Biological Responses in Cancer, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor Angiogenesis Factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman, Angiogenesis and Cancer, Sem Cancer Biol. (1992)), while bFGF is released from endothelial tumors (Ensolli, B et al).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkless et al., J. Biol. Chem. 249:4295-4305 (1974); Strickland & Beers, J. Biol. Chem. 251:5694-5702 (1976); Whur et al., Br. J. Cancer 42:305-312 (1980); Gullino, Angiogenesis, Tumor Vascularization, and Potential Interference with Tumor Growth, in Biological Responses in Cancer, pp. 178-184 (Mihich (ed.) 1985); Freshney, Anticancer Res. 5:111-130 (1985). For example, tumor specific marker levels are monitored in methods to identify and characterize compounds that modulate cancer-associated sequences of the invention.

Invasiveness into Matrigel to Identify and Characterize Modulators

The degree of invasiveness into Matrigel or an extracellular matrix constituent can be used as an assay to identify and characterize compounds that modulate cancer associated sequences. Tumor cells exhibit a positive correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells. Techniques described in Cancer Res. 1999; 59:6010; Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells is measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeled the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Evaluation of Tumor Growth *In Vivo* to Identify and Characterize Modulators

Effects of cancer-associated sequences on cell growth are tested in transgenic or immune-suppressed organisms. Transgenic organisms are prepared in a variety of art-accepted ways. For example, knock-out transgenic organisms, e.g., mammals such as mice, are made, in which a cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice are made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in

the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

To prepare transgenic chimeric animals, e.g., mice, a DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells some of which are derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi et al., *Science* 244:1288 (1989)). Chimeric mice can be derived according to US Patent 6,365,797, issued 2 April 2002; US Patent 6,107,540 issued 22 August 2000; Hogan et al., *Manipulating the Mouse Embryo: A laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, a genetically athymic "nude" mouse (see, e.g., Giovanella et al., *J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley et al., *Br. J. Cancer* 38:263 (1978); Selby et al., *Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts produce invasive tumors in a high proportion of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing cancer-associated sequences are injected subcutaneously or orthotopically. Mice are then separated into groups, including control groups and treated experimental groups (e.g. treated with a modulator). After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions, or weight) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

In Vitro Assays to Identify and Characterize Modulators

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as Western blotting, ELISA and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e. g., Northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or P-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art (Davis GF, *supra*; Gonzalez, J. & Negulescu, P. *Curr. Opin. Biotechnol.* 1998: 9:624).

As outlined above, in vitro screens are done on individual genes and gene products. That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself is performed.

In one embodiment, screening for modulators of expression of specific gene(s) is performed. Typically, the expression of only one or a few genes is evaluated. In another embodiment, screens are designed to first find compounds

that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

Binding Assays to Identify and Characterize Modulators

In binding assays in accordance with the invention, a purified or isolated gene product of the invention is generally used. For example, antibodies are generated to a protein of the invention, and immunoassays are run to determine the amount and/or location of protein. Alternatively, cells comprising the cancer proteins are used in the assays.

Thus, the methods comprise combining a cancer protein of the invention and a candidate compound such as a ligand, and determining the binding of the compound to the cancer protein of the invention. Preferred embodiments utilize the human cancer protein; animal models of human disease can also be developed and used. Also, other analogous mammalian proteins also can be used as appreciated by those of skill in the art. Moreover, in some embodiments variant or derivative cancer proteins are used.

Generally, the cancer protein of the invention, or the ligand, is non-diffusibly bound to an insoluble support. The support can, e.g., be one having isolated sample receiving areas (a microtiter plate, an array, etc.). The insoluble supports can be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports can be solid or porous and of any convenient shape.

Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharide, nylon, nitrocellulose, or Teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition to the support is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies which do not sterically block either the ligand binding site or activation sequence when attaching the protein to the support, direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or ligand/binding agent to the support, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

Once a cancer protein of the invention is bound to the support, and a test compound is added to the assay. Alternatively, the candidate binding agent is bound to the support and the cancer protein of the invention is then added. Binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc.

Of particular interest are assays to identify agents that have a low toxicity for human cells. A wide variety of assays can be used for this purpose, including proliferation assays, cAMP assays, labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

A determination of binding of the test compound (ligand, binding agent, modulator, etc.) to a cancer protein of the invention can be done in a number of ways. The test compound can be labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein of the invention to a solid support, adding a labeled candidate compound (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps can be utilized as appropriate.

In certain embodiments, only one of the components is labeled, e.g., a protein of the invention or ligands labeled. Alternatively, more than one component is labeled with different labels, e.g., 125 I, for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

Competitive Binding to Identify and Characterize Modulators

In one embodiment, the binding of the "test compound" is determined by competitive binding assay with a "competitor." The competitor is a binding moiety that binds to the target molecule (e.g., a cancer protein of the invention). Competitors include compounds such as antibodies, peptides, binding partners, ligands, etc. Under certain circumstances, the competitive binding between the test compound and the competitor displaces the test compound. In one embodiment, the test compound is labeled. Either the test compound, the competitor, or both, is added to the protein for a time sufficient to allow binding. Incubations are performed at a temperature that facilitates optimal activity, typically between four and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening; typically between zero and one hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In one embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the post-test compound wash solution indicates displacement by the test compound. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor indicates that the test compound binds to the cancer protein with higher affinity than the competitor. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, indicates that the test compound binds to and thus potentially modulates the cancer protein of the invention.

Accordingly, the competitive binding methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins of the invention. In this embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, the cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. For example the structure of the cancer protein is modeled and used in rational drug design to synthesize agents that interact with that site, agents which generally do not bind to site-modified proteins. Moreover, such drug candidates that affect the activity of a native cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of such proteins.

Positive controls and negative controls can be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples occurs for a time sufficient to allow for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples can be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents can be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., can be used. The mixture of components is added in an order that provides for the requisite binding.

Use of Polynucleotides to Down-regulate or Inhibit a Protein of the Invention.

Polynucleotide modulators of cancer can be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand-binding molecule, as described in WO 91/04753. Suitable ligand-binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer can be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Inhibitory and Antisense Nucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide or inhibitory small nuclear RNA (snRNA), i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein of the invention, mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally occurring nucleotides, or synthetic species formed from naturally occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprised by this invention so long as they function effectively to hybridize with nucleotides of the invention. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 12 nucleotides, preferably from about 12 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (Cancer Res. 48:2659 (1988 and van der Krol et al. (BioTechniques 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different

kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto et al., *Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel et al., *Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0360257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang et al., *Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada et al., *Human Gene Therapy* 1:39-45 (1994); Leavitt et al., *Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt et al., *Human Gene Therapy* 5: 1151-120 (1994); and Yamada et al., *Virology* 205: 121-126 (1994)).

Use of Modulators in Phenotypic Screening

In one embodiment, a test compound is administered to a population of cancer cells, which have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the modulator is added to the cells in such a manner as to allow the modulator to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, a nucleic acid encoding a proteinaceous agent (i.e., a peptide) is put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used. Once the modulator has been administered to the cells, the cells are washed if desired and are allowed to incubate under preferably physiological conditions for some period. The cells are then harvested and a new gene expression profile is generated. Thus, e.g., cancer tissue is screened for agents that modulate, e.g., induce or suppress, the cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. Similarly, altering a biological function or a signaling pathway is indicative of modulator activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype are devised. With this approach, the drug target need not be known and need not be represented in the original gene/protein expression screening platform, nor does the level of transcript for the target protein need to change. The modulator inhibiting function will serve as a surrogate marker.

As outlined above, screens are done to assess genes or gene products. That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself is performed.

Use of Modulators to Affect Peptides of the Invention

Measurements of cancer polypeptide activity, or of the cancer phenotype are performed using a variety of assays. For example, the effects of modulators upon the function of a cancer polypeptide(s) are measured by examining parameters described above. A physiological change that affects activity is used to assess the influence of a test compound on the polypeptides of this invention. When the functional outcomes are determined using intact cells or animals, a variety of effects can be assessed such as, in the case of a cancer associated with solid tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., by Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGNIP.

Methods of Identifying Characterizing Cancer-associated Sequences

Expression of various gene sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes are determined. In one embodiment, the invention provides methods for identifying cells containing

variant cancer genes, e.g., determining the presence of, all or part, the sequence of at least one endogenous cancer gene in a cell. This is accomplished using any number of sequencing techniques. The invention comprises methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one gene of the invention in the individual. This is generally done in at least one tissue of the individual, e.g., a tissue set forth in Table I, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced gene to a known cancer gene, i.e., a wild-type gene to determine the presence of family members, homologues, mutations or variants. The sequence of all or part of the gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This is done using any number of known homology programs, such as BLAST, Bestfit, etc. The presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome. The cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

XIV.) Kits/Articles of Manufacture

For use in the laboratory, prognostic, prophylactic, diagnostic and therapeutic applications described herein, kits are within the scope of the invention. Such kits can comprise a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used in the method, along with a label or insert comprising instructions for use, such as a use described herein. For example, the container(s) can comprise a probe that is or can be detectably labeled. Such probe can be an antibody or polynucleotide specific for a protein or a gene or message of the invention, respectively. Where the method utilizes nucleic acid hybridization to detect the target nucleic acid, the kit can also have containers containing nucleotide(s) for amplification of the target nucleic acid sequence. Kits can comprise a container comprising a reporter, such as a biotin-binding protein, such as avidin or streptavidin, bound to a reporter molecule, such as an enzymatic, fluorescent, or radioisotope label; such a reporter can be used with, e.g., a nucleic acid or antibody. The kit can include all or part of the amino acid sequences in Figure 2 or Figure 3 or analogs thereof, or a nucleic acid molecule that encodes such amino acid sequences.

The kit of the invention will typically comprise the container described above and one or more other containers associated therewith that comprise materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes; carrier, package, container, vial and/or tube labels listing contents and/or instructions for use, and package inserts with instructions for use.

A label can be present on or with the container to indicate that the composition is used for a specific therapy or non-therapeutic application, such as a prognostic, prophylactic, diagnostic or laboratory application, and can also indicate directions for either *in vivo* or *in vitro* use, such as those described herein. Directions and/or other information can also be included on an insert(s) or label(s) which is included with or on the kit. The label can be on or associated with the container. A label can be on a container when letters, numbers or other characters forming the label are molded or etched into the container itself; a label can be associated with a container when it is present within a receptacle or carrier that also holds the container, e.g., as a package insert. The label can indicate that the composition is used for diagnosing, treating, prophylaxing or prognosing a condition, such as a neoplasia of a tissue set forth in Table I.

The terms "kit" and "article of manufacture" can be used as synonyms.

In another embodiment of the invention, an article(s) of manufacture containing compositions, such as amino acid sequence(s), small molecule(s), nucleic acid sequence(s), and/or antibody(s), e.g., materials useful for the diagnosis, prognosis, prophylaxis and/or treatment of neoplasias of tissues such as those set forth in Table I is provided. The article of manufacture typically comprises at least one container and at least one label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers can be formed from a variety of materials such as glass, metal or plastic. The container can hold amino acid sequence(s), small molecule(s), nucleic acid sequence(s), cell population(s) and/or antibody(s). In one embodiment, the container holds a polynucleotide for use in examining the mRNA expression profile of a cell, together with reagents used for this purpose. In another embodiment a container comprises an antibody, binding fragment thereof or specific binding protein for use in evaluating protein expression of 109P1D4 in cells and tissues, or for relevant laboratory, prognostic, diagnostic, prophylactic and therapeutic purposes; indications and/or directions for such uses can be included on or with such container, as can reagents and other compositions or tools used for these purposes. In another embodiment, a container comprises materials for eliciting a cellular or humoral immune response, together with associated indications and/or directions. In another embodiment, a container comprises materials for adoptive immunotherapy, such as cytotoxic T cells (CTL) or helper T cells (HTL), together with associated indications and/or directions; reagents and other compositions or tools used for such purpose can also be included.

The container can alternatively hold a composition that is effective for treating, diagnosis, prognosing or prophylaxing a condition and can have a sterile access port (for example the container can be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agents in the composition can be an antibody capable of specifically binding 109P1D4 and modulating the function of 109P1D4.

The article of manufacture can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and/or dextrose solution. It can further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, stirrers, needles, syringes, and/or package inserts with indications and/or instructions for use.

EXAMPLES:

Various aspects of the invention are further described and illustrated by way of the several examples that follow, none of which is intended to limit the scope of the invention.

Example 1: SSH-Generated Isolation of cDNA Fragment of the 109P1D4 Gene

To isolate genes that are over-expressed in prostate cancer we used the Suppression Subtractive Hybridization (SSH) procedure using cDNA derived from prostate cancer tissues. The 109P1D4 SSH cDNA sequence was from an experiment where cDNA derived from LNCaP cells that was androgen-deprived (by growing in the presence of charcoal-stripped serum) was subtracted from cDNA derived from LNCaP cells that were stimulated with mibolerone for 9 hours.

Materials and Methods

Human Tissues:

The patient cancer and normal tissues were purchased from different sources such as the NDRI (Philadelphia, PA). mRNA for some normal tissues were purchased from different companies such as Clontech, Palo Alto, CA.

RNA Isolation:

Tissues were homogenized in Trizol reagent (Life Technologies, Gibco BRL) using 10 ml/g tissue to isolate total RNA. Poly A RNA was purified from total RNA using Qiagen's Oligotex mRNA Mini and Midi kits. Total and mRNA were quantified by spectrophotometric analysis (O.D. 260/280 nm) and analyzed by gel electrophoresis.

Oligonucleotides:

The following HPLC purified oligonucleotides were used.

DPNCDN (cDNA synthesis primer):

5'TTTTGATCAAGCTT₃₀3' (SEQ ID NO: 44)

Adaptor 1:

5'CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGGCAG3' (SEQ ID NO: 45)

3'GGCCCGTCCTAG5' (SEQ ID NO: 46)

Adaptor 2:

5'GTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAG3' (SEQ ID NO: 47)

3'CGGCTCCTAG5' (SEQ ID NO: 48)

PCR primer 1:

5'CTAATACGACTCACTATAGGGC3' (SEQ ID NO: 49)

Nested primer (NP)1:

5'TCGAGCGGCCGCCGGGCAGGA3' (SEQ ID NO: 50)

Nested primer (NP)2:

5'AGCGTGGTCGCGGCCGAGGA3' (SEQ ID NO: 51)

Suppression Subtractive Hybridization:

Suppression Subtractive Hybridization (SSH) was used to identify cDNAs corresponding to genes that may be differentially expressed in prostate cancer. The SSH reaction utilized cDNA from LNCaP prostate cancer cells.

The 109P1D4 SSH sequence was derived from cDNA subtraction of LNCaP stimulated with mibolerone minus LNCaP in the absence of androgen. The SSH DNA sequence (Figure 1) was identified.

The cDNA derived from androgen-deprived LNCaP cells was used as the source of the "driver" cDNA, while the cDNA from androgen-stimulated LNCaP cells was used as the source of the "tester" cDNA. Double stranded cDNAs corresponding to tester and driver cDNAs were synthesized from 2 µg of poly(A)⁺ RNA isolated from the relevant xenograft tissue, as described above, using CLONTECH's PCR-Select cDNA Subtraction Kit and 1 µg of oligonucleotide DPNCDN as primer. First- and second-strand synthesis were carried out as described in the Kit's user manual protocol (CLONTECH Protocol No. PT1117-1, Catalog No. K1804-1). The resulting cDNA was digested with Dpn II for 3 hrs at 37°C. Digested cDNA was extracted with phenol/chloroform (1:1) and ethanol precipitated.

Tester cDNA was generated by diluting 1 µl of Dpn II digested cDNA from the relevant tissue source (see above) (400 ng) in 5 µl of water. The diluted cDNA (2 µl, 160 ng) was then ligated to 2 µl of Adaptor 1 and Adaptor 2 (10 µM), in separate ligation reactions, in a total volume of 10 µl at 16°C overnight, using 400 µl of T4 DNA ligase (CLONTECH). Ligation was terminated with 1 µl of 0.2 M EDTA and heating at 72°C for 5 min.

The first hybridization was performed by adding 1.5 µl (600 ng) of driver cDNA to each of two tubes containing 1.5 µl (20 ng) Adaptor 1- and Adaptor 2- ligated tester cDNA. In a final volume of 4 µl, the samples were overlaid with mineral oil, denatured in an MJ Research thermal cycler at 98°C for 1.5 minutes, and then were allowed to hybridize for 8 hrs at 68°C. The two hybridizations were then mixed together with an additional 1 µl of fresh denatured driver cDNA and were allowed to hybridize overnight at 68°C. The second hybridization was then diluted in 200 µl of 20 mM Hepes, pH 8.3, 50 mM NaCl, 0.2 mM EDTA, heated at 70°C for 7 min. and stored at -20°C.

PCR Amplification, Cloning and Sequencing of Gene Fragments Generated from SSH:

To amplify gene fragments resulting from SSH reactions, two PCR amplifications were performed. In the primary PCR reaction 1 μ l of the diluted final hybridization mix was added to 1 μ l of PCR primer 1 (10 μ M), 0.5 μ l dNTP mix (10 μ M), 2.5 μ l 10 x reaction buffer (CLONTECH) and 0.5 μ l 50 x Advantage cDNA polymerase Mix (CLONTECH) in a final volume of 25 μ l. PCR 1 was conducted using the following conditions: 75°C for 5 min., 94°C for 25 sec., then 27 cycles of 94°C for 10 sec, 66°C for 30 sec, 72°C for 1.5 min. Five separate primary PCR reactions were performed for each experiment. The products were pooled and diluted 1:10 with water. For the secondary PCR reaction, 1 μ l from the pooled and diluted primary PCR reaction was added to the same reaction mix as used for PCR 1, except that primers NP1 and NP2 (10 μ M) were used instead of PCR primer 1. PCR 2 was performed using 10-12 cycles of 94°C for 10 sec, 68°C for 30 sec, and 72°C for 1.5 minutes. The PCR products were analyzed using 2% agarose gel electrophoresis.

The PCR products were inserted into pCR2.1 using the T/A vector cloning kit (Invitrogen). Transformed *E. coli* were subjected to blue/white and ampicillin selection. White colonies were picked and arrayed into 96 well plates and were grown in liquid culture overnight. To identify inserts, PCR amplification was performed on 1 μ l of bacterial culture using the conditions of PCR1 and NP1 and NP2 as primers. PCR products were analyzed using 2% agarose gel electrophoresis.

Bacterial clones were stored in 20% glycerol in a 96 well format. Plasmid DNA was prepared, sequenced, and subjected to nucleic acid homology searches of the GenBank, dBest, and NCI-CGAP databases.

RT-PCR Expression Analysis:

First strand cDNAs can be generated from 1 μ g of mRNA with oligo (dT)12-18 priming using the Gibco-BRL Superscript Preamplification system. The manufacturer's protocol was used which included an incubation for 50 min at 42°C with reverse transcriptase followed by RNase H treatment at 37°C for 20 min. After completing the reaction, the volume can be increased to 200 μ l with water prior to normalization. First strand cDNAs from 16 different normal human tissues can be obtained from Clontech.

Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'ATATCGCCGCGCTCGTCGACAA3' (SEQ ID NO: 52) and 5'AGCCACACGCAGCTCATTGTAGAAGG 3' (SEQ ID NO: 53) to amplify β -actin. First strand cDNAs (5 μ l) were amplified in a total volume of 50 μ l containing 0.4 μ M primers, 0.2 μ M each dNTPs, 1X PCR buffer (Clontech, 10 mM Tris-HCL, 1.5 mM MgCl₂, 50 mM KCl, pH8.3) and 1X KlenTaq DNA polymerase (Clontech). Five μ l of the PCR reaction can be removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycler under the following conditions: Initial denaturation can be at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 base pair β -actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β -actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization can be required to achieve equal band intensities in all tissues after 22 cycles of PCR.

To determine expression levels of the 109P1D4 gene, 5 μ l of normalized first strand cDNA were analyzed by PCR using 26, and 30 cycles of amplification. Semi-quantitative expression analysis can be achieved by comparing the PCR products at cycle numbers that give light band intensities. The primers used for RT-PCR were designed using the 109P1D4 SSH sequence and are listed below:

109P1D4.1

5'- TGGTCTTTCAGGTAATTGCTGTTG - 3' (SEQ ID NO: 54)

109P1D4.2

5'- CTCCATCAATGTTATGTTGCCTGT - 3' (SEQ ID NO: 55)

A typical RT-PCR expression analysis is shown in Figure 15.

Example 2: Isolation of Full Length 109P1D4 encoding DNA

The 109P1D4 SSH sequence of 192 bp (Figure 1) exhibited homology to protocadherin 11 (PCDH11), a cell adhesion molecule related to the calcium dependent cadherins. The human cDNA sequence encodes a 1021 amino acid protein with an N-terminal leader sequence and a transmembrane domain. 109P1D4 v.1 of 4603bp was cloned from human prostate cancer xenograft LAPC-9AD cDNA library, revealing an ORF of 1021 amino acids (Figure 2 and Figure 3). Other variants (Transcript and SNP) of 109P1D4 were also identified and these are listed sequentially in Figure 2 and Figure 3.

Example 3: Chromosomal Mapping of 109P1D4

Chromosomal localization can implicate genes in disease pathogenesis. Several chromosome mapping approaches are available including fluorescent *in situ* hybridization (FISH), human/hamster radiation hybrid (RH) panels (Walter et al., 1994; Nature Genetics 7:22; Research Genetics, Huntsville AL), human-rodent somatic cell hybrid panels such as is available from the Coriell Institute (Camden, New Jersey), and genomic viewers utilizing BLAST homologies to sequenced and mapped genomic clones (NCBI, Bethesda, Maryland).

109P1D4 maps to chromosome Xq21.3 using 109P1D4 sequence and the NCBI BLAST tool: located on the World Wide Web at: (ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs). 109P1D4 was also identified on chromosome Yp11.2, a region of 99% identity to Xq21.

Example 4: Expression Analysis of 109P1D4 in Normal Tissues and Patient Specimens

Expression analysis by RT-PCR and Northern analysis demonstrated that normal tissue expression of a gene of Figure 2 is restricted predominantly to the tissues set forth in Table I.

Therapeutic applications for a gene of Figure 2 include use as a small molecule therapy and/or a vaccine (T cell or antibody) target. Diagnostic applications for a gene of Figure 2 include use as a diagnostic marker for local and/or metastasized disease. The restricted expression of a gene of Figure 2 in normal tissues makes it useful as a tumor target for diagnosis and therapy. Expression analysis of a gene of Figure 2 provides information useful for predicting susceptibility to advanced stage disease, rate of progression, and/or tumor aggressiveness. Expression status of a gene of Figure 2 in patient samples, tissue arrays and/or cell lines may be analyzed by: (i) immunohistochemical analysis; (ii) *in situ* hybridization; (iii) RT-PCR analysis on laser capture micro-dissected samples; (iv) Western blot analysis; and (v) Northern analysis.

RT-PCR analysis and Northern blotting were used to evaluate gene expression in a selection of normal and cancerous urological tissues. The results are summarized in Figures 15-19.

Figure 14 shows expression of 109P1D4 in lymphoma cancer patient specimens. RNA was extracted from peripheral blood lymphocytes, cord blood isolated from normal individuals, and from lymphoma patient cancer specimens. Northern blots with 10µg of total RNA were probed with the 109P1D4 sequence. Size standards in kilobases are on the side. Results show expression of 109P1D4 in lymphoma patient specimens but not in the normal blood cells tested.

Figure 15 shows expression of 109P1D4 by RT-PCR. First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), prostate cancer pool, bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, cancer metastasis pool, and pancreas cancer pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 109P1D4, was performed at 30 cycles of amplification. Results show strong expression of 109P1D4 in all cancer pools

tested. Very low expression was detected in the vital pools.

Figure 16 shows expression of 109P1D4 in normal tissues. Two multiple tissue northern blots (Clontech), both with 2 µg of mRNA/lane, were probed with the 109P1D4 SSH fragment. Size standards in kilobases (kb) are indicated on the side. Results show expression of approximately 10 kb 109P1D4 transcript in ovary. Weak expression was also detected in placenta and brain, but not in the other normal tissues tested.

Figure 17 shows expression of 109P1D4 in human cancer cell lines. RNA was extracted from a number of human prostate and bone cancer cell lines. Northern blots with 10 µg of total RNA/lane were probed with the 109P1D4 SSH fragment. Size standards in kilobases (kb) are indicated on the side. Results show expression of 109P1D4 in LAPC-9AD, LAPC-9AI, LNCaP prostate cancer cell lines, and in the bone cancer cell lines, SK-ES-1 and RD-ES.

Extensive expression of 109P1D4 in normal tissues is shown in Figure 18A. A cDNA dot blot containing 76 different samples from human tissues was analyzed using a 109P1D4 SSH probe. Expression was only detected in multiple areas of the brain, placenta, ovary, and fetal brain, amongst all tissues tested.

Figure 18B shows expression of 109P1D4 in patient cancer specimens. Expression of 109P1D4 was assayed in a panel of human cancers (T) and their respective matched normal tissues (N) on RNA dot blots. Upregulated expression of 109P1D4 in tumors compared to normal tissues was observed in uterus, lung and stomach. The expression detected in normal adjacent tissues (isolated from diseased tissues) but not in normal tissues (isolated from healthy donors) may indicate that these tissues are not fully normal and that 109P1D4 may be expressed in early stage tumors.

Figure 19 shows 109P1D4 expression in lung cancer patient specimens. RNA was extracted from normal lung, prostate cancer xenograft LAPC-9AD, bone cancer cell line RD-ES, and lung cancer patient tumors. Northern blots with 10 µg of total RNA were probed with 109P1D4. Size standards in kilobases are on the side. Results show strong expression of 109P1D4 in lung tumor tissues as well as the RD-ES cell line, but not in normal lung.

The restricted expression of 109P1D4 in normal tissues and the expression detected in cancer patient specimens suggest that 109P1D4 is a potential therapeutic target and a diagnostic marker for human cancers.

Example 5: Splice Variants of 109P1D4

Transcript variants are variants of mature mRNA from the same gene which arise by alternative transcription or alternative splicing. Alternative transcripts are transcripts from the same gene but start transcription at different points. Splice variants are mRNA variants spliced differently from the same transcript. In eukaryotes, when a multi-exon gene is transcribed from genomic DNA, the initial RNA is spliced to produce functional mRNA, which has only exons and is used for translation into an amino acid sequence. Accordingly, a given gene can have zero to many alternative transcripts and each transcript can have zero to many splice variants. Each transcript variant has a unique exon makeup, and can have different coding and/or non-coding (5' or 3' end) portions, from the original transcript. Transcript variants can code for similar or different proteins with the same or a similar function or can encode proteins with different functions, and can be expressed in the same tissue at the same time, or in different tissues at the same time, or in the same tissue at different times, or in different tissues at different times. Proteins encoded by transcript variants can have similar or different cellular or extracellular localizations, e.g., secreted versus intracellular.

Transcript variants are identified by a variety of art-accepted methods. For example, alternative transcripts and splice variants are identified by full-length cloning experiment, or by use of full-length transcript and EST sequences. First, all human ESTs were grouped into clusters which show direct or indirect identity with each other. Second, ESTs in the same cluster were further grouped into sub-clusters and assembled into a consensus sequence. The original gene sequence is compared to the consensus sequence(s) or other full-length sequences. Each consensus sequence is a potential splice

variant for that gene. Even when a variant is identified that is not a full-length clone, that portion of the variant is very useful for antigen generation and for further cloning of the full-length splice variant, using techniques known in the art.

Moreover, computer programs are available in the art that identify transcript variants based on genomic sequences. Genomic-based transcript variant identification programs include FgenesH (A. Salamov and V. Solovyev, "Ab Initio gene finding in Drosophila genomic DNA," *Genome Research*. 2000 April;10(4):516-22); Grail (URL compbio.ornl.gov/Grail-bin/EmptyGrailForm) and GenScan (URL genes.mit.edu/GENSCAN.html). For a general discussion of splice variant identification protocols see., e.g., Southan, C., A genomic perspective on human proteases, *FEBS Lett*. 2001 Jun 8; 498(2-3):214-8; de Souza, S.J., *et al.*, Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags, *Proc. Natl Acad Sci U S A*. 2000 Nov 7; 97(23):12690-3.

To further confirm the parameters of a transcript variant, a variety of techniques are available in the art, such as full-length cloning, proteomic validation, PCR-based validation, and 5' RACE validation, etc. (see e.g., Proteomic Validation: Brennan, S.O., *et al.*, Albumin banks peninsula: a new termination variant characterized by electrospray mass spectrometry, *Biochem Biophys Acta*. 1999 Aug 17;1433(1-2):321-6; Ferranti P, *et al.*, Differential splicing of pre-messenger RNA produces multiple forms of mature caprine alpha(s1)-casein, *Eur J Biochem*. 1997 Oct 1;249(1):1-7. For PCR-based Validation: Wellmann S, *et al.*, Specific reverse transcription-PCR quantification of vascular endothelial growth factor (VEGF) splice variants by LightCycler technology, *Clin Chem*. 2001 Apr;47(4):654-60; Jia, H.P., *et al.*, Discovery of new human beta-defensins using a genomics-based approach, *Gene*. 2001 Jan 24; 263(1-2):211-8. For PCR-based and 5' RACE Validation: Brigle, K.E., *et al.*, Organization of the murine reduced folate carrier gene and identification of variant splice forms, *Biochem Biophys Acta*. 1997 Aug 7; 1353(2): 191-8).

It is known in the art that genomic regions are modulated in cancers. When the genomic region to which a gene maps is modulated in a particular cancer, the alternative transcripts or splice variants of the gene are modulated as well. Disclosed herein is that 109P1D4 has a particular expression profile related to cancer. Alternative transcripts and splice variants of 109P1D4 may also be involved in cancers in the same or different tissues, thus serving as tumor-associated markers/antigens.

Using the full-length gene and EST sequences, 8 transcript variants were identified, designated as 109P1D4 v.2, v.3, v.4, v.5, v.6, v.7, v.8 and v.9. The boundaries of the exon in the original transcript, 109P1D4 v.1, were shown in Table LI. Compared with 109P1D4 v.1, transcript variant 109P1D4 v.3 has spliced out 2069-2395 from variant 109P1D4 v.1, as shown in Figure 12. Variant 109P1D4 v.4 spliced out 1162-2096 of variant 109P1D4 v.1. Variant 109P1D4 v.5 added one exon to the 5' and extended 2 bp to the 5' end and 288 bp to the 3' end of variant 109P1D4 v.1. Theoretically, each different combination of exons in spatial order, e.g. exon 1 of v.5 and exons 1 and 2 of v.3 or v.4, is a potential splice variant.

Tables LII through LV are set forth on a variant-by-variant basis. Tables LII(a)-(h) show nucleotide sequence of the transcript variants. Tables LIII(a)-(h) show the alignment of the transcript variants with nucleic acid sequence of 109P1D4 v.1. Tables LIV(a)-(h) lay out amino acid translation of the transcript variants for the identified reading frame orientation. Tables LV(a)-(h) displays alignments of the amino acid sequence encoded by the splice variants with that of 109P1D4 v.1.

Example 6: Single Nucleotide Polymorphisms of 109P1D4

A Single Nucleotide Polymorphism (SNP) is a single base pair variation in a nucleotide sequence at a specific location. At any given point of the genome, there are four possible nucleotide base pairs: A/T, C/G, G/C and T/A. Genotype refers to the specific base pair sequence of one or more locations in the genome of an individual. Haplotype refers to the base pair sequence of more than one location on the same DNA molecule (or the same chromosome in higher organisms),

often in the context of one gene or in the context of several tightly linked genes. SNP that occurs on a cDNA is called cSNP. This cSNP may change amino acids of the protein encoded by the gene and thus change the functions of the protein. Some SNP cause inherited diseases; others contribute to quantitative variations in phenotype and reactions to environmental factors including diet and drugs among individuals. Therefore, SNP and/or combinations of alleles (called haplotypes) have many applications, including diagnosis of inherited diseases, determination of drug reactions and dosage, identification of genes responsible for diseases, and analysis of the genetic relationship between individuals (P. Nowotny, J. M. Kwon and A. M. Goate, "SNP analysis to dissect human traits," *Curr. Opin. Neurobiol.* 2001 Oct; 11(5):637-641; M. Pirmohamed and B. K. Park, "Genetic susceptibility to adverse drug reactions," *Trends Pharmacol. Sci.* 2001 Jun; 22(6):298-305; J. H. Riley, C. J. Allan, E. Lai and A. Roses, "The use of single nucleotide polymorphisms in the isolation of common disease genes," *Pharmacogenomics*. 2000 Feb; 1(1):39-47; R. Judson, J. C. Stephens and A. Windemuth, "The predictive power of haplotypes in clinical response," *Pharmacogenomics*. 2000 Feb; 1(1):15-26).

SNP are identified by a variety of art-accepted methods (P. Bean, "The promising voyage of SNP target discovery," *Am. Clin. Lab.* 2001 Oct-Nov; 20(9):18-20; K. M. Weiss, "In search of human variation," *Genome Res.* 1998 Jul; 8(7):691-697; M. M. She, "Enabling large-scale pharmacogenetic studies by high-throughput mutation detection and genotyping technologies," *Clin. Chem.* 2001 Feb; 47(2):164-172). For example, SNP can be identified by sequencing DNA fragments that show polymorphism by gel-based methods such as restriction fragment length polymorphism (RFLP) and denaturing gradient gel electrophoresis (DGGE). They can also be discovered by direct sequencing of DNA samples pooled from different individuals or by comparing sequences from different DNA samples. With the rapid accumulation of sequence data in public and private databases, one can discover SNP by comparing sequences using computer programs (Z. Gu, L. Hillier and P. Y. Kwok, "Single nucleotide polymorphism hunting in cyberspace," *Hum. Mutat.* 1998; 12(4):221-225). SNP can be verified and genotype or haplotype of an individual can be determined by a variety of methods including direct sequencing and high throughput microarrays (P. Y. Kwok, "Methods for genotyping single nucleotide polymorphisms," *Annu. Rev. Genomics Hum. Genet.* 2001; 2:235-258; M. Kokoris, K. Dix, K. Moynihan, J. Mathis, B. Erwin, P. Grass, B. Hines and A. Duesterhoeft, "High-throughput SNP genotyping with the Masscode system," *Mol. Diagn.* 2000 Dec; 5(4):329-340).

Using the methods described above, SNP were identified in the original transcript, 109P4D4 v.1, and its variants (see Figure 2J and Figure 2K). These alleles of the SNP, though shown separately here, can occur in different combinations (haplotypes) and in any one of the transcript variants (such as 109P4D4 v.4 or v.5) that contains the site of the SNP. Transcript variants v.4 and v.5 contained those SNP in the exons shared with variant v.3, and transcript variant v.9 contained all the SNP occurred in variant v.6 (see Figure 10).

Example 7: Production of Recombinant 109P1D4 in Prokaryotic Systems

To express recombinant 109P1D4 and 109P1D4 variants in prokaryotic cells, the full or partial length 109P1D4 and 109P1D4 variant cDNA sequences are cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 109P1D4 variants are expressed: the full length sequence presented in Figures 2 and 3, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 109P1D4, variants, or analogs thereof.

A. *In vitro* transcription and translation constructs:

pCRII: To generate 109P1D4 sense and anti-sense RNA probes for RNA *in situ* investigations, pCRII constructs (Invitrogen, Carlsbad CA) are generated encoding either all or fragments of the 109P1D4 cDNA. The pCRII vector has Sp6 and T7 promoters flanking the insert to drive the transcription of 109P1D4 RNA for use as probes in RNA *in situ* hybridization experiments. These probes are used to analyze the cell and tissue expression of 109P1D4 at the RNA level. Transcribed

109P1D4 RNA representing the cDNA amino acid coding region of the 109P1D4 gene is used in *in vitro* translation systems such as the TnT™ Coupled Reticulolysate System (Promega, Corp., Madison, WI) to synthesize 109P1D4 protein.

B. Bacterial Constructs:

pGEX Constructs: To generate recombinant 109P1D4 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 109P1D4 cDNA protein coding sequence are cloned into the pGEX family of GST-fusion vectors (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 109P1D4 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag is generated by adding 6 histidine codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission™ recognition site in pGEX-6P-1, may be employed such that it permits cleavage of the GST tag from 109P1D4-related protein. The ampicillin resistance gene and pBR322 origin permits selection and maintenance of the pGEX plasmids in *E. coli*.

pMAL Constructs: To generate, in bacteria, recombinant 109P1D4 proteins that are fused to maltose-binding protein (MBP), all or parts of the 109P1D4 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 109P1D4 protein sequences with MBP fused at the amino-terminus and a 6X His epitope tag at the carboxyl-terminus. The MBP and 6X His tags permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His epitope tag is generated by adding 6 histidine codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 109P1D4. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 24-419 of 109P1D4 variant 1 was cloned into the pMAL-c2X vector and was used to express the fusion protein.

pET Constructs: To express 109P1D4 in bacterial cells, all or parts of the 109P1D4 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 109P1D4 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His and S-Tag™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 109P1D4 protein are expressed as amino-terminal fusions to NusA. In 2 embodiments, amino acids 24-419 and 24-815 were cloned into pET43.1 vector and used to express the fusion protein.

C. Yeast Constructs:

pESC Constructs: To express 109P1D4 in the yeast species *Saccharomyces cerevisiae* for generation of recombinant protein and functional studies, all or parts of the 109P1D4 cDNA protein coding sequence are cloned into the pESC family of vectors each of which contain 1 of 4 selectable markers, HIS3, TRP1, LEU2, and URA3 (Stratagene, La Jolla, CA). These vectors allow controlled expression from the same plasmid of up to 2 different genes or cloned sequences containing either Flag™ or Myc epitope tags in the same yeast cell. This system is useful to confirm protein-protein interactions of 109P1D4. In addition, expression in yeast yields similar post-translational modifications, such as glycosylations and phosphorylations, that are found when expressed in eukaryotic cells.

pESP Constructs: To express 109P1D4 in the yeast species *Saccharomyces pombe*, all or parts of the 109P1D4 cDNA protein coding sequence are cloned into the pESP family of vectors. These vectors allow controlled high level of

expression of a 109P1D4 protein sequence that is fused at either the amino terminus or at the carboxyl terminus to GST which aids purification of the recombinant protein. A Flag™ epitope tag allows detection of the recombinant protein with anti-Flag™ antibody.

Example 8: Production of Recombinant 109P1D4 in Higher Eukaryotic Systems

A. Mammalian Constructs:

To express recombinant 109P1D4 in eukaryotic cells, the full or partial length 109P1D4 cDNA sequences were cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 109P1D4 were expressed in these constructs, amino acids 1 to 1021 or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 109P1D4 v.1; amino acids 1 to 1054, 1 to 1347, 1 to 1337, 1 to 1310, 1 to 1037, 1 to 1048, 1 to 1340 of v.2, v.3, v.4, v.5, v.6, v.7, and v.8 respectively; or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 109P1D4 variants, or analogs thereof.

The constructs can be transfected into any one of a wide variety of mammalian cells such as 293T cells. Transfected 293T cell lysates can be probed with the anti-109P1D4 polyclonal serum, described herein.

pcDNA4/HisMax Constructs: To express 109P1D4 in mammalian cells, a 109P1D4 ORF, or portions thereof, of 109P1D4 are cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

pcDNA3.1/MycHis Constructs: To express 109P1D4 in mammalian cells, a 109P1D4 ORF, or portions thereof, of 109P1D4 with a consensus Kozak translation initiation site was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The complete ORF of 109P1D4 v.1 was cloned into the pcDNA3.1/MycHis construct to generate 109P1D4.pcDNA3.1/MycHis.

pcDNA3.1/CT-GFP-TOPO Construct: To express 109P1D4 in mammalian cells and to allow detection of the recombinant proteins using fluorescence, a 109P1D4 ORF, or portions thereof, with a consensus Kozak translation initiation site are cloned into pcDNA3.1/CT-GFP-TOPO (Invitrogen, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the Green Fluorescent Protein (GFP) fused to the carboxyl-terminus facilitating non-invasive, *in vivo* detection and cell biology studies. The pcDNA3.1CT-GFP-TOPO vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The

Neomycin resistance gene allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*. Additional constructs with an amino-terminal GFP fusion are made in pcDNA3.1/NT-GFP-TOPO spanning the entire length of a 109P1D4 protein.

PAPtag: A 109P1D4 ORF, or portions thereof, is cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of a 109P1D4 protein while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of a 109P1D4 protein. The resulting recombinant 109P1D4 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with 109P1D4 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

pTag5: A 109P1D4 ORF, or portions thereof, were cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 109P1D4 protein with an amino-terminal IgGκ signal sequence and myc and 6X His epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 109P1D4 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 109P1D4 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

pSecFc: A 109P1D4 ORF, or portions thereof, is also cloned into psecFc. The psecFc vector was assembled by cloning the human immunoglobulin G1 (IgG) Fc (hinge, CH2, CH3 regions) into pSecTag2 (Invitrogen, California). This construct generates an IgG1 Fc fusion at the carboxyl-terminus of the 109P1D4 proteins, while fusing the IgGκ signal sequence to N-terminus. 109P1D4 fusions utilizing the murine IgG1 Fc region are also used. The resulting recombinant 109P1D4 proteins are optimized for secretion into the media of transfected mammalian cells, and can be used as immunogens or to identify proteins such as ligands or receptors that interact with 109P1D4 protein. Protein expression is driven from the CMV promoter. The hygromycin resistance gene present in the vector allows for selection of mammalian cells that express the recombinant protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

pSRα Constructs: To generate mammalian cell lines that express 109P1D4 constitutively, 109P1D4 ORF, or portions thereof, were cloned into pSRα constructs. Amphotropic and ecotropic retroviruses were generated by transfection of pSRα constructs into the 293T-10A1 packaging line or co-transfection of pSRα and a helper plasmid (containing deleted packaging sequences) into the 293 cells, respectively. The retrovirus is used to infect a variety of mammalian cell lines, resulting in the integration of the cloned gene, 109P1D4, into the host cell-lines. Protein expression is driven from a long terminal repeat (LTR). The Neomycin resistance gene present in the vector allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permit selection and maintenance of the plasmid in *E. coli*. The retroviral vectors can thereafter be used for infection and generation of various cell lines using, for example, PC3, NIH 3T3, TsuPr1, 293 or rat-1 cells.

Additional pSRα constructs are made that fuse an epitope tag such as the FLAG™ tag to the carboxyl-terminus of 109P1D4 sequences to allow detection using anti-Flag antibodies. For example, the FLAG™ sequence 5' GAT TAC AAG GAT GAC GAC GAT AAG 3' (SEQ ID NO: 56) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His fusion proteins of the full-length 109P1D4 proteins.

Additional Viral Vectors: Additional constructs are made for viral-mediated delivery and expression of 109P1D4. High virus titer leading to high level expression of 109P1D4 is achieved in viral delivery systems such as adenoviral vectors and herpes amplicon vectors. A 109P1D4 coding sequence or fragments thereof are amplified by PCR and subcloned into the AdEasy shuttle vector (Stratagene). Recombination and virus packaging are performed according to the manufacturer's instructions to generate adenoviral vectors. Alternatively, 109P1D4 coding sequences or fragments thereof are cloned into the HSV-1 vector (Imgenex) to generate herpes viral vectors. The viral vectors are thereafter used for infection of various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

Regulated Expression Systems: To control expression of 109P1D4 in mammalian cells, coding sequences of 109P1D4, or portions thereof, are cloned into regulated mammalian expression systems such as the T-Rex System (Invitrogen), the GeneSwitch System (Invitrogen) and the tightly-regulated Ecdysone System (Stratagene). These systems allow the study of the temporal and concentration dependent effects of recombinant 109P1D4. These vectors are thereafter used to control expression of 109P1D4 in various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

B. Baculovirus Expression Systems

To generate recombinant 109P1D4 proteins in a baculovirus expression system, 109P1D4 ORF, or portions thereof, are cloned into the baculovirus transfer vector pBlueBac 4.5 (Invitrogen), which provides a His-tag at the N-terminus. Specifically, pBlueBac-109P1D4 is co-transfected with helper plasmid pBac-N-Blue (Invitrogen) into SF9 (*Spodoptera frugiperda*) insect cells to generate recombinant baculovirus (see Invitrogen Instruction manual for details). Baculovirus is then collected from cell supernatant and purified by plaque assay.

Recombinant 109P1D4 protein is then generated by infection of HighFive insect cells (Invitrogen) with purified baculovirus. Recombinant 109P1D4 protein can be detected using anti-109P1D4 or anti-His-tag antibody. 109P1D4 protein can be purified and used in various cell-based assays or as immunogen to generate polyclonal and monoclonal antibodies specific for 109P1D4.

Example 9: Antigenicity Profiles and Secondary Structure

Figure(s) 5A-I, Figure 6A-I, Figure 7A-I, Figure 8A-I, and Figure 9A-I depict graphically five amino acid profiles of 109P1D4 variants 1 through 9, each assessment available by accessing the ProtScale website located on the World Wide Web at (.expasy.ch/cgi-bin/protscale.pl) on the ExPasy molecular biology server.

These profiles: Figure 5, Hydrophilicity, (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828); Figure 6, Hydropathicity, (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132); Figure 7, Percentage Accessible Residues (Janin J., 1979 Nature 277:491-492); Figure 8, Average Flexibility, (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255); Figure 9, Beta-turn (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294); and optionally others available in the art, such as on the ProtScale website, were used to identify antigenic regions of each of the 109P1D4 variant proteins. Each of the above amino acid profiles of 109P1D4 variants were generated using the following ProtScale parameters for analysis: 1) A window size of 9; 2) 100% weight of the window edges compared to the window center; and, 3) amino acid profile values normalized to lie between 0 and 1.

Hydrophilicity (Figure 5), Hydropathicity (Figure 6) and Percentage Accessible Residues (Figure 7) profiles were used to determine stretches of hydrophilic amino acids (i.e., values greater than 0.5 on the Hydrophilicity and Percentage Accessible Residues profile, and values less than 0.5 on the Hydropathicity profile). Such regions are likely to be exposed to the aqueous environment, be present on the surface of the protein, and thus available for immune recognition, such as by antibodies.

Average Flexibility (Figure 8) and Beta-turn (Figure 9) profiles determine stretches of amino acids (i.e., values

greater than 0.5 on the Beta-turn profile and the Average Flexibility profile) that are not constrained in secondary structures such as beta sheets and alpha helices. Such regions are also more likely to be exposed on the protein and thus accessible to immune recognition, such as by antibodies.

Antigenic sequences of the 109P1D4 variant proteins indicated, e.g., by the profiles set forth in Figure 5, Figure 6, Figure 7, Figure 8, and/or Figure 9 are used to prepare immunogens, either peptides or nucleic acids that encode them, to generate therapeutic and diagnostic anti-109P1D4 antibodies. The immunogen can be any 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50 or more than 50-contiguous amino acids, or the corresponding nucleic acids that encode them, from the 109P1D4 protein variants listed in Figures 2 and 3. In particular, peptide immunogens of the invention can comprise, a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Hydrophilicity profiles of Figure 5; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value less than 0.5 in the Hydrophobicity profile of Figure 6; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profiles of Figure 7; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Average Flexibility profiles on Figure 8; and, a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figures 9. Peptide immunogens of the invention can also comprise nucleic acids that encode any of the foregoing.

All immunogens of the invention, peptide or nucleic acid, can be embodied in human unit dose form, or comprised by a composition that includes a pharmaceutical excipient compatible with human physiology.

The secondary structure of 109P1D4 protein variants, namely the predicted presence and location of alpha helices, extended strands, and random coils, are predicted from the primary amino acid sequence using the HNN - Hierarchical Neural Network method (NPS@: Network Protein Sequence Analysis TIBS 2000 March Vol. 25, No 3 [291]:147-150 Combet C., Blanchet C., Geourjon C. and Deléage G., http://pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_nn.html), accessed from the ExPasy molecular biology server located on the World Wide Web at (www.expasy.ch/tools/). This analysis for protein variants 1 through 9 are shown in Figure 13A through 13I respectively. The percent of structure for each variant comprised of alpha helix, extended strand, and random coil is also indicated.

Analysis for the potential presence of transmembrane domains in 109P1D4 variant proteins was carried out using a variety of transmembrane prediction algorithms accessed from the ExPasy molecular biology server located on the World Wide Web at (www.expasy.ch/tools/). Shown graphically in figures 13J-R are the results of analyses using the TMpred program (top panels) and the TMHMM program (bottom panels) of 109P1D4 protein variants 1 through 9 respectively. Analyses of the variants using other structural prediction programs are summarized in Table VI and Table L.

Example 10: Generation of 109P1D4 Polyclonal Antibodies

Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. In addition to immunizing with a full length 109P1D4 protein variant, computer algorithms are employed in design of immunogens that, based on amino acid sequence analysis contain characteristics of being antigenic and available for recognition by the immune system of the immunized host (see the Example entitled "Antigenicity Profiles and Secondary Structure"). Such regions would be predicted to be hydrophilic, flexible, in beta-turn conformations, and be exposed on the surface of the protein (see, e.g., Figure 5, Figure 6, Figure 7, Figure 8, or Figure 9 for

amino acid profiles that indicate such regions of 109P1D4 protein variant 1).

For example, recombinant bacterial fusion proteins or peptides containing hydrophilic, flexible, beta-turn regions of 109P1D4 protein variants are used as antigens to generate polyclonal antibodies in New Zealand White rabbits or monoclonal antibodies as described in the example entitled "Generation of 109P1D4 Monoclonal Antibodies (mAbs)". For example, in 109P1D4 variant 1, such regions include, but are not limited to, amino acids 22-39, amino acids 67-108, amino acids 200-232, amino acids 454-499, amino acids 525-537, amino acids 640-660, amino acids 834-880, and amino acids 929-942. It is useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include, but are not limited to, keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. In 2 embodiments, peptides encoding amino acids 77-90 and amino acids 929-942 of 109P1D4 variant 1 were synthesized, conjugated to KLH, and used to immunize separate rabbits. Alternatively the immunizing agent may include all or portions of the 109P1D4 variant proteins, analogs or fusion proteins thereof. For example, the 109P1D4 variant 1 amino acid sequence can be fused using recombinant DNA techniques to any one of a variety of fusion protein partners that are well known in the art, such as glutathione-S-transferase (GST) and HIS tagged fusion proteins. In 1 embodiment, amino acids 24-419 of 109P1D4 variant 1 was fused to NUSa using recombinant techniques and the pET43.1 expression vector, expressed, purified and used to immunize a rabbit. Such fusion proteins are purified from induced bacteria using the appropriate affinity matrix.

Other recombinant bacterial fusion proteins that may be employed include maltose binding protein, LacZ, thioredoxin, NusA, or an immunoglobulin constant region (see the section entitled "Production of 109P1D4 in Prokaryotic Systems" and Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubel et al. eds., 1995; Linsley, P.S., Brady, W., Urnes, M., Grosmaire, L., Damle, N., and Ledbetter, J.(1991) J.Exp. Med. 174, 561-566).

In addition to bacterial derived fusion proteins, mammalian expressed protein antigens are also used. These antigens are expressed from mammalian expression vectors such as the Tag5 and Fc-fusion vectors (see the section entitled "Production of Recombinant 109P1D4 in Eukaryotic Systems"), and retain post-translational modifications such as glycosylations found in native protein. In one embodiment, amino acids 24-812 of 109P1D4 variant 1 was cloned into the Tag5 mammalian secretion vector, and expressed in 293T cells (See Figure 20). The recombinant protein is purified by metal chelate chromatography from tissue culture supernatants of 293T cells stably expressing the recombinant vector. The purified Tag5 109P1D4 protein is then used as immunogen.

During the immunization protocol, it is useful to mix or emulsify the antigen in adjuvants that enhance the immune response of the host animal. Examples of adjuvants include, but are not limited to, complete Freund's adjuvant (CFA) and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

In a typical protocol, rabbits are initially immunized subcutaneously with up to 200 µg, typically 100-200 µg, of fusion protein or peptide conjugated to KLH mixed in complete Freund's adjuvant (CFA). Rabbits are then injected subcutaneously every two weeks with up to 200 µg, typically 100-200 µg, of the immunogen in incomplete Freund's adjuvant (IFA). Test bleeds are taken approximately 7-10 days following each immunization and used to monitor the titer of the antiserum by ELISA.

To test reactivity and specificity of immune serum, such as the rabbit serum derived from immunization with the NUSa-fusion of 109P1D4 variant 1 protein, the full-length 109P1D4 variant 1 cDNA is cloned into pCDNA 3.1 myc-his expression vector (Invitrogen, see the Example entitled "Production of Recombinant 109P1D4 in Eukaryotic Systems"). After transfection of the constructs into 293T cells, cell lysates are probed with the anti-109P1D4 serum to determine specific reactivity to denatured 109P1D4 protein using the Western blot technique. Probing with anti-His antibody serves as a positive control for expression of 109P1D4 in the transfected cells (See Figure 21). In addition, the immune serum is tested

by fluorescence microscopy, flow cytometry and immunoprecipitation against 293T and other recombinant 109P1D4-expressing cells to determine specific recognition of native protein. Western blot, immunoprecipitation, fluorescent microscopy, and flow cytometric techniques using cells that endogenously express 109P1D4 are also carried out to test reactivity and specificity.

Anti-serum from rabbits immunized with 109P1D4 variant fusion proteins, such as GST and MBP fusion proteins, are purified by depletion of antibodies reactive to the fusion partner sequence by passage over an affinity column containing the fusion partner either alone or in the context of an irrelevant fusion protein. For example, antiserum derived from a NUSa-109P1D4 variant 1 fusion protein is first purified by passage over a column of MBP protein covalently coupled to AffiGel matrix (BioRad, Hercules, Calif.). The antiserum is then affinity purified by passage over a column composed of a NUSa-109P1D4 fusion protein covalently coupled to Affigel matrix. The serum is then further purified by protein G affinity chromatography to isolate the IgG fraction. Sera from other His-tagged antigens and peptide immunized rabbits as well as fusion partner depleted sera are affinity purified by passage over a column matrix composed of the original protein immunogen or free peptide.

Example 11: Generation of 109P1D4 Monoclonal Antibodies (mAbs)

In one embodiment, therapeutic mAbs to 109P1D4 variants comprise those that react with epitopes specific for each variant protein or specific to sequences in common between the variants that would disrupt or modulate the biological function of the 109P1D4 variants, for example those that would disrupt the interaction with ligands and binding partners. Immunogens for generation of such mAbs include those designed to encode or contain the entire 109P1D4 protein variant sequence, regions predicted to contain functional motifs, and regions of the 109P1D4 protein variants predicted to be antigenic from computer analysis of the amino acid sequence (see, e.g., Figure 5, Figure 6, Figure 7, Figure 8, or Figure 9, and the Example entitled "Antigenicity Profiles and Secondary Structure"). Immunogens include peptides, recombinant bacterial proteins, and mammalian expressed Tag 5 proteins and human and murine IgG FC fusion proteins. In addition, cells engineered to express high levels of a respective 109P1D4 variant, such as 293T-109P1D4 variant 1 or 300.19-109P1D4 variant 1 murine Pre-B cells, are used to immunize mice.

To generate mAbs to a 109P1D4 variant, mice are first immunized intraperitoneally (IP) with, typically, 10-50 µg of protein immunogen or 10⁷ 109P1D4-expressing cells mixed in complete Freund's adjuvant. Mice are then subsequently immunized IP every 2-4 weeks with, typically, 10-50 µg of protein immunogen or 10⁷ cells mixed in incomplete Freund's adjuvant. Alternatively, MPL-TDM adjuvant is used in immunizations. In addition to the above protein and cell-based immunization strategies, a DNA-based immunization protocol is employed in which a mammalian expression vector encoding a 109P1D4 variant sequence is used to immunize mice by direct injection of the plasmid DNA. For example, amino acids 24-812 of 109P1D4 of variant 1 is cloned into the Tag5 mammalian secretion vector and the recombinant vector will then be used as immunogen. In another example the same amino acids are cloned into an Fc-fusion secretion vector in which the 109P1D4 variant 1 sequence is fused at the amino-terminus to an IgK leader sequence and at the carboxyl-terminus to the coding sequence of the human or murine IgG Fc region. This recombinant vector is then used as immunogen. The plasmid immunization protocols are used in combination with purified proteins expressed from the same vector and with cells expressing the respective 109P1D4 variant.

Alternatively, mice may be immunized directly into their footpads. In this case, 10-50 µg of protein immunogen or 10⁷ 254P1D6B-expressing cells are injected sub-cutaneously into the footpad of each hind leg. The first immunization is given with Titermax (Sigma™) as an adjuvant and subsequent injections are given with Alum-gel in conjunction with CpG oligonucleotide sequences with the exception of the final injection which is given with PBS. Injections are given twice weekly

(every three to four days) for a period of 4 weeks and mice are sacrificed 3-4 days after the final injection, at which point lymph nodes immediately draining from the footpad are harvested and the B-cells are collected for use as antibody producing fusion partners.

During the immunization protocol, test bleeds are taken 7-10 days following an injection to monitor titer and specificity of the immune response. Once appropriate reactivity and specificity is obtained as determined by ELISA, Western blotting, immunoprecipitation, fluorescence microscopy, and flow cytometric analyses, fusion and hybridoma generation is then carried out with established procedures well known in the art (see, e.g., Harlow and Lane, 1988).

In one embodiment for generating 109P1D4 monoclonal antibodies, a Tag5 antigen of variant 1 encoding amino acids 14-812 is expressed in 293T cells and purified from conditioned media. Balb C mice are initially immunized intraperitoneally with 25 µg of the Tag5 109P1D4 variant 1 protein mixed in complete Freund's adjuvant. Mice are subsequently immunized every two weeks with 25 µg of the antigen mixed in incomplete Freund's adjuvant for a total of three immunizations. ELISA using the Tag5 antigen determines the titer of serum from immunized mice. Reactivity and specificity of serum to full length 109P1D4 variant 1 protein is monitored by Western blotting, immunoprecipitation and flow cytometry using 293T cells transfected with an expression vector encoding the 109P1D4 variant 1 cDNA (see e.g., the Example entitled "Production of Recombinant 109P1D4 in Higher Eukaryotic Systems" and Figure 21). Other recombinant 109P1D4 variant 1-expressing cells or cells endogenously expressing 109P1D4 variant 1 are also used. Mice showing the strongest reactivity are rested and given a final injection of antigen in PBS and then sacrificed four days later. The spleens of the sacrificed mice are harvested and fused to SPO/2 myeloma cells using standard procedures (Harlow and Lane, 1988). Supernatants from HAT selected growth wells are screened by ELISA, Western blot, immunoprecipitation, fluorescent microscopy, and flow cytometry to identify 109P1D4 specific antibody-producing clones.

To generate monoclonal antibodies that are specific for a 109P1D4 variant protein, immunogens are designed to encode sequences unique for each variant. In one embodiment, an antigenic peptide composed of amino acids 1-29 of 109P1D4 variant 2 is coupled to KLH to derive monoclonal antibodies specific to 109P1D4 variant 2. In another embodiment, an antigenic peptide comprised of amino acids 1-23 of 109P1D4 variant 6 is coupled to KLH and used as immunogen to derive variant 6 specific MAbs. In another example, a GST-fusion protein encoding amino acids 1001-1347 of variant 3 is used as immunogen to generate antibodies that would recognize variants 3, 4, 5, and 8, and distinguish them from variants 1, 2, 6, 7 and 9. Hybridoma supernatants are then screened on the respective antigen and then further screened on cells expressing the specific variant and cross-screened on cells expressing the other variants to derive variant-specific monoclonal antibodies.

The binding affinity of 109P1D4 variant specific monoclonal antibodies are determined using standard technologies. Affinity measurements quantify the strength of antibody to epitope binding and are used to help define which 109P1D4 variant monoclonal antibodies preferred for diagnostic or therapeutic use, as appreciated by one of skill in the art. The BIAcore system (Uppsala, Sweden) is a preferred method for determining binding affinity. The BIAcore system uses surface plasmon resonance (SPR, Welford K. 1991, Opt. Quant. Elect. 23:1; Morton and Myszka, 1998, Methods in Enzymology 295: 268) to monitor biomolecular interactions in real time. BIAcore analysis conveniently generates association rate constants, dissociation rate constants, equilibrium dissociation constants, and affinity constants. Alternatively, equilibrium binding analysis of MAbs on 109P1D4-expressing cells can be used to determine affinity.

Example 12: HLA Class I and Class II Binding Assays

HLA class I and class II binding assays using purified HLA molecules are performed in accordance with disclosed protocols (e.g., PCT publications WO 94/20127 and WO 94/03205; Sidney *et al.*, *Current Protocols in Immunology* 18.3.1

(1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). Briefly, purified MHC molecules (5 to 500 nM) are incubated with various unlabeled peptide inhibitors and 1-10 nM 125 I-radiolabeled probe peptides as described. Following incubation, MHC-peptide complexes are separated from free peptide by gel filtration and the fraction of peptide bound is determined. Typically, in preliminary experiments, each MHC preparation is titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays are performed using these HLA concentrations.

Since under these conditions $[label] < [HLA]$ and $IC_{50} \geq [HLA]$, the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μ g/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For database purposes, and inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation is accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Binding assays as outlined above may be used to analyze HLA supermotif and/or HLA motif-bearing peptides (see Table IV).

Example 13: Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

HLA vaccine compositions of the invention can include multiple epitopes. The multiple epitopes can comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification and confirmation of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage is performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in the Example entitled "Antigenicity Profiles" and Tables VIII-XXI and XXII-XLIX employ the protein sequence data from the gene product of 109P1D4 set forth in Figures 2 and 3, the specific search peptides used to generate the tables are listed in Table VII.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs are performed as follows. All translated 109P1D4 protein sequences are analyzed using a text string search software program to identify potential peptide sequences containing appropriate HLA binding motifs; such programs are readily produced in accordance with information in the art in view of known motif/supermotif disclosures. Furthermore, such calculations can be made mentally.

Identified A2-, A3-, and DR-supermotif sequences are scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms account for the impact of different amino acids at different positions, and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2j} \times a_{3k} \dots \times a_{ni}$$

where a_{ij} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide

irrespective of the sequence of the rest of the peptide.

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all *i* positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying *j* is calculated relative to the remainder of the group, and used as the estimate of *j*. For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Protein sequences from 109P1D4 are scanned utilizing motif identification software, to identify 8-, 9- 10- and 11-mer sequences containing the HLA-A2-supermotif main anchor specificity. Typically, these sequences are then scored using the protocol described above and the peptides corresponding to the positive-scoring sequences are synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule).

These peptides are then tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). Peptides that bind to at least three of the five A2-supertype alleles tested are typically deemed A2-supertype cross-reactive binders. Preferred peptides bind at an affinity equal to or less than 500 nM to three or more HLA-A2 supertype molecules.

Selection of HLA-A3 supermotif-bearing epitopes

The 109P1D4 protein sequence(s) scanned above is also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. Peptides corresponding to the HLA A3 supermotif-bearing sequences are then synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the molecules encoded by the two most prevalent A3-supertype alleles. The peptides that bind at least one of the two alleles with binding affinities of ≤ 500 nM, often ≤ 200 nM, are then tested for binding cross-reactivity to the other common A3-supertype alleles (e.g., A*3101, A*3301, and A*6801) to identify those that can bind at least three of the five HLA-A3-supertype molecules tested.

Selection of HLA-B7 supermotif bearing epitopes

The 109P1D4 protein(s) scanned above is also analyzed for the presence of 8-, 9- 10-, or 11-mer peptides with the HLA-B7-supermotif. Corresponding peptides are synthesized and tested for binding to HLA-B*0702, the molecule encoded by the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Peptides binding B*0702 with IC_{50} of ≤ 500 nM are identified using standard methods. These peptides are then tested for binding to other common B7-supertype molecules (e.g., B*3501, B*5101, B*5301, and B*5401). Peptides capable of binding to three or more of the five B7-supertype alleles tested are thereby identified.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine compositions. An analysis of the 109P1D4 protein can also be performed to identify HLA-A1- and A24-motif-containing sequences.

High affinity and/or cross-reactive binding epitopes that bear other motif and/or supermotifs are identified using analogous methodology.

Example 14: Confirmation of Immunogenicity

Cross-reactive candidate CTL A2-supermotif-bearing peptides that are identified as described herein are selected to confirm *in vitro* immunogenicity. Confirmation is performed using the following methodology:

Target Cell Lines for Cellular Screening:

The .221A2.1 cell line, produced by transferring the HLA-A2.1 gene into the HLA-A, -B, -C null mutant human B-lymphoblastoid cell line 721.221, is used as the peptide-loaded target to measure activity of HLA-A2.1-restricted CTL. This cell line is grown in RPMI-1640 medium supplemented with antibiotics, sodium pyruvate, nonessential amino acids and 10% (v/v) heat inactivated FCS. Cells that express an antigen of interest, or transfectants comprising the gene encoding the antigen of interest, can be used as target cells to confirm the ability of peptide-specific CTLs to recognize endogenous antigen.

Primary CTL Induction Cultures:

Generation of Dendritic Cells (DC): PBMCs are thawed in RPMI with 30 µg/ml DNase, washed twice and resuspended in complete medium (RPMI-1640 plus 5% AB human serum, non-essential amino acids, sodium pyruvate, L-glutamine and penicillin/streptomycin). The monocytes are purified by plating 10×10^6 PBMC/well in a 6-well plate. After 2 hours at 37°C, the non-adherent cells are removed by gently shaking the plates and aspirating the supernatants. The wells are washed a total of three times with 3 ml RPMI to remove most of the non-adherent and loosely adherent cells. Three ml of complete medium containing 50 ng/ml of GM-CSF and 1,000 U/ml of IL-4 are then added to each well. TNFα is added to the DCs on day 6 at 75 ng/ml and the cells are used for CTL induction cultures on day 7.

Induction of CTL with DC and Peptide: CD8+ T-cells are isolated by positive selection with Dynal immunomagnetic beads (Dynabeads® M-450) and the detach-bead® reagent. Typically about $200\text{--}250 \times 10^6$ PBMC are processed to obtain 24×10^6 CD8+ T-cells (enough for a 48-well plate culture). Briefly, the PBMCs are thawed in RPMI with 30 µg/ml DNase, washed once with PBS containing 1% human AB serum and resuspended in PBS/1% AB serum at a concentration of 20×10^6 cells/ml. The magnetic beads are washed 3 times with PBS/AB serum, added to the cells (140 µl beads/ 20×10^6 cells) and incubated for 1 hour at 4°C with continuous mixing. The beads and cells are washed 4x with PBS/AB serum to remove the nonadherent cells and resuspended at 100×10^6 cells/ml (based on the original cell number) in PBS/AB serum containing 100 µl/ml detach-bead® reagent and 30 µg/ml DNase. The mixture is incubated for 1 hour at room temperature with continuous mixing. The beads are washed again with PBS/AB/DNase to collect the CD8+ T-cells. The DC are collected and centrifuged at 1300 rpm for 5-7 minutes, washed once with PBS with 1% BSA, counted and pulsed with 40 µg/ml of peptide at a cell concentration of $1\text{--}2 \times 10^6$ /ml in the presence of 3 µg/ml β₂-microglobulin for 4 hours at 20°C. The DC are then irradiated (4,200 rads), washed 1 time with medium and counted again.

Setting up induction cultures: 0.25 ml cytokine-generated DC (at 1×10^5 cells/ml) are co-cultured with 0.25 ml of CD8+ T-cells (at 2×10^6 cell/ml) in each well of a 48-well plate in the presence of 10 ng/ml of IL-7. Recombinant human IL-10 is added the next day at a final concentration of 10 ng/ml and human IL-2 is added 48 hours later at 10 IU/ml.

Restimulation of the induction cultures with peptide-pulsed adherent cells: Seven and fourteen days after the primary induction, the cells are restimulated with peptide-pulsed adherent cells. The PBMCs are thawed and washed twice with RPMI and DNase. The cells are resuspended at 5×10^6 cells/ml and irradiated at ~4200 rads. The PBMCs are plated at 2×10^6 in 0.5 ml complete medium per well and incubated for 2 hours at 37°C. The plates are washed twice with RPMI by tapping the plate gently to remove the nonadherent cells and the adherent cells pulsed with 10 µg/ml of peptide in the

presence of 3 $\mu\text{g/ml}$ β_2 microglobulin in 0.25ml RPMI/5%AB per well for 2 hours at 37°C. Peptide solution from each well is aspirated and the wells are washed once with RPMI. Most of the media is aspirated from the induction cultures (CD8+ cells) and brought to 0.5 ml with fresh media. The cells are then transferred to the wells containing the peptide-pulsed adherent cells. Twenty four hours later recombinant human IL-10 is added at a final concentration of 10 ng/ml and recombinant human IL-2 is added the next day and again 2-3 days later at 50IU/ml (Tsai *et al.*, *Critical Reviews in Immunology* 18(1-2):65-75, 1998). Seven days later, the cultures are assayed for CTL activity in a ^{51}Cr release assay. In some experiments the cultures are assayed for peptide-specific recognition in the *in situ* IFN γ ELISA at the time of the second restimulation followed by assay of endogenous recognition 7 days later. After expansion, activity is measured in both assays for a side-by-side comparison.

Measurement of CTL lytic activity by ^{51}Cr release.

Seven days after the second restimulation, cytotoxicity is determined in a standard (5 hr) ^{51}Cr release assay by assaying individual wells at a single E:T. Peptide-pulsed targets are prepared by incubating the cells with 10 $\mu\text{g/ml}$ peptide overnight at 37°C.

Adherent target cells are removed from culture flasks with trypsin-EDTA. Target cells are labeled with 200 μCi of ^{51}Cr sodium chromate (Dupont, Wilmington, DE) for 1 hour at 37°C. Labeled target cells are resuspended at 10^6 per ml and diluted 1:10 with K562 cells at a concentration of $3.3 \times 10^6/\text{ml}$ (an NK-sensitive erythroblastoma cell line used to reduce non-specific lysis). Target cells (100 μl) and effectors (100 μl) are plated in 96 well round-bottom plates and incubated for 5 hours at 37°C. At that time, 100 μl of supernatant are collected from each well and percent lysis is determined according to the formula:

$$[(\text{cpm of the test sample} - \text{cpm of the spontaneous } ^{51}\text{Cr release sample}) / (\text{cpm of the maximal } ^{51}\text{Cr release sample} - \text{cpm of the spontaneous } ^{51}\text{Cr release sample})] \times 100.$$

Maximum and spontaneous release are determined by incubating the labeled targets with 1% Triton X-100 and media alone, respectively. A positive culture is defined as one in which the specific lysis (sample- background) is 10% or higher in the case of individual wells and is 15% or more at the two highest E:T ratios when expanded cultures are assayed.

In situ Measurement of Human IFN γ Production as an Indicator of Peptide-specific and Endogenous Recognition

Immulon 2 plates are coated with mouse anti-human IFN γ monoclonal antibody (4 $\mu\text{g/ml}$ 0.1M NaHCO_3 , pH8.2) overnight at 4°C. The plates are washed with Ca^{2+} , Mg^{2+} -free PBS/0.05% Tween 20 and blocked with PBS/10% FCS for two hours, after which the CTLs (100 $\mu\text{l/well}$) and targets (100 $\mu\text{l/well}$) are added to each well, leaving empty wells for the standards and blanks (which received media only). The target cells, either peptide-pulsed or endogenous targets, are used at a concentration of 1×10^6 cells/ml. The plates are incubated for 48 hours at 37°C with 5% CO_2 .

Recombinant human IFN-gamma is added to the standard wells starting at 400 pg or 1200pg/100 microliter/well and the plate incubated for two hours at 37°C. The plates are washed and 100 μl of biotinylated mouse anti-human IFN-gamma monoclonal antibody (2 microgram/ml in PBS/3%FCS/0.05% Tween 20) are added and incubated for 2 hours at room temperature. After washing again, 100 microliter HRP-streptavidin (1:4000) are added and the plates incubated for one hour at room temperature. The plates are then washed 6x with wash buffer, 100 microliter/well developing solution (TMB 1:1) are added, and the plates allowed to develop for 5-15 minutes. The reaction is stopped with 50 microliter/well 1M H_3PO_4 and read at OD450. A culture is considered positive if it measured at least 50 pg of IFN-gamma/well above background and is twice the background level of expression.

CTL Expansion.

Those cultures that demonstrate specific lytic activity against peptide-pulsed targets and/or tumor targets are expanded over a two week period with anti-CD3. Briefly, 5×10^4 CD8+ cells are added to a T25 flask containing the following:

1×10^6 irradiated (4,200 rad) PBMC (autologous or allogeneic) per ml, 2×10^5 irradiated (8,000 rad) EBV-transformed cells per ml, and OKT3 (anti-CD3) at 30ng per ml in RPMI-1640 containing 10% (v/v) human AB serum, non-essential amino acids, sodium pyruvate, 25 μ M 2-mercaptoethanol, L-glutamine and penicillin/streptomycin. Recombinant human IL2 is added 24 hours later at a final concentration of 200IU/ml and every three days thereafter with fresh media at 50IU/ml. The cells are split if the cell concentration exceeds 1×10^6 /ml and the cultures are assayed between days 13 and 15 at E:T ratios of 30, 10, 3 and 1:1 in the ^{51}Cr release assay or at 1×10^6 /ml in the *in situ* IFN γ assay using the same targets as before the expansion.

Cultures are expanded in the absence of anti-CD3 $^+$ as follows. Those cultures that demonstrate specific lytic activity against peptide and endogenous targets are selected and 5×10^4 CD8 $^+$ cells are added to a T25 flask containing the following: 1×10^6 autologous PBMC per ml which have been peptide-pulsed with 10 μ g/ml peptide for two hours at 37°C and irradiated (4,200 rad); 2×10^5 irradiated (8,000 rad) EBV-transformed cells per ml RPMI-1640 containing 10%(v/v) human AB serum, non-essential AA, sodium pyruvate, 25mM 2-ME, L-glutamine and gentamicin.

Immunogenicity of A2 supermotif-bearing peptides

A2-supermotif cross-reactive binding peptides are tested in the cellular assay for the ability to induce peptide-specific CTL in normal individuals. In this analysis, a peptide is typically considered to be an epitope if it induces peptide-specific CTLs in at least individuals, and preferably, also recognizes the endogenously expressed peptide.

Immunogenicity can also be confirmed using PBMCs isolated from patients bearing a tumor that expresses 109P1D4. Briefly, PBMCs are isolated from patients, re-stimulated with peptide-pulsed monocytes and assayed for the ability to recognize peptide-pulsed target cells as well as transfected cells endogenously expressing the antigen.

Evaluation of A*03/A11 immunogenicity

HLA-A3 supermotif-bearing cross-reactive binding peptides are also evaluated for immunogenicity using methodology analogous for that used to evaluate the immunogenicity of the HLA-A2 supermotif peptides.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified as set forth herein are confirmed in a manner analogous to the confirmation of A2-and A3-supermotif-bearing peptides.

Peptides bearing other supermotifs/motifs, e.g., HLA-A1, HLA-A24 *etc.* are also confirmed using similar methodology

Example 15: Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged to confer upon the peptide certain characteristics, e.g. greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analoging peptides to exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

Peptide engineering strategies are implemented to further increase the cross-reactivity of the epitopes. For example, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide is confirmed as binding one or all supertype members and then analoged to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

The selection of analogs for immunogenicity in a cellular screening analysis is typically further restricted by the capacity of the parent wild type (WT) peptide to bind at least weakly, *i.e.*, bind at an IC_{50} of 5000nM or less, to three or more A2 supertype alleles. The rationale for this requirement is that the WT peptides must be present endogenously in sufficient quantity to be biologically relevant. Analoged peptides have been shown to have increased immunogenicity and cross-reactivity by T cells specific for the parent epitope (see, *e.g.*, Parkhurst *et al.*, *J. Immunol.* 157:2539, 1996; and Pogue *et al.*, *Proc. Natl. Acad. Sci. USA* 92:8166, 1995).

In the cellular screening of these peptide analogs, it is important to confirm that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, target cells that endogenously express the epitope.

Analoging of HLA-A3 and B7-supermotif-bearing peptides

Analogues of HLA-A3 supermotif-bearing epitopes are generated using strategies similar to those employed in analoging HLA-A2 supermotif-bearing peptides. For example, peptides binding to 3/5 of the A3-supertype molecules are engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity are then confirmed as having A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, peptides binding 3 or more B7-supertype alleles can be improved, where possible, to achieve increased cross-reactive binding or greater binding affinity or binding half life. B7 supermotif-bearing peptides are, for example, engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at primary anchor residues of other motif and/or supermotif-bearing epitopes is performed in a like manner.

The analog peptides are then confirmed for immunogenicity, typically in a cellular screening assay. Again, it is generally important to demonstrate that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, targets that endogenously express the epitope.

Analoging at Secondary Anchor Residues

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide with an F residue at position 1 is analyzed. The peptide is then analoged to, for example, substitute L for F at position 1. The analoged peptide is evaluated for increased binding affinity, binding half life and/or increased cross-reactivity. Such a procedure identifies analoged peptides with enhanced properties.

Engineered analogs with sufficiently improved binding capacity or cross-reactivity can also be tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. Analoged peptides are additionally tested for the ability to stimulate a recall response using PBMC from patients with 109P1D4-expressing tumors.

Other analoging strategies

Another form of peptide analoging, unrelated to anchor positions, involves the substitution of a cysteine with α -amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the

peptide structurally so as to reduce binding capacity. Substitution of α -amino butyric acid for cysteine not only alleviates this problem, but has been shown to improve binding and crossbinding capabilities in some instances (see, e.g., the review by Sette *et al.*, In: *Persistent Viral Infections*, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999).

Thus, by the use of single amino acid substitutions, the binding properties and/or cross-reactivity of peptide ligands for HLA supertype molecules can be modulated.

Example 16: Identification and confirmation of 109P1D4-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif are identified and confirmed as outlined below using methodology similar to that described for HLA Class I peptides.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify 109P1D4-derived, HLA class II HTL epitopes, a 109P1D4 antigen is analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences are selected comprising a DR-supermotif, comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates sequences for the presence of secondary anchors. Using allele-specific selection tables (see, e.g., Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The 109P1D4-derived peptides identified above are tested for their binding capacity for various common HLA-DR molecules. All peptides are initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least two of these three DR molecules are then tested for binding to DR2w2 β 1, DR2w2 β 2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least two of the four secondary panel DR molecules, and thus cumulatively at least four of seven different DR molecules, are screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least seven of the ten DR molecules comprising the primary, secondary, and tertiary screening assays are considered cross-reactive DR binders. 109P1D4-derived peptides found to bind common HLA-DR alleles are of particular interest.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is a relevant criterion in the selection of HTL epitopes. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, target 109P1D4 antigens are analyzed for sequences carrying one of the two DR3-specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides are then synthesized and confirmed as having the ability to bind DR3 with an affinity of 1 μ M or better, i.e., less than 1 μ M. Peptides are found that meet this binding criterion and qualify as HLA class II high affinity binders.

DR3 binding epitopes identified in this manner are included in vaccine compositions with DR supermotif-bearing peptide epitopes.

Similarly to the case of HLA class I motif-bearing peptides, the class II motif-bearing peptides are analogized to

improve affinity or cross-reactivity. For example, aspartic acid at position 4 of the 9-mer core sequence is an optimal residue for DR3 binding, and substitution for that residue often improves DR 3 binding.

Example 17: Immunogenicity of 109P1D4-derived HTL epitopes

This example determines immunogenic DR supermotif- and DR3 motif-bearing epitopes among those identified using the methodology set forth herein.

Immunogenicity of HTL epitopes are confirmed in a manner analogous to the determination of immunogenicity of CTL epitopes, by assessing the ability to stimulate HTL responses and/or by using appropriate transgenic mouse models. Immunogenicity is determined by screening for: 1.) *in vitro* primary induction using normal PBMC or 2.) recall responses from patients who have 109P1D4-expressing tumors.

Example 18: Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles are determined. Gene frequencies for each HLA allele are calculated from antigen or allele frequencies utilizing the binomial distribution formulae $gf=1-(\text{SQRT}(1-af))$ (see, e.g., Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies are calculated, and the cumulative antigen frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data is not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies is assumed. To obtain total potential supertype population coverage no linkage disequilibrium is assumed, and only alleles confirmed to belong to each of the superotypes are included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations are made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., $\text{total}=A+B*(1-A)$). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups. Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%, see, e.g., Table IV (G). An analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Immunogenicity studies in humans (e.g., Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. The use of highly cross-reactive binding peptides is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

With a sufficient number of epitopes (as disclosed herein and from the art), an average population coverage is

predicted to be greater than 95% in each of five major ethnic populations. The game theory Monte Carlo simulation analysis, which is known in the art (see e.g., Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), can be used to estimate what percentage of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize the vaccine epitopes described herein. A preferred percentage is 90%. A more preferred percentage is 95%.

Example 19: CTL Recognition Of Endogenously Processed Antigens After Priming

This example confirms that CTL induced by native or analoged peptide epitopes identified and selected as described herein recognize endogenously synthesized, i.e., native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ⁵¹Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of peptide, and also tested on ⁵¹Cr labeled target cells bearing the endogenously synthesized antigen, i.e. cells that are stably transfected with 109P1D4 expression vectors.

The results demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized 109P1D4 antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that are being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (e.g., transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 20: Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice, by use of a 109P1D4-derived CTL and HTL peptide vaccine compositions. The vaccine composition used herein comprise peptides to be administered to a patient with a 109P1D4-expressing tumor. The peptide composition can comprise multiple CTL and/or HTL epitopes. The epitopes are identified using methodology as described herein. This example also illustrates that enhanced immunogenicity can be achieved by inclusion of one or more HTL epitopes in a CTL vaccine composition; such a peptide composition can comprise an HTL epitope conjugated to a CTL epitope. The CTL epitope can be one that binds to multiple HLA family members at an affinity of 500 nM or less, or analogs of that epitope. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are used to confirm the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, and are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline, or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngeneic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (e.g., Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991)

***In vitro* CTL activation:** One week after priming, spleen cells (30x10⁶ cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10x10⁶ cells/flask) in 10 ml of culture medium/T25 flask.

After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of $200\ \mu\text{l}$ of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of $1\ \mu\text{g/ml}$. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of $200\ \mu\text{l}$) in U-bottom 96-well plates. After a six hour incubation period at 37°C , a $0.1\ \text{ml}$ aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a six hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (i.e., 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000) - (1/500,000)] \times 10^6 = 18\ \text{LU}$.

The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using, for example, CTL epitopes as outlined above in the Example entitled "Confirmation of Immunogenicity." Analyses similar to this may be performed to confirm the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures, it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 21: Selection of CTL and HTL epitopes for inclusion in a 109P1D4-specific vaccine.

This example illustrates a procedure for selecting peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (i.e., minigene) that encodes peptide(s), or can be single and/or polyepitopic peptides.

The following principles are utilized when selecting a plurality of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that are correlated with 109P1D4 clearance. The number of epitopes used depends on observations of patients who spontaneously clear 109P1D4. For example, if it has been observed that patients who spontaneously clear 109P1D4-expressing cells generate an immune response to at least three (3) epitopes from 109P1D4 antigen, then at least three epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less; or HLA Class I peptides with high binding scores from the BIMAS web site, at URL bimas.dcrt.nih.gov/.

In order to achieve broad coverage of the vaccine through out a diverse population, sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. In one embodiment, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating polyepitopic compositions, or a minigene that encodes same, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as

those employed when selecting a peptide comprising nested epitopes. For example, a protein sequence for the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. Epitopes may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. A multi-epitopic peptide can be generated synthetically, recombinantly, or via cleavage from the native source. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polypeptidic peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes. This embodiment provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent the creating of any analogs) directs the immune response to multiple peptide sequences that are actually present in 109P1D4, thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions. Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude to an immune response that controls or clears cells that bear or overexpress 109P1D4.

Example 22: Construction of "Minigene" Multi-Epitope DNA Plasmids

This example discusses the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of B cell, CTL and/or HTL epitopes or epitope analogs as described herein.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes. HLA class I supermotif or motif-bearing peptide epitopes derived 109P1D4, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from 109P1D4 to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the li protein may be fused to one or more HTL epitopes as described in the art, wherein the CLIP sequence of the li protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid of this example contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides that can, for example, average about 70 nucleotides in length with 15 nucleotide

overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C for 1 min.

For example, a minigene is prepared as follows. For a first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: In an example using eight oligonucleotides, i.e., four pairs of primers, oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 23: The Plasmid Construct and the Degree to Which It Induces Immunogenicity.

The degree to which a plasmid construct, for example a plasmid constructed in accordance with the previous Example, is able to induce immunogenicity is confirmed *in vitro* by determining epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (see, e.g., Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by diseased or transfected target cells, and then determining the concentration of peptide necessary to obtain equivalent levels of lysis or lymphokine release (see, e.g., Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Alternatively, immunogenicity is confirmed through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analyzed using cytotoxicity and proliferation assays, respectively, as detailed e.g., in Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to confirm the capacity of a DNA minigene construct containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ⁵¹Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine.

It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes, whereby it is also found that the minigene elicits appropriate immune responses directed toward the provided epitopes.

To confirm the capacity of a class II epitope-encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitopes that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ³H-thymidine incorporation proliferation assay, (see, *e.g.*, Alexander *et al.* *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in the previous Example, can also be confirmed as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (see, *e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10⁷ pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an alpha, beta and/or gamma IFN ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes. The use of prime boost protocols in humans is described below in the Example entitled "Induction of CTL Responses Using a Prime Boost Protocol."

Example 24: Peptide Compositions for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent 109P1D4 expression in persons who are at risk for tumors that bear this antigen. For example, a polypeptidic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in the above Examples, which are also selected to target greater than 80% of the population, is administered to individuals at risk for a 109P1D4-associated tumor.

For example, a peptide-based composition is provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against 109P1D4-associated disease.

Alternatively, a composition typically comprising transfecting agents is used for the administration of a nucleic acid-

based vaccine in accordance with methodologies known in the art and disclosed herein.

Example 25: Polyepitopic Vaccine Compositions Derived from Native 109P1D4 Sequences

A native 109P1D4 polypeptide sequence is analyzed, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polypeptide that comprise multiple epitopes. The "relatively short" regions are preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct or overlapping, "nested" epitopes can be used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

The vaccine composition will include, for example, multiple CTL epitopes from 109P1D4 antigen and at least one HTL epitope. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally, such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup(s) that is presently unknown. Furthermore, this embodiment (excluding an analoged embodiment) directs the immune response to multiple peptide sequences that are actually present in native 109P1D4, thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing peptide or nucleic acid vaccine compositions.

Related to this embodiment, computer programs are available in the art which can be used to identify in a target sequence, the greatest number of epitopes per sequence length.

Example 26: Polyepitopic Vaccine Compositions from Multiple Antigens

The 109P1D4 peptide epitopes of the present invention are used in conjunction with epitopes from other target tumor-associated antigens, to create a vaccine composition that is useful for the prevention or treatment of cancer that expresses 109P1D4 and such other antigens. For example, a vaccine composition can be provided as a single polypeptide that incorporates multiple epitopes from 109P1D4 as well as tumor-associated antigens that are often expressed with a target cancer associated with 109P1D4 expression, or can be administered as a composition comprising a cocktail of one or more discrete epitopes. Alternatively, the vaccine can be administered as a minigene construct or as dendritic cells which have been loaded with the peptide epitopes *in vitro*.

Example 27: Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific antibodies, CTL or HTL directed to 109P1D4. Such an analysis can be performed in a manner described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In this Example, peptides in accordance with the invention are used as a reagent for diagnostic or

prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, 109P1D4 HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of disease or following immunization comprising a 109P1D4 peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5' triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive non-diseased donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the 109P1D4 epitope, and thus the status of exposure to 109P1D4, or exposure to a vaccine that elicits a protective or therapeutic response.

Example 28: Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from 109P1D4-associated disease or who have been vaccinated with a 109P1D4 vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any 109P1D4 vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 μ g/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 μ g/ml to each well and HBV core 128-140 epitope is added at 1 μ g/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 μ l/well of complete RPMI. On days 3 and 10, 100 μ l of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with non-diseased control subjects as previously described (Rehermann, *et al.*, *Nature Med.*

2:1104,1108, 1996; Rehmann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehmann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al.* *J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μ M, and labeled with 100 μ Ci of 51 Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well 51 Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(experimental\ release - spontaneous\ release) / (maximum\ release - spontaneous\ release)]$. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to 109P1D4 or a 109P1D4 vaccine.

Similarly, Class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 μ g/ml synthetic peptide of the invention, whole 109P1D4 antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μ Ci 3 H-thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for 3 H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of 3 H-thymidine incorporation in the presence of antigen divided by the 3 H-thymidine incorporation in the absence of antigen.

Example 29: Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 individuals are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μ g of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μ g peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μ g of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient

centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 30: Phase II Trials in Patients Expressing 109P1D4

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to patients having cancer that expresses 109P1D4. The main objectives of the trial are to determine an effective dose and regimen for inducing CTLs in cancer patients that express 109P1D4, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of these patients, as manifested, e.g., by the reduction and/or shrinking of lesions. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65 and represent diverse ethnic backgrounds. All of them have a tumor that expresses 109P1D4.

Clinical manifestations or antigen-specific T-cell responses are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of 109P1D4-associated disease.

Example 31: Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol similar in its underlying principle to that used to confirm the efficacy of a DNA vaccine in transgenic mice, such as described above in the Example entitled "The Plasmid Construct and the Degree to Which It Induces Immunogenicity," can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization may be performed using an expression vector, such as that constructed in the Example entitled "Construction of 'Minigene' Multi-Epitope DNA Plasmids" in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of response sufficient to achieve a therapeutic or protective immunity against 109P1D4 is generated.

Example 32: Administration of Vaccine Compositions Using Dendritic Cells (DC)

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction, respectively, of the target cells that bear the 109P1D4 protein from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-comprising peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides, and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (see, e.g., *Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although 2.5×10^6 DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC generated after treatment with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10} . Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoiectin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5×10^8 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoiectin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

Alternatively, *ex vivo* CTL or HTL responses to 109P1D4 antigens can be induced by incubating, in tissue culture, the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cells, *i.e.*, tumor cells.

Example 33: An Alternative Method of Identifying and Confirming Motif-Bearing Peptides

Another method of identifying and confirming motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can be transfected with nucleic acids that express the antigen of interest, e.g. 109P1D4. Peptides produced by endogenous antigen processing of peptides produced as a result of transfection will then bind to HLA molecules within the cell and be transported and displayed on the cell's surface. Peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, e.g., by mass spectral analysis (e.g., Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express endogenous HLA molecules can be transfected with an expression

construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can then be transfected with nucleic acids that encode 109P1D4 to isolate peptides corresponding to 109P1D4 that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

Example 34: Complementary Polynucleotides

Sequences complementary to the 109P1D4-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring 109P1D4. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using, e.g., OLIGO 4.06 software (National Biosciences) and the coding sequence of 109P1D4. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to a 109P1D4-encoding transcript.

Example 35: Purification of Naturally-occurring or Recombinant 109P1D4 Using 109P1D4-Specific Antibodies

Naturally occurring or recombinant 109P1D4 is substantially purified by immunoaffinity chromatography using antibodies specific for 109P1D4. An immunoaffinity column is constructed by covalently coupling anti-109P1D4 antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing 109P1D4 are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of 109P1D4 (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/109P1D4 binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and GCR.P is collected.

Example 36: Identification of Molecules Which Interact with 109P1D4

109P1D4, or biologically active fragments thereof, are labeled with 125 I Bolton-Hunter reagent. (See, e.g., Bolton *et al.* (1973) *Biochem. J.* 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled 109P1D4, washed, and any wells with labeled 109P1D4 complex are assayed. Data obtained using different concentrations of 109P1D4 are used to calculate values for the number, affinity, and association of 109P1D4 with the candidate molecules.

Example 37: In Vivo Assay for 109P1D4 Tumor Growth Promotion

The effect of a 109P1D4 protein on tumor cell growth is evaluated *in vivo* by gene overexpression in tumor-bearing mice. For example, SCID mice are injected subcutaneously on each flank with 1×10^6 of either PC3, DU145 or 3T3 cells containing tkNeo empty vector or a nucleic acid sequence of the invention. At least two strategies can be used: (1) Constitutive expression under regulation of a promoter such as a constitutive promoter obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine

papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), or from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, provided such promoters are compatible with the host cell systems, and (2) Regulated expression under control of an inducible vector system, such as ecdysone, tet, etc., provided such promoters are compatible with the host cell systems. Tumor volume is then monitored at the appearance of palpable tumors and followed over time to determine if the cells expressing a gene of the invention grow at a faster rate and whether tumors of a 109P1D4 protein-expressing cells demonstrate characteristics of altered aggressiveness (e.g. enhanced metastasis, vascularization, reduced responsiveness to chemotherapeutic drugs).

Additionally, mice can be implanted with 1×10^5 of the same cells orthotopically to determine if a protein of the invention has an effect on local growth in the prostate or on the ability of the cells to metastasize, specifically to lungs, lymph nodes, and bone marrow.

The assay is also useful to determine the inhibitory effect of candidate therapeutic compositions, such as for example, 109P1D4 protein-related intrabodies, 109P1D4 gene-related antisense molecules and ribozymes.

Example 38: 109P1D4 Monoclonal Antibody-mediated Inhibition of Tumors *In Vivo*

The significant expression of 109P1D4 proteins in the cancer tissues of Table I and its restrictive expression in normal tissues, together with its expected cell surface expression, makes 109P1D4 proteins excellent targets for antibody therapy. Similarly, 109P1D4 proteins are a target for T cell-based immunotherapy. Thus, for 109P1D4 genes expressed, e.g., in prostate cancer, the therapeutic efficacy of anti-109P1D4 protein mAbs in human prostate cancer xenograft mouse models is evaluated by using androgen-independent LAPC-4 and LAPC-9 xenografts (Craft, N., *et al.*, Cancer Res, 1999, 59(19): p. 5030-6) and the androgen independent recombinant cell line PC3-of 109P1D4 (see, e.g., Kaighn, M.E., *et al.*, Invest Urol, 1979, 17(1): p. 16-23); analogous models are used for other cancers.

Antibody efficacy on tumor growth and metastasis formation is studied, e.g., in a mouse orthotopic prostate cancer xenograft models and mouse kidney xenograft models. The antibodies can be unconjugated, as discussed in this Example, or can be conjugated to a therapeutic modality, as appreciated in the art. Anti-109P1D4 protein mAbs inhibit formation of both the androgen-dependent LAPC-9 and androgen-independent PC3-109P1D4 protein tumor xenografts. Anti-109P1D4 protein mAbs also retard the growth of established orthotopic tumors and prolonged survival of tumor-bearing mice. These results indicate the utility of anti-109P1D4 protein mAbs in the treatment of local and advanced stages of prostate cancer. (See, e.g., (Saffran, D., *et al.*, PNAS 10:1073-1078 or World Wide Web URL www.pnas.org/cgi/doi/10.1073/pnas.051624698).

Administration of the anti-109P1D4 protein mAbs lead to retardation of established orthotopic tumor growth and inhibition of metastasis to distant sites, resulting in a significant prolongation in the survival of tumor-bearing mice. These studies indicate that proteins of the invention are attractive targets for immunotherapy and demonstrate the therapeutic potential of anti-109P1D4 protein mAbs for the treatment of local and metastatic cancer. This example demonstrates that unconjugated 109P1D4 protein-related monoclonal antibodies are effective to inhibit the growth of human prostate tumor xenografts and human kidney xenografts grown in SCID mice; accordingly a combination of such efficacious monoclonal antibodies is also effective.

Tumor Inhibition using multiple unconjugated mAbs

Materials and Methods

109P1D4 Protein-related Monoclonal Antibodies:

Monoclonal antibodies are raised against proteins of the invention as described in the Example entitled "Generation of 109P1D4 Monoclonal Antibodies". The antibodies are characterized by ELISA, Western blot, FACS, and

immunoprecipitation for their capacity to bind to the respective protein of the invention. Epitope mapping data for, e.g., the anti-109P1D4 protein mAbs, as determined by ELISA and Western analysis, indicate that the antibodies recognize epitopes on the respective 109P1D4 protein. Immunohistochemical analysis of prostate cancer tissues and cells with these antibodies is performed.

The monoclonal antibodies are purified from ascites or hybridoma tissue culture supernatants by Protein-G Sepharose chromatography, dialyzed against PBS, filter sterilized, and stored at -20°C. Protein determinations are performed by a Bradford assay (Bio-Rad, Hercules, CA). A therapeutic monoclonal antibody or a cocktail comprising a mixture of individual monoclonal antibodies is prepared and used for the treatment of mice receiving subcutaneous or orthotopic injections of LAPC-9 prostate tumor xenografts.

Cancer Xenografts and Cell Lines

The LAPC-9 xenograft, which expresses a wild-type androgen receptor and produces prostate-specific antigen (PSA), is passaged in 6- to 8-week-old male ICR-severe combined immunodeficient (SCID) mice (Taconic Farms) by s.c. trocar implant (Craft, N., et al., supra). The prostate carcinoma cell line PC3 (American Type Culture Collection) is maintained in RPMI supplemented with L-glutamine and 10% FBS.

Recombinant PC3 and 3T3- cell populations expressing a protein of the invention are generated by retroviral gene transfer as described in Hubert, R.S., et al., STEAP: a prostate-specific cell-surface antigen highly expressed in human prostate tumors. *Proc Natl Acad Sci U S A*, 1999. 96(25): p. 14523-8. Anti-protein of the invention staining is detected by using an FITC-conjugated goat anti-mouse antibody (Southern Biotechnology Associates) followed by analysis on a Coulter Epics-XL flow cytometer.

Xenograft Mouse Models

Subcutaneous (s.c.) tumors are generated by injection of 1×10^6 LAPC-9, PC3, recombinant PC3-protein of the invention, 3T3 or recombinant 3T3-protein of the invention cells mixed at a 1:1 dilution with Matrigel (Collaborative Research) in the right flank of male SCID mice. To test antibody efficacy on tumor formation, i.p. antibody injections are started on the same day as tumor-cell injections. As a control, mice are injected with either purified mouse IgG (ICN) or PBS; or a purified monoclonal antibody that recognizes an irrelevant antigen not expressed in human cells. In preliminary studies, no difference is found between mouse IgG or PBS on tumor growth. Tumor sizes are determined by vernier caliper measurements, and the tumor volume is calculated as length x width x height. Mice with s.c. tumors greater than 1.5 cm in diameter are sacrificed. PSA levels are determined by using a PSA ELISA kit (Anogen, Mississauga, Ontario). Circulating levels of, e.g., anti-109P1D4 protein mAbs are determined by a capture ELISA kit (Bethyl Laboratories, Montgomery, TX). (See, e.g., Saffran, D., et al., PNAS 10:1073-1078 or www.pnas.org/cgi/doi/10.1073/pnas.051624698)

Orthotopic injections are performed under anesthesia by using ketamine/xylazine. For prostate orthotopic studies, an incision is made through the abdominal muscles to expose the bladder and seminal vesicles, which then are delivered through the incision to expose the dorsal prostate. LAPC-9 or PC3 cells (5×10^5) mixed with Matrigel are injected into each dorsal lobe in a 10- μ l volume. To monitor tumor growth, mice are bled on a weekly basis for determination of PSA levels. The mice are segregated into groups for the appropriate treatments, with anti-protein of the invention or control mAbs being injected i.p.

Anti-109P1D4 Protein mAbs Inhibit Growth of Respective 109P1D4 Protein-Expressing Xenograft-Cancer Tumors

The effect of anti-109P1D4 protein mAbs on tumor formation is tested by using LAPC-9 and recombinant PC3-protein of the invention orthotopic models. As compared with the s.c. tumor model, the orthotopic model, which requires injection of tumor cells directly in the mouse prostate or kidney, respectively, results in a local tumor growth, development of metastasis in distal sites, deterioration of mouse health, and subsequent death (Saffran, D., et al., PNAS supra; Fu, X., et al.,

Int J Cancer, 1992. 52(6): p. 987-90; Kubota, T., J Cell Biochem, 1994. 56(1): p. 4-8). The features make the orthotopic model more representative of human disease progression and allowed us to follow the therapeutic effect of mAbs on clinically relevant end points.

Accordingly, tumor cells are injected into the mouse prostate or kidney, and 2 days later, the mice are segregated into two groups and treated with either: a) 200-500 μ g, of anti-109P1D4 protein Ab, or b) PBS three times per week for two to five weeks.

A major advantage of the orthotopic prostate-cancer model is the ability to study the development of metastases. Formation of metastasis in mice bearing established orthotopic tumors is studied by IHC analysis on lung sections using an antibody against a prostate-specific cell-surface protein STEAP expressed at high levels in LAPC-9 xenografts (Hubert, R.S., *et al.*, Proc Natl Acad Sci U S A, 1999. 96(25): p. 14523-8).

Mice bearing established orthotopic LAPC-9 or recombinant PC3-109P1D4 protein tumors are administered 1000 μ g injections of either anti-109P1D4 protein mAbs or PBS over a 4-week period. Mice in both groups are allowed to establish a high tumor burden (PSA levels greater than 300 ng/ml for LAPC-9), to ensure a high frequency of metastasis formation in mouse lungs. Mice then are killed and their prostate and lungs are analyzed for the presence of tumor cells by IHC analysis.

These studies demonstrate a broad anti-tumor efficacy of anti-109P1D4 protein antibodies on initiation and progression of prostate cancer in xenograft mouse models. Anti-109P1D4 protein antibodies inhibit tumor formation of both androgen-dependent and androgen-independent tumors, retard the growth of already established tumors, and prolong the survival of treated mice. Moreover, anti-109P1D4 protein mAbs demonstrate a dramatic inhibitory effect on the spread of local prostate tumor to distal sites, even in the presence of a large tumor burden. Thus, anti-109P1D4 protein mAbs are efficacious on major clinically relevant end points (tumor growth), prolongation of survival, and health.

Example 39: Therapeutic and Diagnostic use of Anti-109P1D4 Antibodies in Humans.

Anti-109P1D4 monoclonal antibodies are safely and effectively used for diagnostic, prophylactic, prognostic and/or therapeutic purposes in humans. Western blot and immunohistochemical analysis of cancer tissues and cancer xenografts with anti-109P1D4 mAb show strong extensive staining in carcinoma but significantly lower or undetectable levels in normal tissues. Detection of 109P1D4 in carcinoma and in metastatic disease demonstrates the usefulness of the mAb as a diagnostic and/or prognostic indicator. Anti-109P1D4 antibodies are therefore used in diagnostic applications such as immunohistochemistry of kidney biopsy specimens to detect cancer from suspect patients.

As determined by flow cytometry, anti-109P1D4 mAb specifically binds to carcinoma cells. Thus, anti-109P1D4 antibodies are used in diagnostic whole body imaging applications, such as radioimmunoscinigraphy and radioimmunotherapy, (see, e.g., Potamianos S., *et al.* Anticancer Res 20(2A):925-948 (2000)) for the detection of localized and metastatic cancers that exhibit expression of 109P1D4. Shedding or release of an extracellular domain of 109P1D4 into the extracellular milieu, such as that seen for alkaline phosphodiesterase B10 (Meerson, N. R., Hepatology 27:563-568 (1998)), allows diagnostic detection of 109P1D4 by anti-109P1D4 antibodies in serum and/or urine samples from suspect patients.

Anti-109P1D4 antibodies that specifically bind 109P1D4 are used in therapeutic applications for the treatment of cancers that express 109P1D4. Anti-109P1D4 antibodies are used as an unconjugated modality and as conjugated form in which the antibodies are attached to one of various therapeutic or imaging modalities well known in the art, such as a prodrugs, enzymes or radioisotopes. In preclinical studies, unconjugated and conjugated anti-109P1D4 antibodies are tested for efficacy of tumor prevention and growth inhibition in the SCID mouse cancer xenograft models, e.g., kidney cancer

models AGS-K3 and AGS-K6, (see, e.g., the Example entitled "109P1D4 Monoclonal Antibody-mediated Inhibition of Bladder and Lung Tumors *In Vivo*"). Either conjugated and unconjugated anti-109P1D4 antibodies are used as a therapeutic modality in human clinical trials either alone or in combination with other treatments as described in following Examples.

Example 40: Human Clinical Trials for the Treatment and Diagnosis of Human Carcinomas through use of Human Anti-109P1D4 Antibodies *In vivo*

Antibodies are used in accordance with the present invention which recognize an epitope on 109P1D4, and are used in the treatment of certain tumors such as those listed in Table I. Based upon a number of factors, including 109P1D4 expression levels, tumors such as those listed in Table I are presently preferred indications. In connection with each of these indications, three clinical approaches are successfully pursued.

I.) **Adjunctive therapy:** In adjunctive therapy, patients are treated with anti-109P1D4 antibodies in combination with a chemotherapeutic or antineoplastic agent and/or radiation therapy. Primary cancer targets, such as those listed in Table I, are treated under standard protocols by the addition anti-109P1D4 antibodies to standard first and second line therapy. Protocol designs address effectiveness as assessed by reduction in tumor mass as well as the ability to reduce usual doses of standard chemotherapy. These dosage reductions allow additional and/or prolonged therapy by reducing dose-related toxicity of the chemotherapeutic agent. Anti-109P1D4 antibodies are utilized in several adjunctive clinical trials in combination with the chemotherapeutic or antineoplastic agents adriamycin (advanced prostate carcinoma), cisplatin (advanced head and neck and lung carcinomas), taxol (breast cancer), and doxorubicin (preclinical).

II.) **Monotherapy:** In connection with the use of the anti-109P1D4 antibodies in monotherapy of tumors, the antibodies are administered to patients without a chemotherapeutic or antineoplastic agent. In one embodiment, monotherapy is conducted clinically in end stage cancer patients with extensive metastatic disease. Patients show some disease stabilization. Trials demonstrate an effect in refractory patients with cancerous tumors.

III.) **Imaging Agent:** Through binding a radionuclide (e.g., iodine or yttrium (^{131}I , ^{90}Y) to anti-109P1D4 antibodies, the radiolabeled antibodies are utilized as a diagnostic and/or imaging agent. In such a role, the labeled antibodies localize to both solid tumors, as well as, metastatic lesions of cells expressing 109P1D4. In connection with the use of the anti-109P1D4 antibodies as imaging agents, the antibodies are used as an adjunct to surgical treatment of solid tumors, as both a pre-surgical screen as well as a post-operative follow-up to determine what tumor remains and/or returns. In one embodiment, a (^{111}In)-109P1D4 antibody is used as an imaging agent in a Phase I human clinical trial in patients having a carcinoma that expresses 109P1D4 (by analogy see, e.g., Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991)). Patients are followed with standard anterior and posterior gamma camera. The results indicate that primary lesions and metastatic lesions are identified.

Dose and Route of Administration

As appreciated by those of ordinary skill in the art, dosing considerations can be determined through comparison with the analogous products that are in the clinic. Thus, anti-109P1D4 antibodies can be administered with doses in the range of 5 to 400 mg/m², with the lower doses used, e.g., in connection with safety studies. The affinity of anti-109P1D4 antibodies relative to the affinity of a known antibody for its target is one parameter used by those of skill in the art for determining analogous dose regimens. Further, anti-109P1D4 antibodies that are fully human antibodies, as compared to the chimeric antibody, have slower clearance; accordingly, dosing in patients with such fully human anti-109P1D4 antibodies can be lower, perhaps in the range of 50 to 300 mg/m², and still remain efficacious. Dosing in mg/m², as opposed to the conventional measurement of dose in mg/kg, is a measurement based on surface area and is a convenient dosing measurement that is designed to include patients of all sizes from infants to adults.

Three distinct delivery approaches are useful for delivery of anti-109P1D4 antibodies. Conventional intravenous delivery is one standard delivery technique for many tumors. However, in connection with tumors in the peritoneal cavity, such as tumors of the ovaries, biliary duct, other ducts, and the like, intraperitoneal administration may prove favorable for obtaining high dose of antibody at the tumor and to also minimize antibody clearance. In a similar manner, certain solid tumors possess vasculature that is appropriate for regional perfusion. Regional perfusion allows for a high dose of antibody at the site of a tumor and minimizes short term clearance of the antibody.

Clinical Development Plan (CDP)

Overview: The CDP follows and develops treatments of anti-109P1D4 antibodies in connection with adjunctive therapy, monotherapy, and as an imaging agent. Trials initially demonstrate safety and thereafter confirm efficacy in repeat doses. Trials are open label comparing standard chemotherapy with standard therapy plus anti-109P1D4 antibodies. As will be appreciated, one criteria that can be utilized in connection with enrollment of patients is 109P1D4 expression levels in their tumors as determined by biopsy.

As with any protein or antibody infusion-based therapeutic, safety concerns are related primarily to (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 109P1D4. Standard tests and follow-up are utilized to monitor each of these safety concerns. Anti-109P1D4 antibodies are found to be safe upon human administration.

Example 41: Human Clinical Trial Adjunctive Therapy with Human Anti-109P1D4 Antibody and Chemotherapeutic Agent

A phase I human clinical trial is initiated to assess the safety of six intravenous doses of a human anti-109P1D4 antibody in connection with the treatment of a solid tumor, e.g., a cancer of a tissue listed in Table I. In the study, the safety of single doses of anti-109P1D4 antibodies when utilized as an adjunctive therapy to an antineoplastic or chemotherapeutic agent as defined herein, such as, without limitation: cisplatin, topotecan, doxorubicin, adriamycin, taxol, or the like, is assessed. The trial design includes delivery of six single doses of an anti-109P1D4 antibody with dosage of antibody escalating from approximately about 25 mg/m² to about 275 mg/m² over the course of the treatment in accordance with the following schedule:

	Day 0	Day 7	Day 14	Day 21	Day 28	Day 35
mAb Dose	25	75	125	175	225	275
	mg/m ²	mg/m ²	mg/m ²	mg/m ²	mg/m ²	mg/m ²
Chemotherapy	+	+	+	+	+	+
(standard dose)						

Patients are closely followed for one-week following each administration of antibody and chemotherapy. In particular, patients are assessed for the safety concerns mentioned above: (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the human antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 109P1D4. Standard tests and follow-up are utilized to monitor each of these safety concerns. Patients are also assessed for clinical outcome, and particularly reduction in tumor mass as evidenced by MRI or other imaging.

The anti-109P1D4 antibodies are demonstrated to be safe and efficacious, Phase II trials confirm the efficacy and refine optimum dosing.

Example 42: Human Clinical Trial: Monotherapy with Human Anti-109P1D4 Antibody

Anti-109P1D4 antibodies are safe in connection with the above-discussed adjunctive trial, a Phase II human clinical trial confirms the efficacy and optimum dosing for monotherapy. Such trial is accomplished, and entails the same safety and outcome analyses, to the above-described adjunctive trial with the exception being that patients do not receive chemotherapy concurrently with the receipt of doses of anti-109P1D4 antibodies.

Example 43: Human Clinical Trial: Diagnostic Imaging with Anti-109P1D4 Antibody

Once again, as the adjunctive therapy discussed above is safe within the safety criteria discussed above, a human clinical trial is conducted concerning the use of anti-109P1D4 antibodies as a diagnostic imaging agent. The protocol is designed in a substantially similar manner to those described in the art, such as in Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991). The antibodies are found to be both safe and efficacious when used as a diagnostic modality.

Example 44: 109P1D4 Functional Assays

I. Phosphorylation of 109P1D4 on tyrosine residues

One hallmark of the cancer cell phenotype is the active signal transduction of surface bound receptor molecules, such as the EGF receptor, through tyrosine phosphorylation of their cytoplasmic domains and their subsequent interaction with cytosolic signaling molecules. To address the possibility that 109P1D4 is phosphorylated on its cytoplasmic tyrosine residues, 293T cells were transfected with the 109P1D4 gene in an expression plasmid such that the 109P1D4 gene was fused with a Myc/His tag, and were then stimulated with pervanadate (a 1:1 mixture of Na_2VO_4 and H_2O_2). After solubilization of the cells in Triton X-100, the 109P1D4 protein was immunoprecipitated with anti-His polyclonal antibody (pAb), subjected to SDS-PAGE and Western blotted with anti-phosphotyrosine. Equivalent immunoprecipitates were Western blotted with anti-His antibody. In Figure 22, 109P1D4 exhibits tyrosine phosphorylation only upon cell treatment with pervanadate and not without treatment. This suggests that pervanadate, which inhibits intracellular protein tyrosine phosphatases (PTPs), allows the accumulation of phosphotyrosine (tyrosine kinase activity) on 109P1D4. Further, a large amount of the 109P1D4 protein is sequestered into the insoluble fraction upon pervanadate activation, suggesting its association with cytoskeletal components. Similar effects of partial insolubility in Triton X-100 have been observed for cadherins, proteins that are related to protocadherins based on homology of their extracellular domains. Cadherins are known to interact with cytoskeletal proteins including actin, which are not readily soluble in the detergent conditions used in this study. Together, these data indicate that 109P1D4 is a surface receptor with the capacity to be phosphorylated on tyrosine and to bind to signaling molecules that possess SH2 or PTB binding domains, including but not limited to, phospholipase-Cy1, Grb2, Shc, Crk, PI-3-kinase p85 subunit, rasGAP, Src-family kinases and abl-family kinases. Such interactions are important for downstream signaling through 109P1D4, leading to changes in adhesion, proliferation, migration or elaboration of secreted factors. In addition, 109P1D4 protein interacts with cytoskeletal components such as actin that facilitates its cell adhesion functions. These phenotypes are enhanced in 109P1D4 expressing tumor cells and contribute to their increased capacity to metastasize and grow in vivo.

Thus, when 109P1D4 plays a role in cell signaling and phosphorylation, it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 45: 109P1D4 RNA Interference (RNAI)

RNA interference (RNAi) technology is implemented to a variety of cell assays relevant to oncology. RNAi is a post-transcriptional gene silencing mechanism activated by double-stranded RNA (dsRNA). RNAi induces specific mRNA degradation leading to changes in protein expression and subsequently in gene function. In mammalian cells, these dsRNAs called short interfering RNA (siRNA) have the correct composition to activate the RNAi pathway targeting for degradation, specifically some mRNAs. See, Elbashir S.M., *et. al.*, Duplexes of 21-nucleotide RNAs Mediate RNA interference in Cultured Mammalian Cells, Nature 411(6836):494-8 (2001). Thus, RNAi technology is used successfully in mammalian cells to silence targeted genes.

Loss of cell proliferation control is a hallmark of cancerous cells; thus, assessing the role of 109P1D4 in cell survival/proliferation assays is relevant. Accordingly, RNAi was used to investigate the function of the 109P1D4 antigen. To generate siRNA for 109P1D4, algorithms were used that predict oligonucleotides that exhibit the critical molecular parameters (G:C content, melting temperature, etc.) and have the ability to significantly reduce the expression levels of the 109P1D4 protein when introduced into cells. Accordingly, three targeted sequences for the 109P1D4 siRNA are: 5' AAGAGGATACTGGTGAGATCT 3' (SEQ ID NO: 57)(oligo 109P1D4.a), 5' AAGAGCAATGGTGCTGGTAAA 3' (SEQ ID NO: 58)(oligo 109P1D4.c), and 5' AACACCAGAAGGAGACAAGAT 3' (SEQ ID NO: 59)(oligo 109P1D4.d). In accordance with this Example, 109P1D4 siRNA compositions are used that comprise siRNA (double stranded, short interfering RNA) that correspond to the nucleic acid ORF sequence of the 109P1D4 protein or subsequences thereof. Thus, siRNA subsequences are used in this manner are generally 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 or more than 35 contiguous RNA nucleotides in length. These siRNA sequences are complementary and non-complementary to at least a portion of the mRNA coding sequence. In a preferred embodiment, the subsequences are 19-25 nucleotides in length, most preferably 21-23 nucleotides in length. In preferred embodiments, these siRNA achieve knockdown of 109P1D4 antigen in cells expressing the protein and have functional effects as described below.

The selected siRNAs (109P1D4.a, 109P1D4.c, 109P1D4.d oligos) were tested in LNCaP cells in the ³H-thymidine incorporation assay (measures cellular proliferation). Moreover, the oligonucleotides achieved knockdown of 109P1D4 antigen in cells expressing the protein and had functional effects as described below using the following protocols.

Mammalian siRNA transfections: The day before siRNA transfection, the different cell lines were plated in media (RPMI 1640 with 10% FBS w/o antibiotics) at 2x10³ cells/well in 80 μ (96 well plate format) for the proliferation assay. In parallel with the 109P1D4 specific siRNA oligo, the following sequences were included in every experiment as controls: a) Mock transfected cells with Lipofectamine 2000 (Invitrogen, Carlsbad, CA) and annealing buffer (no siRNA); b) Luciferase-4 specific siRNA (targeted sequence: 5'-AAGGGACGAAGACGAACACUUCTT-3') (SEQ ID NO: 60); and, c) Eg5 specific siRNA (targeted sequence: 5'-AACTGAAGACCTGAAGACAATAA-3') (SEQ ID NO: 61). siRNAs were used at 10nM and μ g/ml Lipofectamine 2000 final concentration.

The procedure was as follows: The siRNAs were first diluted in OPTIMEM (serum-free transfection media, Invitrogen) at 0.1 μ M (10-fold concentrated) and incubated 5-10 min RT. Lipofectamine 2000 was diluted at 10 μ g/ml (10-fold concentrated) for the total number transfections and incubated 5-10 minutes at room temperature (RT). Appropriate amounts of diluted 10-fold concentrated Lipofectamine 2000 were mixed 1:1 with diluted 10-fold concentrated siRNA and incubated at RT for 20-30" (5-fold concentrated transfection solution). 20 μ l of the 5-fold concentrated transfection solutions were added to the respective samples and incubated at 37°C for 96 hours before analysis.

³H-Thymidine incorporation assay: The proliferation assay is a ³H-thymidine incorporation method for determining the proliferation of viable cells by uptake and incorporation of label into DNA.

The procedure was as follows: Cells growing in log phase are trypsinized, washed, counted and plated in 96-well

plates at 1000-4000 cells/well in 10% FBS. After 4-8 hrs, the media is replaced. The cells are incubated for 24-72 hrs, pulsed with ^3H -Thy at 1.5 $\mu\text{Ci/ml}$ for 14 hrs, harvested onto a filtermat and counted in scintillation cocktail on a Microbeta triluor or other counter.

In order to address the function of 109P1D4 in cells, 109P1D4 was silenced by transfecting the endogenously expressing 109P1D4 cell line (LNCaP) with the 109P1D4 specific siRNAs (109P1D4.a, 109P1D4.c, and 109P1D4.d) along with negative siRNA controls (Luc4, targeted sequence not represented in the human genome), a positive siRNA control (targeting Eg5) and no siRNA oligo (LF2K) (Figure 23). The results indicated that when these cells are treated with siRNA specifically targeting the 109P1D4 mRNA, the resulting "109P1D4 deficient cells" showed diminished cell proliferation as measured by this assay (e.g., see oligo 109P1D4.a treated cells).

These data indicate that 109P1D4 plays an important role in the proliferation of cancer cells and that the lack of 109P1D4 clearly decreases the survival potential of these cells. It is to be noted that 109P1D4 is constitutively expressed in many tumor cell lines. 109P1D4 serves a role in malignancy; its expression is a primary indicator of disease, where such disease is often characterized by high rates of uncontrolled cell proliferation and diminished apoptosis. Correlating cellular phenotype with gene knockdown following RNAi treatments is important, and allows one to draw valid conclusions and rule out toxicity or other non-specific effects of these reagents. To this end, assays to measure the levels of expression of both protein and mRNA for the target after RNAi treatments are important, including Western blotting, FACS staining with antibody, immunoprecipitation, Northern blotting or RT-PCR (Taqman or standard methods). Any phenotypic effect of the siRNAs in these assays should be correlated with the protein and/or mRNA knockdown levels in the same cell lines. 109P1D4 protein is reduced after treatment with siRNA oligos described above (e.g., 109P1D4.a, etc.)

A method to analyze 109P1D4 related cell proliferation is the measurement of DNA synthesis as a marker for proliferation. Labeled DNA precursors (i.e. ^3H -Thymidine) are used and their incorporation to DNA is quantified. Incorporation of the labeled precursor into DNA is directly proportional to the amount of cell division occurring in the culture. Another method used to measure cell proliferation is performing clonogenic assays. In these assays, a defined number of cells are plated onto the appropriate matrix and the number of colonies formed after a period of growth following siRNA treatment is counted.

In 109P1D4 cancer target validation, complementing the cell survival/proliferation analysis with apoptosis and cell cycle profiling studies are considered. The biochemical hallmark of the apoptotic process is genomic DNA fragmentation, an irreversible event that commits the cell to die. A method to observe fragmented DNA in cells is the immunological detection of histone-complexed DNA fragments by an immunoassay (i.e. cell death detection ELISA) which measures the enrichment of histone-complexed DNA fragments (mono- and oligo-nucleosomes) in the cytoplasm of apoptotic cells. This assay does not require pre-labeling of the cells and can detect DNA degradation in cells that do not proliferate in vitro (i.e. freshly isolated tumor cells).

The most important effector molecules for triggering apoptotic cell death are caspases. Caspases are proteases that when activated cleave numerous substrates at the carboxy-terminal site of an aspartate residue mediating very early stages of apoptosis upon activation. All caspases are synthesized as pro-enzymes and activation involves cleavage at aspartate residues. In particular, caspase 3 seems to play a central role in the initiation of cellular events of apoptosis. Assays for determination of caspase 3 activation detect early events of apoptosis. Following RNAi treatments, Western blot detection of active caspase 3 presence or proteolytic cleavage of products (i.e. PARP) found in apoptotic cells further support an active induction of apoptosis. Because the cellular mechanisms that result in apoptosis are complex, each has its advantages and limitations. Consideration of other criteria/endpoints such as cellular morphology, chromatin condensation, membrane blebbing, apoptotic bodies help to further support cell death as apoptotic. Since not all the gene targets that

regulate cell growth are anti-apoptotic, the DNA content of permeabilized cells is measured to obtain the profile of DNA content or cell cycle profile. Nuclei of apoptotic cells contain less DNA due to the leaking out to the cytoplasm (sub-G1 population). In addition, the use of DNA stains (i.e., propidium iodide) also differentiate between the different phases of the cell cycle in the cell population due to the presence of different quantities of DNA in G0/G1, S and G2/M. In these studies the subpopulations can be quantified.

For the 109P1D4 gene, RNAi studies facilitate the understanding of the contribution of the gene product in cancer pathways. Such active RNAi molecules have use in identifying assays to screen for mAbs that are active anti-tumor therapeutics. Further, siRNA are administered as therapeutics to cancer patients for reducing the malignant growth of several cancer types, including those listed in Table I. When 109P1D4 plays a role in cell survival, cell proliferation, tumorigenesis, or apoptosis, it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Throughout this application, various website data content, publications, patent applications and patents are referenced. (Websites are referenced by their Uniform Resource Locator, or URL, addresses on the World Wide Web.)

The present invention is not to be limited in scope by the embodiments disclosed herein, which are intended as single illustrations of individual aspects of the invention, and any that are functionally equivalent are within the scope of the invention. Various modifications to the models and methods of the invention, in addition to those described herein, will become apparent to those skilled in the art from the foregoing description and teachings, and are similarly intended to fall within the scope of the invention. Such modifications or other embodiments can be practiced without departing from the true scope and spirit of the invention.

TABLES:

TABLE I: Tissues that Express 109P1D4 when malignant:

Prostate
Bladder
Kidney
Colon
Lymphoma
Lung
Pancreas
Ovary
Breast
Uterus
Stomach
Rectum
Cervix
Lymph Node
Bone

TABLE II: Amino Acid Abbreviations

SINGLE LETTER	THREE LETTER	FULL NAME
F	Phe	phenylalanine
L	Leu	leucine
S	Ser	serine
Y	Tyr	tyrosine
C	Cys	cysteine
W	Trp	tryptophan
P	Pro	proline
H	His	histidine
Q	Gln	glutamine
R	Arg	arginine
I	Ile	isoleucine
M	Met	methionine
T	Thr	threonine
N	Asn	asparagine
K	Lys	lysine
V	Val	valine
A	Ala	alanine
D	Asp	aspartic acid
E	Glu	glutamic acid
G	Gly	glycine

[illegible]

TABLE IV:
HLA Class I/II Motifs/Supermotifs

TABLE IV (A): HLA Class I Supermotifs/Motifs

SUPERMOTIF	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T ILVMS		F WY
A2	L IVMATQ		I VMATL
A3	V SMATLI		R K
A24	Y FWIVLMT		F IYWLM
B7	P		V ILFMWYA
B27	R HK		F YLWMIVA
B44	E D		F WYLMVA
B58	A TS		F WYLI/MA
B62	Q LIVMP		F WYMI/VLA
MOTIFS			
A1	T SM		Y
A1		D EAS	Y
A2.1	L MVQIAT		V LIMAT
A3	L MVISATFCGD		K YRHFA
A11	V TMLISAGNCDF		K RYH
A24	Y FWM		F LIW
A*3101	M VTALIS		R K
A*3301	M VALFIST		R K
A*6801	A VTMSLI		R K
B*0702	P		L MFWYAIV
B*3501	P		L MFWYIVA
B51	P		L IVFWYAM
B*5301	P		I MFWYALV
B*5401	P		A TIVLMFWY

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE IV (B): HLA Class II Supermotif

1	6	9
W, F, Y, V, J, L	A, V, I, L, P, C, S, T	A, V, I, L, C, S, T, M, Y

TABLE IV (C): HLA Class II Motifs

MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred deleterious	FMYLIVW	M	T	W	I	VSTCPALIM	MH R		MH WDE
DR1	preferred deleterious	MFLIVWY			PAMQ FD		VMATSPLIC	M GDE	D	AVM
DR7	preferred deleterious	MFLIVWY	M	W	A		IVMSACTPL	M GRD		IV G
DR3	<u>MOTIFS</u>	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6			
Motif a preferred		LIVMFY			D					
Motif b preferred		LIVMFAY			DNQEST		KRH			
DR Supermotif		MFLIVWY					VMSTACPLI			

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (D): HLA Class I Supermotifs

	POSITION:	1	2	3	4	5	6	7	8	C-terminus
<u>SUPER-MOTIFS</u>										
A1			1° Anchor TILVMS							1° Anchor FWY
A2			1° Anchor LIVMATQ							1° Anchor LIVMAT
A3	Preferred deleterious		1° Anchor VSMATLI	YFW (4/5) DE (4/5)		YFW (3/5)	YFW (4/5)	P (4/5)		1° Anchor RK
A24			1° Anchor YFWIVLMT							1° Anchor FIYWLM
B7	Preferred deleterious	FWY (5/5) LIVM (3/5) DE (3/5); P(5/5); G(4/5); A(3/5); QN(3/5)	1° Anchor P	FWY (4/5)		DE (3/5)	G (4/5)	QN (4/5)	FWY (3/5) DE (4/5)	1° Anchor VILFMWYA
B27			1° Anchor RHK							1° Anchor FYLWMIVA
B44			1° Anchor ED							1° Anchor FWYLIMVA
B58			1° Anchor ATS							1° Anchor FWYLIVMA
B62			1° Anchor QLIVMP							1° Anchor FWYMI/VA

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (E): HLA Class I Motifs

	POSITION 1	2	3	4	5	6	7	8	9	C-terminus
A1 9-mer	preferred GFYW	<u>1°Anchor</u> STM	DEA	YFW		P	DEQN	YFW	or C-terminus <u>1°Anchor</u> Y	
	deleterious DE		RHKLVMP	A	G	A				
A1 9-mer	preferred GRHK	ASTCLIVM	<u>1°Anchor</u> DEAS	GSTC		ASTC	LIVM	DE	<u>1°Anchor</u> Y	
	deleterious A	RHKDEPYFW		DE	PQN	RHK	PG	GP		
A1 10-mer	preferred YFW	<u>1°Anchor</u> STM	DEAQN	A	YFWQN		PASTC	GDE	P	<u>1°Anchor</u> Y
	deleterious GP		RHKGLIVM	DE	RHK	QNA	RHKYFW	RHK	A	
A1 10-mer	preferred YFW	STCLIVM	<u>1°Anchor</u> DEAS	A	YFW		PG	G	YFW	<u>1°Anchor</u> Y
	deleterious RHK	RHKDEPYFW			P	G		PRHK	QN	
A2.1 9-mer	preferred YFW	<u>1°Anchor</u> LMIVQAT	YFW	STC	YFW		A	P	<u>1°Anchor</u> VLIMAT	
	deleterious DEP		DERKH			RKH	DERKH			
	POSITION: 1	2	3	4	5	6	7	8	9	C-Terminus
A2.1 10-mer	preferred AYFW	<u>1°Anchor</u> LMIVQAT	LVIM	G		G		FYWL VIM		<u>1°Anchor</u> VLIMAT
	deleterious DEP		DE	RKHA	P		RKH	DERKHK	RKH	
A3	preferred RHK	<u>1°Anchor</u> LMVISATFCGD	YFW	PRHKYF W	A	YFW		P	<u>1°Anchor</u> KYRHFA	
	deleterious DEP		DE							
A11	preferred A	<u>1°Anchor</u> VTLMISAGNCD F	YFW	YFW	A	YFW	YFW	P	<u>1°Anchor</u> KRYH	
	deleterious DEP						A	G		
A24 9-mer	preferred YFWRHK	<u>1°Anchor</u> YFWM		STC			YFW	YFW	<u>1°Anchor</u> FLIW	
	deleterious DEG		DE	G	QNP	DERHKG		AQN		
A24 10-mer	Preferred	<u>1°Anchor</u> YFWM		P	YFWP		P			<u>1°Anchor</u> FLIW
	Deleterious		GDE	QN	RHK	DE	A	QN	DEA	
A3101 Preferred	RHK	<u>1°Anchor</u> MVTALIS	YFW	P		YFW	YFW	AP	<u>1°Anchor</u> RK	
	Deleterious DEP		DE		ADE	DE	DE	DE		
A3301 Preferred		<u>1°Anchor</u> MVALFIST	YFW				AYFW		<u>1°Anchor</u> RK	
	Deleterious GP		DE							
A6801 Preferred	YFWSTC	<u>1°Anchor</u> AVTMSLI			YFWLIV M		YFW	P	<u>1°Anchor</u> RK	
	deleterious GP		DEG		RHK			A		
B0702 Preferred	RHKFWY	<u>1°Anchor</u> P	RHK		RHK	RHK	RHK	PA	<u>1°Anchor</u> LMFWYA/ V	
	deleterious DEQNP		DEP	DE	DE	GDE	QN	DE		

POSITION	1	2	3	4	5	6	7	8	9	C-terminus
									or C-terminus	
A1 9-mer	preferred	GFYW	<u>1°Anchor</u> STM	DEA	YFW		P	DEQN	YFW	<u>1°Anchor</u> Y
	deleterious	DE		RHKLIVMP	A	G	A			
A1 9-mer	preferred	GRHK	ASTCLIVM	<u>1°Anchor</u> DEAS	GSTC		ASTC	LIVM	DE	<u>1°Anchor</u> Y
	deleterious	A	RHKDEPYFW		DE	PQN	RHK	PG	GP	
B3501	Preferred	FWYLIVM	<u>1°Anchor</u> P	FWY				FWY		<u>1°Anchor</u> LMFWY/V A
	deleterious	AGP			G	G				
B51	Preferred	LIVMFWY	<u>1°Anchor</u> P	FWY	STC	FWY		G	FWY	<u>1°Anchor</u> LIVFWYA M
	deleterious	AGPDER HKSTC				DE	G	DEQN	GDE	
B5301	preferred	LIVMFWY	<u>1°Anchor</u> P	FWY	STC	FWY		LIVMFWYFWY		<u>1°Anchor</u> IMFWYAL V
	deleterious	AGPQN					G	RHKQN	DE	
B5401	preferred	FWY	<u>1°Anchor</u> P	FWYLIVM		LIVM		ALIVM	FWYA	<u>1°Anchor</u> ATIVLMF WY
	deleterious	GPQNDE		GDESTC		RHKDE	DE	QNDGE	DE	

TABLE IV (F):

Summary of HLA-supertypes								
Overall phenotypic frequencies of HLA-supertypes in different ethnic populations								
Specificity			Phenotypic frequency					
Supertype	Position 2	C-Terminus	Caucasian	N.A. Black	Japanese	Chinese	Hispanic	Average
B7	P	AILMVFWY	43.2	55.1	57.1	43.0	49.3	49.5
A3		AILMVST	37.5	42.1	45.8	52.7	43.1	44.2
A2		AILMVT	45.8	39.0	42.4	45.9	43.0	42.2
A24	YF (WIVLMT)	FI (YWLM)	23.9	38.9	58.6	40.1	38.3	40.0
B44	E (D)	FWYLIMVA	43.0	21.2	42.9	39.1	39.0	37.0
A1	TI (LVMS)	FWY	47.1	16.1	21.8	14.7	26.3	25.2
B27	RHK	FYL (WMI)	28.4	26.1	13.3	13.9	35.3	23.4
B62	QL (IVMP)	FWY (MIV)	12.6	4.8	36.5	25.4	11.1	18.1
B58	ATS	FWY (LIV)	10.0	25.1	1.6	9.0	5.9	10.3

TABLE IV (G):

Calculated population coverage afforded by different HLA-supertype combinations

HLA-supertypes		Phenotypic frequency					
		Caucasian	N.A. Blacks	Japanese	Chinese	Hispanic	Average
A2, A3 and B7 A2, A3, B7, A24, B44 and A1 A2, A3, B7, A24, B44, A1, B27, B62, and B 58		83.0	86.1	87.5	88.4	86.3	86.2
		99.5	98.1	100.0	99.5	99.4	99.3
		99.9	99.6	100.0	99.8	99.9	99.8

Motifs indicate the residues defining supertype specificities. The motifs incorporate residues determined on the basis of published data to be recognized by multiple alleles within the supertype. Residues within brackets are additional residues also predicted to be tolerated by multiple alleles within the supertype.

Table V: Frequently Occurring Motifs

Name	avrg. % identity	Description	Potential Function
zf-C2H2	34%	Zinc finger, C2H2 type	Nucleic acid-binding protein functions as transcription factor, nuclear location probable
cytochrome_b_N	68%	Cytochrome b(N-terminal)/b6/pefB	membrane bound oxidase, generate superoxide
Ig	19%	Immunoglobulin domain	domains are one hundred amino acids long and include a conserved intradomain disulfide bond.
WD40	18%	WD domain, G-beta repeat	tandem repeats of about 40 residues, each containing a Trp-Asp motif. Function in signal transduction and protein interaction
PDZ	23%	PDZ domain	may function in targeting signaling molecules to sub-membranous sites
LRR	28%	Leucine Rich Repeat	short sequence motifs involved in protein-protein interactions
Pkinase	23%	Protein kinase domain	conserved catalytic core common to both serine/threonine and tyrosine protein kinases containing an ATP binding site and a catalytic site

PH	16%	PH domain	pleckstrin homology involved in intracellular signaling or as constituents of the cytoskeleton
EGF	34%	EGF-like domain	30-40 amino-acid long found in the extracellular domain of membrane-bound proteins or in secreted proteins
Rvt	49%	Reverse transcriptase (RNA-dependent DNA polymerase)	
Ank	25%	Ank repeat	Cytoplasmic protein, associates integral membrane proteins to the cytoskeleton
Oxidored_q1	32%	NADH-Ubiquinone/plastoquinone (complex I), various chains	membrane associated. Involved in proton translocation across the membrane
Efhand	24%	EF hand	calcium-binding domain, consists of a 12 residue loop flanked on both sides by a 12 residue alpha-helical domain
Rvp	79%	Retroviral aspartyl protease	Aspartyl or acid proteases, centered on a catalytic aspartyl residue
Collagen	42%	Collagen triple helix repeat (20 copies)	extracellular structural proteins involved in formation of connective tissue. The sequence consists of the G-X-Y and the polypeptide chains forms a triple helix.
Fn3	20%	Fibronectin type III domain	Located in the extracellular ligand-binding region of receptors and is about 200 amino acid residues long with two pairs of cysteines involved in disulfide bonds
7tm_1	19%	7 transmembrane receptor (rhodopsin family)	seven hydrophobic transmembrane regions, with the N-terminus located extracellularly while the C-terminus is cytoplasmic. Signal through G proteins

Table VI: Post-translational modifications of 109P1D4

O-glycosylation sites

231 S
 238 S
 240 T
 266 T
 346 T
 467 T
 551 T
 552 S
 555 T
 595 T
 652 S
 654 S
 660 T
 790 T
 795 T
 798 T
 804 S
 808 S
 923 T
 927 T
 954 T
 979 S
 982 S
 983 S

985 S
986 S
990 S
999 T
1000 T
1006 S
1017 S
1020 T

Serine phosphorylation sites

50 DLNLSLIPN (SEQ ID NO: 62)
147 VINISIPEN (SEQ ID NO: 63)
152 IPENSAINS (SEQ ID NO: 64)
238 ILQVSVTDI (SEQ ID NO: 65)
257 EIEVSIPEN (SEQ ID NO: 66)
428 LDYESTKEY (SEQ ID NO: 67)
480 PENNSPGIQ (SEQ ID NO: 68)
489 LTKVSAMDA (SEQ ID NO: 69)
495 MDADSGPNA (SEQ ID NO: 70)
559 TVFVSIIDQ (SEQ ID NO: 71)
567 QNDNSPVFT (SEQ ID NO: 72)
608 AVTLSILDE (SEQ ID NO: 73)
630 RPNISFDRE (SEQ ID NO: 74)
638 EKQESYTFY (SEQ ID NO: 75)
652 GGRVSRSSS (SEQ ID NO: 76)
654 RVSRSSSAK (SEQ ID NO: 77)
655 VSRSSSAKV (SEQ ID NO: 78)
656 SRSSSAKVT (SEQ ID NO: 79)
714 EVRYSIVGG (SEQ ID NO: 80)
789 LVRKSTEAP (SEQ ID NO: 81)
805 ADVSSPTSD (SEQ ID NO: 82)
808 SSPTSDYVK (SEQ ID NO: 83)
852 NKQNSEWAT (SEQ ID NO: 84)
877 KKKHSPKNL (SEQ ID NO: 85)
898 DDVDSGNGR (SEQ ID NO: 86)
932 FKPDSPLA (SEQ ID NO: 87)
941 RHYKSASPQ (SEQ ID NO: 88)
943 YKSASPQPA (SEQ ID NO: 89)
982 ISKCSSSSS (SEQ ID NO: 90)
983 SKCSSSSSD (SEQ ID NO: 91)
984 KCSSSSSDP (SEQ ID NO: 92)
985 CSSSSSDPY (SEQ ID NO: 93)
990 SDPYSVSDC (SEQ ID NO: 94)
1006 EVPVSVHTR (SEQ ID NO: 95)

Threonine phosphorylation sites

29 EKNYTIREE (SEQ ID NO: 96)
81 IEEDTGEIF (SEQ ID NO: 97)
192 DVIETPEGD (SEQ ID NO: 98)
252 VFKETEIEV (SEQ ID NO: 99)
310 TGLITIKPE (SEQ ID NO: 100)
320 DREETPNHK (SEQ ID NO: 101)
551 VPPLTSNVT (SEQ ID NO: 102)
790 VRKSTEAPV (SEQ ID NO: 103)
856 SEWATPNPE (SEQ ID NO: 104)
924 NWWTTPTTF (SEQ ID NO: 105)
927 TPTTFKPD (SEQ ID NO: 106)
999 GYPVTTFEV (SEQ ID NO: 107)
1000 YPVTTFEVP (SEQ ID NO: 108)

Tyrosine phosphorylation sites

67 FKLVTYKTD (SEQ ID NO: 109)

158 INSKYTLPA (SEQ ID NO: 110)
 215 EKDTYVMKV (SEQ ID NO: 111)
 359 IDIRYIVNP (SEQ ID NO: 112)
 423 ETAAYLDYE (SEQ ID NO: 113)
 426 AYLDYESTK (SEQ ID NO: 114)
 432 STKEYAIKL (SEQ ID NO: 115)
 536 KEDKYLFTI (SEQ ID NO: 116)
 599 TDPDYGDNS (SEQ ID NO: 117)
 642 SYTFYVIAE (SEQ ID NO: 118)
 682 SNCSYELVL (SEQ ID NO: 119)
 713 AEVRYSIVG (SEQ ID NO: 120)
 810 PTSDYVKIL (SEQ ID NO: 121)
 919 TMGKYNWWT (SEQ ID NO: 122)
 989 SSDPYSVSD (SEQ ID NO: 123)
 996 SDCGYPVTT (SEQ ID NO: 124)

Table VII:
Search Peptides

109P1D4 v.1 - 9-mers, 10-mers and 15-mers (SEQ ID NO: 125)

MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLTTA	60
MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF	120
RLVKIRFLIE DINDNAPLEP ATVINISIE NSAINSKYTL PAAVDPDVGI NGVQNYELIK	180
SONIFGLDVI ETPEGDKMPO LIVQKELDRE EKDTYVMKV VEDGGFPQRS STAILQVSVT	240
DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF	300
HLNATTGLIT IKEPLDREET PNHKLVLAS DGGLMPARAM VLVNVTDVND NVPSIDIRYI	360
VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLET	420
AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS	480
PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDR EKEDKYLFTI	540
LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG	600
DNSAVTSLIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT	660
INVVDVNDNK PYFIVPPSNC SYELVLPSTN PGTVVFQVIA VDNDTGMNAE VRYSIVGGNT	720
RDLEAIDQET GNTLMEKCD VTDLGLHRVL VKANDLGQPD SLFSVVIVNL FVNESVTNAT	780
LINELVRKST EAPVTPNTEI ADVSSPTS DY VKILVA AVAG TITVVVVIFI TAVVRCRQAP	840
HLKAAQKNKQ NSWATPNE NRQMIMMKK KKKKKHSPKN LLLNFVTIEE TKADDVDS DG	900
NRVTLDLPID LEEQTMGKYN WVTPTTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH	960
HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PVGIQVSNTT	1020
F	1021

109P1D4 v.2 (both ends diff from v.1)

N' terminal

9-mers aa -30 to 8

MRTERQWVLIQIFQVLCGLIQQTVTSVPGMDLLSGTY (SEQ ID NO: 126)

10-mers aa -30 to 9

MRTERQWVLIQIFQVLCGLIQQTVTSVPGMDLLSGTYI (SEQ ID NO: 127)

15-mers aa -30 to 14

MRTERQWVLIQIFQVLCGLIQQTVTSVPGMDLLSGTYIFAVLL (SEQ ID NO: 128)

109P1D4 v.2

C' Terminal

9 mers: aa 1004 to 1025

PVSVHTRPTDSRTSTIEICSEI (SEQ ID NO: 129)

10 mers: aa 1003 to 1025

VPVSVHTRPTDSRTSTIEICSEI (SEQ ID NO: 130)

15 mers: aa 997 to 1025

VTTFEVPVSVHTRPTDSRTSTIEICSEI (SEQ ID NO: 131)

109P1D4 v.3

9 mers: aa 1004 to 1347 (SEQ ID NO: 132)

PVSVHTRPPMKEVVRSCPTMKESTTMEIWIHPQQRKSEGKVAGKSQRRVTFHLPEGSQESSSDG
 GLGDHDAGSLTSTSHGLPLGYEQEYFDRATPSNRTEGDGNSDPESTFIPGLKKAETVQPTVE
 EASDNCTQECLYGHSDACWMPASLDHSSSSQAQASALCHSPPLSQASTQHHSRVTQTIALCHS
 PPVTQTIALCHSPPIQVSALHHSPLVQATALHHSPPSAQASALCYSPLAQAASISHSPLPQ

VIALHRSQAQSSVSLQQGWVQGADGLCSVDQGVQGSATSQFYTMSERLHPSDDSIKVIPLTTFTF
RQQARPSRGDSPMEEHPL

10 mers: aa 1003 to 1347 (SEQ ID NO: 133)

VPVSVHTRPPMKEVVRSCPTMKESTTMEIWIHPQPQRKSEGVAGKSQRRVTFHLPEGSQESSSD
GGLGDHDAGSLTSTSHGLPLGYPQEEYFDRATPSNRTEGDGNSDPESTFIPGLKKAEEITVQPTV
EEASDNCTQECLLYGHSDACWMPASLDHSSSSQAQASALCHSPPLSQASTQHHSRVTQTIALCH
SPPVTQTIALCHSPPIQVSALHHSPLVQATALHHSPPSAQASALCYSPPLAQAAAISHSSPLP
QVIALHRSQAQSSVSLQQGWVQGADGLCSVDQGVQGSATSQFYTMSERLHPSDDSIKVIPLTTFTF
RQQARPSRGDSPMEEHPL

15 mers: aa 998 to 1347 (SEQ ID NO: 134)

VTTFEVPVSV HTRPPMKEVV RSCPTMKEST TMEIWIHPQP QRKSEGVAG KSQRRVTFHL
PEGSQESSSD GGLGDHDAGS LTSTSHGLPL GYPQEEYFDR ATPSNRTEGD GNSDPESTFI
PGLKKAEEIT VQPTVEEASD NCTQECLLYG HSDACWMPAS LDHSSSSQAQ ASALCHSPPL
SQASTQHHSR RVTQTIALCH SPPVTQTIAL CHSPPIQVS ALHHSPLVQ ATALHHSPPS
AQASALCYSP PLAQAAAISH SSPLQVIAL HRSQAQSSVS LQQGWVQGAD GLCSVDQGVQ
GSATSQFYTM SERLHPSDDS IKVIPLTTFT PRQARPSRG DSPMEEHPL

109P1D4 v.4 (deleting 10 aa, 1039-1048, from v.1)

9-mers aa 1031-1056 (deleting 10 aa, 1039-1048, from v.1)
IWIHPQPQSQRRVTFH (SEQ ID NO: 135)

10-mers aa 1030- 1057 (deleting 10 aa, 1039-1048, from v.1)

EIWIHPQPQSQRRVTFHL (SEQ ID NO: 136)

15-mers aa 1025- 1062 (deleting 10 aa, 1039-1048, from v.1)

ESTTMEIWIHPQPQSQRRVTFHLPEGSQ (SEQ ID NO: 137)

109P1D4 v.5 (deleting 37 aa, 1012-1048, from v.1)

9-mers aa 1004-1056 (deleting 37 aa, 1012-1048, from v.1)
PVSVHTRPSQRRVTFH (SEQ ID NO: 138)

10-mers aa 1003-1057 (deleting 37 aa, 1012-1048, from v.1)

VPVSVHTRPSQRRVTFHL (SEQ ID NO: 139)

15-mers aa 998-1062 (deleting 37 aa, 1012-1048, from v.1)

VTTFEVPVSVHTRPSQRRVTFHLPEGSQ (SEQ ID NO: 140)

109P1D4 v.6 (both ends diff from v.1)

N' terminal

9-mers: aa -23 to 10 (excluding 1 and 2)

MTVGFNSDISSVVRVNTTNCHKCLLSGTYIF (SEQ ID NO: 141)

10-mers: aa -23 to 11 (excluding 1 and 2)

MTVGFNSDISSVVRVNTTNCHKCLLSGTYIFA (SEQ ID NO: 142)

15-mers: aa -23 to 17 (excluding 1 and 2)

MTVGFNSDISSVVRVNTTNCHKCLLSGTYIFAVLLVC (SEQ ID NO: 143)

109P1D4 v.6

C' terminal

9-mers: aa 1004-1016

PVSVHTRPTDSRT (SEQ ID NO: 144)

10-mers: aa 1003-1016

VPVSVHTRPTDSRT (SEQ ID NO: 145)

15-mers: aa 998-1016

VTTFEVPVSVHTRPTDSRT (SEQ ID NO: 146)

109P1D4 v.7 (N-terminal 21 aa diff from those in v.6)

N' terminal

9-mers aa -21 to 10 (excluding 1 and 2)

MFRVGFLIISSSSSLPLLLLSVVRVNTT (SEQ ID NO: 147)

10-mers aa -21 to 11 (excluding 1 and 2)

MFRVGFLIISSSSSLPLLLLSVVRVNTTN (SEQ ID NO: 148)

15-mers aa -21 to 16 (excluding 1 and 2)

MFRVGFLIISSSSSLPLLLLSVVRVNTTNCHKCL (SEQ ID NO: 149)

109P1D4 v.8

9-mers aa 1099-1126 (excluding 1117 and 1118)

TFIPGLKKEITVQPTV (SEQ ID NO: 150)

10-mers aa 1098-1127 (excluding 1117 and 1118)

STFIPGLKKEITVQPTVE (SEQ ID NO: 151)

15-mers aa 1093-1131 (excluding 1117 and 1118)

NSDPESTFIPGLKKEITVQPTVEEASDN (SEQ ID NO: 152)

109P1D4 v.1, v.2 and v.3 SNP variants

A15V

9-mers

TYIFAVLLVCVVFHSGA (SEQ ID NO: 153)

10-mers

GTYIFAVLLVCVVFHSGAQ (SEQ ID NO: 154)

15-mers

MDLLSGTYIFAVLLVCVVFHSGAQEKNYT (SEQ ID NO: 155)

109P1D4 v.1, v.2 and v.3 SNP variants

M34I

9-mers

KNYTIREEIPENVLIGD (SEQ ID NO: 156)

10-mers

EKNYTIREEIPENVLIGDL (SEQ ID NO: 157)

15-mers

HSGAQEKNYTIREEIPENVLIGDLLKDLN (SEQ ID NO: 158)

109P1D4 v.1, v.2 and v.3 SNP variants

M34I and D42N

9-mers

KNYTIREEIPENVLIGN (SEQ ID NO: 159)

10-mers

EKNYTIREEIPENVLIGNL (SEQ ID NO: 160)

15-mers

HSGAQEKNYTIREEIPENVLIGNLLKDLN (SEQ ID NO: 161)

109P1D4 v.1, v.2 and v.3 SNP variants

D42N

9-mers

MPENVLIGNLLKDLNLS (SEQ ID NO: 162)

10-mers

EMPENVLIGNLLKDLNLSL (SEQ ID NO: 163)

15-mers

YTIREEMPENVLIGNLLKDLNLSLIPNKS (SEQ ID NO: 164)

109P1D4 v.1, v.2 and v.3 SNP variants

D42N and M34I

9-mers

IPENVLIGNLLKDLNLS (SEQ ID NO: 165)

10-mers

EIPENVLIGNLLKDLNLSL (SEQ ID NO: 166)

15-mers

YTIREEIPENVLIGNLLKDLNLSLIPNKS (SEQ ID NO: 167)

109P1D4 v.1, v.2 and v.3 SNP variants

A60T

9-mers

IPNKSLTTTMOFKLVYK (SEQ ID NO: 168)

10-mers

LIPNKSLTTTMOFKLVYKT (SEQ ID NO: 169)

15-mers

DLNLSLIPNKSLTTTMOFKLVYKTGDVPLI (SEQ ID NO: 170)

109P1D4 v.1, v.2 and v.3 SNP variants

I154V

9-mers

ISIPENSAVNISKYTLPA (SEQ ID NO: 171)

10-mers

NISIPENSAVNISKYTLPA (SEQ ID NO: 172)

15-mers

PATVINISIPENSAVNISKYTLPAAVDPDV (SEQ ID NO: 173)

109P1D4 v.1, v.2 and v.3 SNP variants

V292I

9-mers

IHFSSNLSNLSNIARRLF (SEQ ID NO: 174)

10-mers

KIHFSNLSNLSNIARRLFH (SEQ ID NO: 175)

15-mers

IGENAKIHFSNLSNLSNIARRLFHLNATT (SEQ ID NO: 176)

109P1D4 v.1, v.2 and v.3 SNP variants

T420N

9-mers

FSNQFLENAAYLDYES (SEQ ID NO: 177)

10-mers

VFSNQFLENAAYLDYEST (SEQ ID NO: 178)

15-mers

FRLRPVFSNQFLENAAYLDYESTKEYAI (SEQ ID NO: 179)

109P1D4 v.1, v.2 and v.3 SNP variants

T486M

9-mers

NNSPGIQLMKVSAMDAD (SEQ ID NO: 180)

10-mers

ENNSPGIQLMKVSAMDADS (SEQ ID NO: 181)

15-mers

TVSIPENNSPGIQLMKVSAMDADSGPNAK (SEQ ID NO: 182)

109P1D4 v.1, v.2 and v.3 SNP variants

T486M and M491T

9-mers

NNSPGIQLMKVSATDAD (SEQ ID NO: 183)

10-mers

ENNSPGIQLMKVSATDADS (SEQ ID NO: 184)

15-mers

TVSIPENNSPGIQLMKVSATDADSGPNAK (SEQ ID NO: 185)

109P1D4 v.1, v.2 and v.3 SNP variants

T486M and M491T and K500E

15-mers

TVSIPENNSPGIQLMKVSATDADSGPNAE (SEQ ID NO: 186)

109P1D4 v.1, v.2 and v.3 SNP variants

T486M and K500E

15-mers

TVSIPENNSPGIQLMKVSAMDADSGPNAE (SEQ ID NO: 187)

109P1D4 v.1, v.2 and v.3 SNP variants

M491T

9-mers

IQLTKVSATDADSGPNA (SEQ ID NO: 188)

10-mers

GIQLTKVSATDADSGPNAK (SEQ ID NO: 189)

15-mers

ENNSPGIQLTKVSATDADSGPNAKINYLL (SEQ ID NO: 190)

109P1D4 v.1, v.2 and v.3 SNP variants

M491T and T486M

9-mers

IQLNKVSATDADSGPNA (SEQ ID NO: 191)

10-mers

GIQLNKVSATDADSGPNAK (SEQ ID NO: 192)

15-mers

ENNSPGIQLNKVSATDADSGPNAKINYLL (SEQ ID NO: 193)

109P1D4 v.1, v.2 and v.3 SNP variants

M491T and T486M and K500E

10-mers

GIQLNKVSATDADSGPNAE (SEQ ID NO: 194)

15-mers

ENNSPGIQLNKVSATDADSGPNAEINYLL (SEQ ID NO: 195)

109P1D4 v.1, v.2 and v.3 SNP variants

M491T and K500E

15-mers

ENNSPGIQLTKVSATDADSGPNAEINYLL (SEQ ID NO: 196)

109P1D4 v.1, v.2 and v.3 SNP variants

K500E

9-mers

DADSGPNAEINYLLGPD (SEQ ID NO: 197)

10-mers

MDADSGPNAEINYLLGPDA (SEQ ID NO: 198)

15-mers

TKVSAMDADSGPNAEINYLLGPDAPPEFS (SEQ ID NO: 199)

109P1D4 v.1, v.2 and v.3 SNP variants

K500E and M491T

10-mers

TDADSGPNAEINYLLGPDA (SEQ ID NO: 200)

15-mers

TKVSATDADSGPNAEINYLLGPDAPPEFS (SEQ ID NO: 201)

109P1D4 v.1, v.2 and v.3 SNP variants

K500E and M491T and T486M

15-mers

MKVSATDADSGPNAEINYLLGPDAPPEFS (SEQ ID NO: 202)

109P1D4 v.1, v.2 and v.3 SNP variants

K500E and T486M

15-mers

MKVSAMDADSGPNAEINYLLGPDAPPEFS (SEQ ID NO: 203)

109P1D4 v.1, v.2 and v.3 SNP variants

C517R
9-mers
APPEFSLDRRTGMLTVV (SEQ ID NO: 204)
10-mers
DAPPEFSLDRRTGMLTVVK (SEQ ID NO: 205)
15-mers
INYLLGPDAPPEFSLDRRTGMLTVVKLDRE (SEQ ID NO: 206)

109P1D4 v.1, v.2 and v.3 SNP variants
N576K
9-mers
PVETHNEYKFYVPENLP (SEQ ID NO: 207)
10-mers
SPVETHNEYKFYVPENLPR (SEQ ID NO: 208)
15-mers
DQNDNSPVETHNEYKFYVPENLPRHGTVG (SEQ ID NO: 209)

109P1D4 v.1, v.2 and v.3 SNP variants
S678Y
9-mers
KPVFIVPPYNCSEYELVLPS (SEQ ID NO: 210)
10-mers
NKPVFIVPPYNCSEYELVLPST (SEQ ID NO: 211)
15-mers
VDVNDNKPVFIVPPYNCSEYELVLPSTNPG (SEQ ID NO: 212)

109P1D4 v.1, v.2 and v.3 SNP variants
S678Y and C680Y
9-mers
KPVFIVPPYNSEYELVLPS (SEQ ID NO: 213)
10-mers
NKPVFIVPPYNSEYELVLPST (SEQ ID NO: 214)
15-mers
VDVNDNKPVFIVPPYNSEYELVLPSTNPG (SEQ ID NO: 215)

109P1D4 v.1, v.2 and v.3 SNP variants
C680Y
9-mers
VFIVPPSNSEYELVLPS (SEQ ID NO: 216)
10-mers
PVFIVPPSNSEYELVLPST (SEQ ID NO: 217)
15-mers
VNDNKPVFIVPPSNSEYELVLPSTNPGTV (SEQ ID NO: 218)

109P1D4 v.1, v.2 and v.3 SNP variants
C680Y and S678Y
9-mers
VFIVPPYNSEYELVLPS (SEQ ID NO: 219)
10-mers
PVFIVPPYNSEYELVLPST (SEQ ID NO: 220)
15-mers
VNDNKPVFIVPPYNSEYELVLPSTNPGTV (SEQ ID NO: 221)

109P1D4 v.1, v.2 and v.3 SNP variants
T790I
9-mers
INELVRKSIEAPVTPNT (SEQ ID NO: 222)
10-mers
LINELVRKSIEAPVTPNTE (SEQ ID NO: 223)
15-mers
VTNATLINELVRKSIEAPVTPNTEIADVS (SEQ ID NO: 224)

109P1D4 v.1, v.2 and v.3 SNP variants

K846M

9-mers

HLKAAQKNMQNSEWATP (SEQ ID NO: 225)

10-mers

PHLKAAQKNMQNSEWATPN (SEQ ID NO: 226)

15-mers

RCRQAPHLKAAQKNMQNSEWATPNPENRQ (SEQ ID NO: 227)

109P1D4 v.1, v.2 and v.3 SNP variants

F855V

9-mers

SPKNLLLNVTIEETKA (SEQ ID NO: 228)

10-mers

HSPKNLLLNVTIEETKAD (SEQ ID NO: 229)

15-mers

KKKKKHSPKNLLLNVTIEETKADDVDS (SEQ ID NO: 230)

109P1D4 v.1, v.2 and v.3 SNP variants

S958L

9-mers

IQPETPLNLKHIIQEL (SEQ ID NO: 231)

10-mers

QIQPETPLNLKHIIQELP (SEQ ID NO: 232)

15-mers

PQPAFQIQPETPLNLKHIIQELPLDNTF (SEQ ID NO: 233)

109P1D4 v.1, v.2 and v.3 SNP variants

K980N

9-mers

FVACDSISNCSSSSSDP (SEQ ID NO: 234)

10-mers

TFVACDSISNCSSSSSDPY (SEQ ID NO: 235)

15-mers

LPLDNTFVACDSISNCSSSSSDPYVSDC (SEQ ID NO: 236)

Tables VIII – XXI:

Table VIII - 109P1D4v.1 – A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
910	DLEEQTMGK	90.000
399	FTDHEIPFR	25.000
189	VIETPEGDK	18.000
594	VTDPDYGDN	12.500
278	IGENAKIHF	11.250
275	DADIGENAK	10.000
492	DADSGPNAK	10.000
370	LSENIPLNT	6.750
929	KPDSPDLAR	6.250
688	STNPGTVWF	5.000
674	IVPPSNCSY	5.000
163	AVDPDVGIN	5.000
113	AILPDEIFR	5.000
242	TNDNHPVFK	5.000
220	KVEDGGFPQ	4.500
797	NTEIADVSS	4.500
951	QPETPLNSK	4.500
807	TSDYVKILV	3.750
329	ASDGGLMPA	3.750
59	TAMQFKLVY	2.500
738	KCDVTDLGL	2.500
354	SIDIRYIVN	2.500
351	NVPSIDIRY	2.500
932	SPDLARHYK	2.500
911	LEEQTMGKY	2.250
789	STEAPVTPN	2.250
253	EIEVSIPIEN	1.800
897	DSDGNRVTL	1.500
479	NSPGIQLTK	1.500
985	SSDPYSVSD	1.500
991	VSDCGYPVT	1.500
68	KTGDVPLIR	1.250
741	VTDLGLHRV	1.250
273	ATDADIGEN	1.250
570	FTHNEYNFY	1.250

Table VIII - 109P1D4v.1 – A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
522	LTVVKLDR	1.250
85	FTTGARIDR	1.250
779	ATLINELVR	1.250
192	TPEGDKMPQ	1.125
858	NPENRQMIM	1.125
148	IPENSAINS	1.125
591	LITVTPDY	1.000
37	NVLIGDLLK	1.000
172	GVQNYELIK	1.000
800	IADVSSPTS	1.000
438	AADAGKPPL	1.000
972	FVACDSISK	1.000
518	RTGMLTVVK	1.000
854	WATPNPENR	1.000
527	KLDREKEDK	1.000
644	KAEDGGRVS	0.900
76	RIEEDTGEI	0.900
204	QKELDREEK	0.900
708	NAEVRYIV	0.900
316	DREETPNHK	0.900
128	LIEDINDNA	0.900
931	DSPDLARHY	0.750
20	HSGAQEKNY	0.750
981	CSSSSSDPY	0.750
55	KSLTTAMQF	0.750
635	KQESYTFYV	0.675
727	DQETGNITL	0.675
69	TGDVPLIRI	0.625
612	ENDDFTIDS	0.625
495	SGPNAKINY	0.625
804	SSPTS DYVK	0.600
221	VEDGGFPQR	0.500
201	LIVQKELDR	0.500
609	ILDENDDFT	0.500
892	KADDVDSGD	0.500

Table VIII - 109P1D4v.1 – A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
895	DVDSGDNRV	0.500
700	AVDNDTGMN	0.500
389	DADHNGRVT	0.500
802	DVSSPTSDY	0.500
645	AEDGGRVSR	0.500
740	DVTDLGLHR	0.500
617	TIDSQTGVI	0.500
725	AIDQETGNI	0.500
304	ATTGLITIK	0.500
241	DTNDNHPVF	0.500
514	SLDCRTGML	0.500
974	ACDSISKCS	0.500
116	PDEIFRLVK	0.450
77	IEEDTGEIF	0.450
475	IPENNSPGI	0.450
258	IPENAPVGT	0.450
109	EVEVAILPD	0.450
401	DHEIPFRLR	0.450
435	KLLAADAGK	0.400
780	TLINELVRK	0.400
256	VSIPENAPV	0.300
940	KSASPQPAF	0.300
851	NSEWATPNP	0.270
744	LGLHRLVK	0.250
704	DTGMNAEVR	0.250
666	VNDNKPVFI	0.250
387	DKDADHNGR	0.250
350	DNVPSIDIR	0.250
459	ENDNAPVFT	0.250
90	RIDREKLCA	0.250

Table IX – 109P1D4v.1-A1-10-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
189	LLETaAYLDY	225.000
682	DLEEgTMGKY	45.000
266	DSGPnAKINY	37.500
142	LSEnPLNTK	27.000
195	YLDYeSTKEY	25.000
416	KAEDgGRVSR	18.000
101	ASDGgLMpAR	15.000
366	VTDPdYGDNS	12.500
389	TIDSqTGVIR	10.000
757	SSDPySVSDC	7.500
122	DNVPsIDIRY	6.250
171	FTDHeIPFRL	6.250
575	VSSPISDYVK	6.000
407	KQESyTFYVK	5.400
445	FIVPpSNGSY	5.000
561	STEApVTPNT	4.500
480	NAEVySIVG	4.500
579	TSDYvKILVA	3.750
381	ILDEnDDFTI	2.500
472	AVDNdTGmNA	2.500
299	KLDReKEDKY	2.500
286	SLDCrTGMLT	2.500
117	VTDVnDNVPS	2.500
250	NNSPgIQLTK	2.500
501	ETGNtLMEK	2.500
476	DTGMnAEVRY	2.500
276	LLGPdAPPEF	2.000
763	VSDCgYPVTT	1.500
735	IQELpLDNTF	1.350
513	VTDLgLHRVL	1.250
45	ATDAiIGENA	1.250
11	VTDTnDNHPV	1.250
630	NPENrQMIMM	1.125
23	ETELeVSIPE	1.125
210	AADAgKPPLN	1.000
264	DADSGpNAKI	1.000
362	GLITvTDPDY	1.000
515	DLGLhRVLVK	1.000

Table IX – 109P1D4v.1- A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
47	DADIgENAKI	1.000
290	RTGMITVVKK	1.000
551	ATLInELVRK	1.000
13	DTNDnHPVFK	1.000
161	DADHnGRVTC	1.000
659	TIEEIKADDV	0.900
25	EIEVsiPENA	0.900
229	KDENdNAPVF	0.900
338	NSPVITHNEY	0.750
60	FSNLvSNIAR	0.750
278	GPDAPeFESL	0.625
335	QNDNsPVFTH	0.625
120	VNDNvPSIDI	0.625
231	ENDNaPVFTQ	0.625
438	VNDNkPVFIV	0.625
80	LITiKEPLDR	0.500
293	MLTVvKKLDR	0.500
105	GLMPaRAMVL	0.500
721	QIQPeTPLNS	0.500
280	DAPPeFSLDC	0.500
592	GTITvVVVIF	0.500
169	TCFTdHEIPF	0.500
49	DIGEnAKIHf	0.500
460	STNPgTVVFQ	0.500
435	VVDVnDNKPV	0.500
746	ACDSISKCSS	0.500
664	KADDvSDSGN	0.500
396	VIRPnISFDR	0.500
332	IIDQnDNSPV	0.500
262	AMDAdSGPNA	0.500
510	KCDViDLGLH	0.500
667	DVDSdGNNRVT	0.500
497	AIDQeTGNI	0.500
713	SASPgPAFQI	0.500
752	KCSSsSSDPY	0.500
550	NATLiNELVR	0.500

Table IX – 109P1D4v.1- A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
83	IKEPIDREET	0.450
544	VNESvTNATL	0.450
610	QAPHIKAAQK	0.400
703	DSPDIARHYK	0.300
28	VSIPeNAPVG	0.300
220	QSAMIFIKVK	0.300
665	ADDVdSDGNR	0.250
218	LNQSaMLFIK	0.250
474	DNDTgMNAEV	0.250
701	KPDSPDLARH	0.250
530	QPDSIFSvVI	0.250
676	TLDLpIDLEE	0.250
233	DNAPvFTQSF	0.250
704	SPDLaRHYKS	0.250
569	NTElaDVSSP	0.225
30	IPENaPVGTS	0.225
303	EKEDrYLFIT	0.225
247	IPENnSPGIQ	0.225
351	VPENIPRHGT	0.225
723	QPETpLNSKH	0.225
201	TKEYaIKLLA	0.225
50	IGENaKIHFS	0.225
175	EIPFrLRPVF	0.200
193	AAYLdYESTK	0.200
598	VVIFITAVVR	0.200
456	LVLPSnTPGT	0.200

Table X – 109P1D4v.1- A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Sequence	Score
356	FLLETAAYL	8198.910
54	ILPDEIFRL	1986.272

Table X - 109P1D4v.1-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Sequence	Score
697	GQPDLSLFS V	385.691
273	GLMPARAM V	257.342
460	GMLTVVKKL	131.296
765	VVIFITAV	90.423
280	MVLNVNVD V	88.043
820	NLLLNFTI	73.343
61	RLVKIRFLI	60.510
549	ILDENDFT	55.992
575	KQESYTFYV	50.389
598	KVTINVDV	48.991
234	NIARRLFL	39.184
479	TILAKDNGV	35.385
704	SVVIVNLFV	33.472
4	KLVTGTGDV	31.646
854	QTMGKYNW V	29.487
174	ILQVSVTDT	29.137
753	ILVAAVAGT	29.137
905	ELPLDNTFV	28.690
238	RLFHLNATT	27.572
121	SQNIFGLDV	26.797
930	SVSDCGYP V	24.952
674	TLMEKCDV T	22.711
223	KIHFSFSL	19.533
711	FVNESVTNA	18.856
556	FTIDSQTV	18.219
855	TMGKYNW T	16.550
939	TTFEVPVSV	14.654
633	TVVFQVAV	13.997
625	VLPSTNPGT	12.668
284	NVTDVNDN V	12.226
308	VVLSENIPL	11.757

Table X - 109P1D4v.1-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Sequence	Score
685	GLHRVLKA	11.426
709	NLFVNESVT	11.305
1	MQFKLVYK T	10.931
299	YIVNPVNDT	10.841
274	LMPARAMV L	10.754
247	GLITKEPL	10.468
210	QLHATDADI	10.433
888	FQIQPETPL	9.963
490	LTSNVTVFV	9.032
843	VTDLPLIDL	7.652
423	QLTKVSAM	7.287
688	RVLVKANDL	6.916
511	THNEYNFY V	6.317
486	GVPLTSNV	6.086
673	ITLMEKCDV	6.076
630	NPGTVVFQ V	6.057
757	AVAGTITVV	5.739
683	DLGLHRVLV	5.216
300	IVNPVNDTV	5.069
766	VVIFITAVV	4.242
472	KEDKYLFTI	3.789
75	NAPLFPATV	3.671
763	TVVVIFIT	3.566
116	YELIKSQNI	3.453
493	NVTVFVSII	3.271
67	FLIEDINDN	3.233
762	ITVVVIFI	3.116
190	KETEIEVSI	2.911
403	APVFTQSFV	2.497
453	FSLDCRTG M	2.263
750	YVKILVAIV	2.254
743	VSSPTSDYV	2.080
662	DLFAIDQET	2.068

Table X - 109P1D4v.1-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Sequence	Score
825	FVTIEETKA	2.000
906	LPLDNTFVA	1.989
352	FSNQFLET	1.956
354	NQFLETAA	1.864
859	YNWVTPT T	1.857
275	MPARAMVL V	1.775
436	GPNKINYL	1.764
266	LVASDGGGL	1.528
681	VTDLGLHRV	1.511
819	KNLLNFVT	1.498
386	LNQSAMLF	1.465
764	VVVIFITA	1.404
708	VNLFVNESV	1.399
309	VLSENIPLN	1.195
515	YNFYVPENL	1.163
322	LITVTDKDA	1.161
777	RQAPHLKA A	1.159
224	IHFSSNLV	1.154
454	SLDCRTGM L	1.111
913	VACDSISK	1.106
267	VLASDGGGL M	1.098
370	KEYAIKLLA	1.082
407	TQSFVTVSI	1.058
169	RSSTAILQV	1.044
735	TPNTEIADV	1.044
420	SPGIQLTKV	1.044
171	STAILQVSV	0.966
756	AAVAGTITV	0.966
264	KLLVLASDG	0.965
366	YESTKEYAI	0.933
946	SVHTRPVG	0.913
658	GNTRDLFAI	0.908
350	PVFSNQFLL	0.882

Table X – 109P1D4v.1-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Sequence	Score
314	IPLNKIAL	0.877

Table XI – 109P1D4v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
274	LMPArAMVLV	196.407
54	ILPDeIFRLV	184.215
701	SLFSvVIVNL	181.794
549	ILDEnDDFTI	168.703
53	AILPDeIFRL	144.981
510	FTHNeYNFYV	141.751
223	KIHFsFSNLV	127.193
279	AMVLvNVTDV	115.534
764	VVVVIFITAV	90.423
99	TLPAaVDPDV	69.552
309	VLSEnIPLNT	51.940
67	FLIEdINDNA	45.911
548	SILDeNDDFT	41.891
273	GLMPaRAMVL	32.407
752	KILVaAVAGT	30.519
904	QELPIDNTFV	27.521
697	GQPDsLFSV	22.523
299	YIVNpVNDTV	21.556
522	NLPRhGTVGL	21.362
761	TITVVVIFI	18.147
625	VLPSINPGTV	15.371
822	LLNFvTIEET	14.277
387	NQSAmLFIKV	13.398
711	FVNEsVTNAT	12.298
703	FSVvVNLfV	11.487
696	LGQPDsLFSV	10.296
5	LVYKiGDVPL	10.169

Table XI – 109P1D4v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
767	VIFiAVVRC	9.882
672	NITLmEKCDV	9.563
855	TMGKyNWVTT	9.149
173	AILQvSVTDT	8.720
123	NIFGIDVIET	8.720
934	CGYPvTTFEV	8.427
489	PLTSnVTVFV	8.416
902	IIQEPLDNT	8.049
936	YPVTiFEVPV	7.936
145	KELDrEEKDT	7.693
646	GMNAeVRYSI	7.535
721	LINEIVRKST	7.142
500	IIDQnDNSPV	6.503
590	RVSRsSSAKV	6.086
629	TNPGiVVFQV	6.057
120	KSQNiFGLDV	6.038
414	SIPEnNSPGI	5.881
402	NAPVTQSFV	5.313
707	IVNLvNESV	5.069
321	ALITVTDKDA	4.968
424	QLTKvSAMDA	4.968
8	KTGDvPLIRI	4.782
265	LLVLaSDGGL	4.721
912	FVACdSISKC	4.599
478	FTILaKDNV	4.444
853	EQTMgKYNWV	4.363
680	DVTDIGLHRV	4.304
230	NLVSniARRL	4.272
765	VVViiTAVV	4.242
300	IVNPvNDTVV	4.242
197	SIPEnAPVGT	4.201
603	VVDVnDNKPV	4.138
624	LVLPSnTPGT	4.101
209	TQLHaTDADI	3.914
675	LMEKcDVTDL	3.861
734	VTPNIeIADV	3.777
636	FQVIaVDNDT	3.476

Table XI – 109P1D4v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
339	FTDHeIPFRL	3.166
454	SLDCrTGMLT	2.981
313	NIPLnTKIAL	2.937
109	GINGvQNYEL	2.937
385	PLNQsAMLFI	2.903
226	FSFSnLVSNI	2.666
757	AVAGiTVV	2.495
370	KEYAiKLLAA	2.488
440	KINyILGPDA	2.391
118	LIKsqNIFGL	2.331
291	NVPSiDIRYI	2.310
753	ILVAaVAGTI	2.306
632	GTVVfQVIAV	2.222
929	YSVSdCGYPV	2.088
377	LAADaGKPPL	2.068
77	PLFPaTVINI	1.953
647	MNAeVRYSiV	1.946
842	RVTLDLPIDL	1.869
307	TVVLsENIPL	1.869
233	SNIArRLFHL	1.860
316	LNTKIALITV	1.775
435	SGPNaKINYL	1.764
606	VNDNkPVFiV	1.689
272	GGLMpPARAMV	1.680
819	KNLLINfVTI	1.676
930	SVSDcGYPVT	1.644
938	VTTFeVPVSV	1.642
755	VAAVaGTITV	1.642
906	LPLDnTFVAC	1.589
422	GIQLiKVSAM	1.571
758	VAGTITVVVV	1.549
104	VDPDvGINGV	1.549
605	DVNDnKPVFI	1.544
620	CSYEiVLPST	1.468
430	AMDAdSGPNA	1.435
85	NIspENSAI	1.435

Table XII – 109P1D4v.1-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
137	KMPQLIVQK	90.000
375	KLLAADAGK	90.000
467	KLDREKEDK	60.000
720	TLINELVRK	45.000
112	GVQNYELIK	36.000
850	DLEEQTMGK	18.000
805	IMMKKKKKK	15.000
803	QMIMMKKKK	15.000
781	HLKAAQKNK	10.000
806	MMKKKKKKK	10.000
230	NLVSNIARR	9.000
460	GMLTVVKKL	6.075
602	NVVDVNDNK	4.500
61	RLVKIRFLI	4.050
247	GLITKEPL	4.050
912	FVACDSISK	4.000
861	WVTPTTFK	3.000
820	NLLNFVTI	2.700
54	ILPDEIFRL	2.700
563	GVIRPNISF	2.700
387	NQSAMLFIK	2.700
244	ATTGLITIK	2.250
767	VIFITAVVR	2.000
590	RVSRSSSAK	2.000
8	KTGDVPLIR	1.800
53	AILPDEIFR	1.800
804	MIMMKKKKK	1.500
273	GLMPARAMV	1.350
356	FLLETAAYL	1.350
685	GLHRVLVKA	1.350
141	LIVQKELDR	1.200
291	NVPSIDIRY	1.200
274	LMPARAMVL	1.200
458	RTGMLTVVK	1.000
695	DLGQPDSLF	0.900
129	VIETPEGDK	0.900
855	TMGKYNWVT	0.900

Table XII – 109P1D4v.1-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
761	TITVVVIF	0.900
320	IALITVTDK	0.900
117	ELIKSQNIF	0.900
58	EIFRLVKIR	0.900
701	SLFSVVIVN	0.900
389	SAMLFIVK	0.675
802	RQMIMMKKK	0.675
760	GTITVVVI	0.608
719	ATLINELVR	0.600
210	QLHATDADI	0.600
614	IVPPSNCYS	0.600
489	PLTSNVTVF	0.600
953	GIQVSNTTF	0.600
39	GIPRDEHCF	0.600
462	LTVVKLDR	0.600
25	FTTGARIDR	0.600
249	ITIKEPLDR	0.600
493	NVTVFVSII	0.540
223	KIHFSFSNL	0.540
576	QESYTFYVK	0.540
709	NLFVNESVT	0.500
238	RLFHLNATT	0.500
419	NSPGIQLTK	0.450
753	ILVAAVAGT	0.450
891	QPETPLNSK	0.450
762	ITVVVIFI	0.405
531	LITVTDPDY	0.400
385	PLNQSAMLF	0.400
869	KPDSPDLAR	0.360
942	EVPSVHTR	0.360
744	SSPTSDYVK	0.300
339	FTDHEIPFR	0.300
174	ILQSVTDT	0.300
548	SILDENDDF	0.300
368	STKEYAIKL	0.270
821	LLNFVTIE	0.270
4	KLVIKTGDV	0.270

Table XII – 109P1D4v.1-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
764	VVVVIFITA	0.270
234	NIARRLFHL	0.270
475	KYLFTILAK	0.270
64	KIRFLIEDI	0.270
680	DVTDLGLHR	0.240
476	YLFTILAKD	0.225
674	TLMEKCDVT	0.225
662	DLFAIDQET	0.225
872	SPDLARHYK	0.200
775	RRCRAPHLK	0.200
510	FTHNEYNFY	0.200
464	VVKLDREK	0.200
779	APHLKAAQK	0.200
684	LGLHRVLVK	0.180
454	SLDCRTGML	0.180
158	KVKVEDGGF	0.180
633	TVVFQVIAV	0.180
769	FITAVVRCR	0.180
598	KVTINVVDV	0.180
742	DVSSPTSDY	0.180
241	HLNATTGLI	0.180
308	VVLSENIPL	0.180
575	KQESYTFYV	0.162
391	MLFIKVKDE	0.150
910	NTFVACDSI	0.150
628	STNPGTVVF	0.150

Table XIII – 109P1D4v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
683	DLGLHRVLVK	36.000
319	KIALITVTDK	18.000
530	GLITVTDPDY	18.000

Table XIII – 109P1D4v.1–A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
575	KQESyTFYVK	16.200
803	QMIMmKKKKK	15.000
805	IMMKkKKKKK	15.000
140	QLIVqKELDR	12.000
467	KLDReKEDKY	12.000
806	MMKKkKKKKK	10.000
347	RLRPvFSNQF	9.000
646	GMNAeVRSI	8.100
273	GLMPaRAMVL	8.100
461	MLTVvKKLDR	8.000
357	LLETaAYLDY	8.000
701	SLFSvVIVNL	6.750
160	KVEDgGFPQR	3.600
361	AAYLdYESTK	3.000
444	LLGPdAPPEF	3.000
458	RTGMITVVKK	3.000
549	ILDEnDDFTI	2.700
77	PLFPaTVINI	2.700
564	VIRPnISFDR	2.700
719	ATLInELVRK	2.250
890	IQPEIPLNSK	2.025
760	GTITvVVVIF	2.025
363	YLDYeSTKEY	2.000
675	LMEKcDVTDL	1.800
55	LPDEiFRLVK	1.800
804	MIMMKKKKKK	1.500
39	GIPReEHCfY	1.200
146	ELDReEKDty	1.200
669	ETGNITLMEK	0.900
613	FIVPpSNCSY	0.900
58	EiFRIVKIRF	0.900
143	VQKEIDREEK	0.900
279	AMVLvNVTDV	0.900
109	GINGvQNYEL	0.810
850	DLEEqTMGKY	0.810
248	LITiKEPLDR	0.800
67	FLIEdINDNA	0.675

Table XIII – 109P1D4v.1–A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
53	AILPdEiFRL	0.608
128	DVIETPEGDK	0.608
766	VViFITA VVR	0.600
522	NLPRhGTVGL	0.600
354	NQFLIETAAY	0.600
761	TITVvVViFi	0.540
309	VLSEnIPLNT	0.450
802	RQMImMKKKK	0.450
123	NIFGIDVIET	0.450
743	VSSPISDYVK	0.450
753	ILVAaVAGTI	0.405
8	KTGDvPLIRI	0.405
557	TIDSqTGVIR	0.400
424	QLTKvSAMDA	0.400
107	DVGInGVQNY	0.360
939	TTFEvPVSVH	0.338
88	IPENsAINSK	0.300
243	NATTgLITIK	0.300
655	IVGGnTRDLF	0.300
823	LNFVIEETK	0.300
16	RIEEtGGEIF	0.300
5	LVYKiGDVPL	0.300
274	LMPArAMVLV	0.300
767	ViFiTAVVRC	0.300
181	DTNDnHPVFK	0.300
463	TVVKkLDREK	0.300
99	TLPAaVDPDV	0.300
508	PVFThNEYNF	0.300
763	TVVVvIFITA	0.270
137	KMPQIIVQKE	0.270
632	GTVVvQVIaV	0.270
265	LLVLaSDGGL	0.270
820	NLLLnFVTIE	0.270
118	LIKSqNIFGL	0.270
310	LSENIPLNTK	0.225
388	QSAMiFIKVK	0.225
241	HLNAITGLIT	0.200

Table XIII – 109P1D4v.1–A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
337	TCFTdHEIPF	0.200
430	AMDAdSGPNA	0.200
778	QAPHIKAAQK	0.200
454	SLDCrTGMLT	0.200
386	LNQSaMLFIK	0.180
418	NNSPgIQLTK	0.180
111	NGVQnYELIK	0.180
905	ELPLdNTFVA	0.180
217	DIGEnAKIHF	0.180
307	TVVLSEnIPL	0.180
385	PLNQsAMLFi	0.180
61	RLVKiRFLIE	0.180
223	KIHFsFSNLV	0.180
422	GIQLiKVSAM	0.180
866	TTFKpDSPDL	0.150
822	LLNFvTIEET	0.150
391	MLFiKVKDEN	0.150
26	TTGaRIDREK	0.150
321	ALITvTDKDA	0.150
339	FTDHeIPFRL	0.135
230	NLVSnIARRL	0.135
356	FLLEIAAYLD	0.135
764	VVVViFITA V	0.135

Table XIV-109P1D4v.1-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
112	GVQNYELIK	12.000
590	RVSRSSSAK	6.000
912	FVACDSISK	4.000
475	KYLFTILAK	3.600
458	RTGMLTVVK	3.000

Table XIV-109P1D4v.1-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
602	NVVDVNDNK	3.000
861	WVTPTTFK	2.000
387	NQSAMLFK	1.800
375	KLLAADAGK	1.800
802	RQMIMMKKK	1.800
137	KMPQLIVQK	1.200
467	KLDREKEDK	1.200
8	KTGDVPLIR	1.200
244	ATTGLITIK	1.000
462	LTVVKLDR	0.600
720	TLINELVRK	0.600
249	ITIKEPLDR	0.600
775	RCRQAPHLK	0.600
719	ATLINELVR	0.600
362	AYLDYESTK	0.600
25	FTTGARIDR	0.400
805	IMMKKKKKK	0.400
804	MIMMKKKKK	0.400
582	YVKAEDGGR	0.400
129	VIETPEGDK	0.400
320	IALITVTDK	0.300
803	QMIMMKKKK	0.300
824	NFVTIEETK	0.300
680	DVTDLGLHR	0.240
869	KPDSPDLAR	0.240
53	AILPDEIFR	0.240
850	DLEEQTMGK	0.240
141	LIVQKELDR	0.240
517	FYVPENLPR	0.240
389	SAMLFIVK	0.200
781	HLKAAQKNK	0.200
872	SPDLARHYK	0.200
806	MMKKKKKKK	0.200
779	APHLKAAQK	0.200
891	QPETPLNSK	0.200
339	FTDHEIPFR	0.200

Table XIV-109P1D4v.1-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
464	VVKLDREK	0.200
563	GVRPNISF	0.180
767	VIFITAVVR	0.160
576	QESYTFYVK	0.120
230	NLVSNIARR	0.120
942	EVPSVHTR	0.120
688	RVLVKANDL	0.090
811	KKKKKHSPK	0.060
684	LGLHRVLVK	0.060
311	SENIPLNTK	0.060
598	KVTINVDV	0.060
215	DADIGENAK	0.060
764	VVVIFITA	0.060
644	DTGMNAEVR	0.060
704	SVVIVNLV	0.060
486	GVPLTSNV	0.060
432	DADSGPNAK	0.060
395	KVKDENDNA	0.060
633	TVVFQVAV	0.060
205	GTSVTQLHA	0.060
158	KVKVEDGGF	0.060
308	VVLSENIPL	0.060
61	RLVKIRFLI	0.054
697	GQPDLSFSV	0.054
575	KQESYTFYV	0.054
22	GEIFTTGAR	0.054
760	GTITVVVVI	0.045
632	GTVFQVIA	0.045
930	SVSDCGYPV	0.040
801	NRQMIMMKK	0.040
744	SSPTSDYVK	0.040
670	TGNITLMEK	0.040
419	NSPGQLTK	0.040
182	TNDNHPVFK	0.040
291	NVPSIDIRY	0.040
794	WATPNPENR	0.040

Table XIV-109P1D4v.1-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
459	TGMLTVVKK	0.040
935	GYPVTTFEV	0.036
152	KDTYVMKVK	0.030
843	VTLDLPIDL	0.030
766	VVIFITAVV	0.030
280	MVLVNVTDV	0.030
266	LVLASDGGL	0.030
762	ITVVVIFI	0.030
765	VVIFITAV	0.030
229	SNLVSNIAR	0.024
58	EIFRLVKIR	0.024
30	RIDREKLCA	0.024
273	GLMPARAMV	0.024
800	ENRQMIMMK	0.024
939	TTFEVPVSV	0.020
614	IVPPSNCSY	0.020
324	TVTDKADADH	0.020
754	LVAAVAGTI	0.020
368	STKEYAIKL	0.020
73	VVRCRQAPH	0.020
946	SVHTRPVGI	0.020
757	AVAGTITVV	0.020
750	YVKILVAAV	0.020

Table XV - 109P1D4v.1-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
575	KQESYTFYVK	3.600
458	RTGMITVVKK	3.000
802	RQMIMMKKKK	1.800
719	ATLINELVRK	1.500
319	KIALITVTDK	1.200

Table XV - 109P1D4v.1-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
160	KVEDgGFPQR	1.200
128	DVIEIPEGDK	0.900
766	VVIFITAVVR	0.600
669	ETGNITLMEK	0.600
911	TFVAcDSISK	0.600
143	VQKEIDREEK	0.600
890	IQPEIPLNSK	0.600
804	MIMMkKKKKK	0.400
805	IMMkKKKKKK	0.400
361	AAYLdYESTK	0.400
55	LPDEIFRLVK	0.400
181	DTNDnHPVFK	0.300
463	TVVKLDREK	0.300
803	QMIMmKKKKK	0.300
564	VIRPnISFDR	0.240
140	QLIVqKELDR	0.240
652	RYSIvGGNTR	0.240
683	DLGLhRVLVK	0.240
778	QAPHIKAQK	0.200
88	IPENsAINSK	0.200
243	NATTgLITIK	0.200
806	MMKkKKKKKK	0.200
149	REEKdTYVMK	0.180
461	MLTVvKKLDR	0.160
516	NFYVpENLPR	0.160
248	LITiKEPLDR	0.160
386	LNQSaMLFIK	0.120
581	FYVKaEDGGR	0.120
842	RVTLdLPIDL	0.120
52	VAILpDEIFR	0.120
584	KAEDgGRVSR	0.120
26	TTGARdDREK	0.100
589	GRVSRsSSAK	0.090
466	KKLDrEKEDK	0.090
632	GTVVfQVIIV	0.090
718	NATLINELVR	0.080
24	IFTTgARIDR	0.080

Table XV - 109P1D4v.1-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
557	TIDSqTGVIR	0.080
418	NNSPgIQLTK	0.080
823	LNFVIEETK	0.080
33	REKLcAGIPR	0.072
566	RPNIsFDREK	0.060
111	NGVQnYELIK	0.060
849	IDLEqQTMGK	0.060
601	INVVdVNDNK	0.060
810	KKKKkKHSPK	0.060
366	YESTkEYAIK	0.060
8	KTGDvPLIRI	0.060
335	RVTCfTDHEI	0.060
307	TVVLsENIPL	0.060
763	TVVVfIFITA	0.060
590	RVSRSsSAKV	0.060
273	GLMPaRAMVL	0.048
760	GTITvVVVIF	0.045
640	AVDNdTGMINA	0.040
449	APPEfSLDCR	0.040
5	LVYKtGDVPL	0.040
743	VSSPISDYVK	0.040
338	CFTDhEIPFR	0.040
374	IKLLaADAGK	0.030
860	NWVTIPTTFK	0.030
764	VVVfITAV	0.030
339	FTDHeIPFRL	0.030
772	AVVRcRQAPH	0.030
266	LVLAsDGGLM	0.030
510	FTHNeYNFYV	0.030
765	VVVfITAVV	0.030
349	RPVFsNQFL	0.027
109	GINGvQNYEL	0.024
646	GMNAeVRYSI	0.024
800	ENRQmIMMKK	0.024
474	DKYLFILAK	0.024
431	MDADsGPNAK	0.020
214	TDADiGENAK	0.020

Table XV - 109P1D4v.1-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
757	AVAGItTVVV	0.020
300	IVNPvNDTVV	0.020
774	VRCRqAPHLK	0.020
707	IVNLfVNESV	0.020
750	YVKIIIAAVA	0.020
255	LDREtTPNHK	0.020
866	TTFKpDSPDL	0.020
207	SVTQIHATDA	0.020
939	TTFEvPVS VH	0.020
457	CRTGmLTVVK	0.020
725	LVRKsTEAPV	0.020
582	YVKAeDGGRV	0.020
655	IVGGnTRDLF	0.020
773	VVRCrQAPHL	0.020
310	LSENiPLNTK	0.020
530	GLITvTDPDY	0.018
446	GPDAPeFSL	0.018
697	GQPDsLFSVV	0.018
53	AILPdEIFRL	0.018
941	FEVPvSVHTR	0.018
556	FTIDsQTGVI	0.015

Table XVI-109P1D4v.1-A24 - 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
47	FYEVEVAIL	300.000
6	VYKTGDVPL	200.000
702	LFSVIVNL	28.000
867	TFKPDSPDL	24.000
858	KYNWVTTPT	21.000
349	RPVFSNQFL	14.400
688	RVLVKANDL	14.400

Table XVI-109P1D4v.1-A24 – 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
59	IFRLVKIRF	14.000
652	RYSIVGGNT	14.000
338	CFTDHEIPF	12.000
621	SYELVLPST	10.500
749	DYVKILVAA	10.500
115	NYELIKSQN	10.500
509	VFTHNEYNF	10.000
223	KIHFSFSNL	9.600
460	GMLTVVKKL	9.240
843	VTLDLPIDL	8.640
46	CFYEVEVAI	8.400
839	DGNRVTLDL	8.400
247	GLITIKEPL	8.400
935	GYPTTTFEV	8.250
514	EYNFYVPEN	8.250
678	KCDVTDLGL	8.000
78	LFPATVINI	7.500
365	DYESTKEYA	7.500
436	GPNAKINYL	7.200
54	ILPDEIFRL	7.200
356	FLLETAAYL	7.200
717	TNATLINEL	6.336
667	DQETGNITL	6.000
274	LMPARAMVL	6.000
417	ENNSPGIQL	6.000
314	IPLNTKIAL	6.000
302	NPVNDTVVL	6.000
308	VVLSENIPL	6.000
92	SAINSKYTL	6.000
538	DYGDNSAVT	6.000
260	TPNHKLLVL	6.000
888	FQIQPETPL	6.000
227	SFSNLVSNI	6.000
266	LVLASDGGI	6.000
231	LVSNIARRL	5.600
515	YNFYVPENL	5.600

Table XVI-109P1D4v.1-A24 – 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
368	STKEYAIKL	5.280
703	FSVVIVNLF	5.040
371	EYAIKLLAA	5.000
110	INGVQNYEL	4.400
28	GARIDREKL	4.400
61	RLVKIRFLI	4.200
378	AADAGKPPL	4.000
837	DSDGNRVTL	4.000
880	KSASPQPAF	4.000
655	IVGGNTRDL	4.000
539	YGDNSAVTL	4.000
234	NIARRLFHL	4.000
618	SNCSYELVL	4.000
542	NSAVTSLIL	4.000
454	SLDCRTGML	4.000
158	KVKVEDGGF	4.000
523	LPRHGTVGL	4.000
16	RIEEDTGEI	3.960
445	LGPDAPPEF	3.960
502	DQNDNSPVF	3.600
548	SILDENDDF	3.600
117	ELIKSQNIF	3.600
605	DVNDNKPVF	3.600
402	NAPVFTQSF	3.600
181	DTNDNHPVF	3.600
71	DINDNAPLF	3.600
628	STNPGTVVF	3.600
860	NWVTTPTTF	3.000
39	GIPRDEHCF	3.000
52	VAIPDEIF	3.000
563	GVIKPNISF	3.000
232	VSNIARRLF	3.000
218	IGENAKIHF	3.000
953	GIQVSNTTF	3.000
220	ENAKIHFSF	2.800
761	TTVVVVVIF	2.800

Table XVI-109P1D4v.1-A24 – 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
492	SNVTVFVSI	2.520
64	KIRFLIEDI	2.400
344	IPFRLRPVF	2.400
817	SPKNLLNLF	2.400
312	ENIPLNTKI	2.376
760	GTITVVVVI	2.100
762	ITVVVVIFI	2.100
695	DLGQPDLSF	2.000
656	VGGNTRDLF	2.000
933	DCGYPVTTF	2.000
593	RSSSAKVTI	2.000
86	ISIPENSAI	1.800
306	DTVLSENI	1.800
287	DVNDNVPSI	1.800
102	AAVDPDVGI	1.800
820	NLLLNFTVI	1.800
647	MNAEVRYSI	1.680
186	HPVFKETEI	1.650
732	APVTPNTEI	1.650
111	NGVQNYELI	1.500
166	FPQRSSTAI	1.500

Table XVII – 109P1D4v.1-A24 – 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
514	EYNFYVPENL	420.000
538	DYGDNSAVTL	240.000
115	NYELIKSQNI	90.000
365	DYESIKEYAI	75.000
6	VYKTgDVPLI	50.000
887	AFQIqPETPL	30.000
355	QFLLeTAAYL	30.000

Table XVII – 109P1D4v.1-A24 – 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
46	CFYEvEAIL	24.000
239	LFHLnATTGL	20.000
59	IFRLvKIRFL	20.000
298	RYIVnPVNDT	18.000
702	LFSvViVNL	16.800
858	KYNWvTPTT	15.000
349	RPVFsnQFLL	12.000
383	KPPLnQSAML	12.000
842	RVTLDLPIDL	9.600
716	VTNAILINEL	9.504
459	TGMLiVVKKL	9.240
138	MPQLiVQKEL	9.240
621	SYELvLPSTN	9.000
749	DYVKILVAHV	9.000
246	TGLiIKKEPL	8.400
230	NLVSniARRL	8.400
436	GPNAKiNYLL	8.400
165	GFPQrSSTAI	7.500
897	NSKHhiQEL	7.392
16	RIEEdTGEIF	7.200
53	AILPdEiFRL	7.200
435	SGPNaKiNYL	7.200
273	GLMPaRAMVL	7.200
453	FSLDcRTGML	7.200
615	VPPSnCSYEL	6.600
109	GINGvQNYEL	6.600
313	NIPLnTKIAL	6.000
878	HYKSaSPQPA	6.000
712	VNESvTNATL	6.000
522	NLPRhGTVGL	6.000
307	TVVLsENIPL	6.000
265	LLVLsSDGGL	6.000
166	FPQRsSTAIL	6.000
675	LMEKcDVTDL	6.000
202	APVGiSVTQL	6.000
233	SNiARLFLH	6.000
301	VNPVnDTVVL	6.000

Table XVII – 109P1D4v.1-A24 – 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
259	ETPNhKLLVL	6.000
132	TPEGdKMPQL	6.000
654	SIVGgNTRDL	6.000
347	RLRPvFSNQF	5.760
701	SLFSvViVNL	5.600
339	FTDHeiPFRL	5.600
481	LAKDnGVPPPL	4.800
377	LAADaGKPPL	4.800
681	VTDLgLHRVL	4.800
368	STKeyAIKLL	4.800
27	TGARiDREKL	4.400
367	ESTKeYAIKL	4.400
903	IQELpLDNTF	4.320
760	GTITvVVVIF	4.200
773	VVRCrQAPHL	4.000
91	NSAiNskYTL	4.000
866	TTFKpDSPDL	4.000
118	LIKSqNIFGL	4.000
693	ANDLgQPDSL	4.000
446	GPDAPPEFSL	4.000
541	DNSAvTLSIL	4.000
5	LVYKiGDVPL	4.000
745	SPTSdYVKIL	4.000
38	AGIPrDEHCF	3.600
816	HSPKnLLLNF	3.600
819	KNLLiNFVTI	3.600
343	EIPFrLRPVF	3.600
547	LSILDENDDF	3.000
952	VGIQvSNTTF	3.000
562	TGViRPNISF	3.000
401	DNAPvFTQSF	2.880
58	EiFRiVKIRF	2.800
444	LLGPdAPPEF	2.640
491	TSNViVFVSI	2.520
452	EFSLdCRTGM	2.500
217	DIGEnAKiHF	2.400
8	KTGDvPLIRI	2.400

Table XVII – 109P1D4v.1-A24 – 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
475	KYLFiLAKD	2.310
335	RVTCiTDEI	2.200
796	TPNPnRQMI	2.160
646	GMNAeVRYSI	2.100
406	FTQSVTVSI	2.100
753	ILVAaVAGTI	2.100
630	NPGTvVFQVI	2.016
655	IVGGnTRDLF	2.000
337	TCFTdHEIPF	2.000
51	EVAiIPDEIF	2.000
231	LVSNiARRLF	2.000
859	YNWViTPTTF	2.000
556	FTIDsQTGVI	1.800
605	DVNDnKPVFI	1.800
664	FAIDqETGNI	1.800
66	RFLiDINDN	1.800
414	SIPEnNSPGI	1.800
731	EAPViPNTEI	1.650
744	SSPTsDYVKI	1.650

Table XVIII – 109P1D4v.1-B7 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
523	LPRHGTVGL	800.000
28	GARiDREKL	180.000
349	RPVFsnQFL	80.000
314	IPLNTKIAL	80.000
436	GPNAKiNYL	80.000
260	TPNHKLLVL	80.000
302	NPVNDTVVL	80.000
732	APVTPNTEI	36.000
76	APLFPATVI	36.000

Table XVIII – 109P1D4v.1-B7 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
796	TPNPENRQM	20.000
655	IVGGNTRDL	20.000
688	RVLVKANDL	20.000
308	VVLSENIPL	20.000
231	LVSNIARRL	20.000
383	KPPLNQSAM	20.000
266	LVLASDGGGL	20.000
92	SAINSKYTL	12.000
403	APVFTQSFV	12.000
378	AADAGKPPL	10.800
166	FPQRSSTAI	8.000
745	SPTSDYVKI	8.000
384	PPLNQSAML	8.000
186	HPVFKETEI	8.000
292	VPSIDIRYI	8.000
894	TPLNSKHHI	8.000
616	PPSNCSYEL	8.000
888	FQIQPETPL	6.000
449	APPEFSLDC	6.000
417	ENNSPGIQL	6.000
798	NPENRQMIM	6.000
102	AAVDPDVGI	5.400
735	TPNTEIADV	4.000
839	DGNRVTLDL	4.000
630	NPGTVVFQV	4.000
275	MPARAMVLV	4.000
460	GMLTVVKKL	4.000
274	LMPARAMVL	4.000
618	SNCSYELVL	4.000
223	KIHFSFSL	4.000
368	STKEYAIKL	4.000
167	PQRSSTAIL	4.000
54	ILPDEIFRL	4.000
420	SPGIQLTKV	4.000
64	KIRFLIEDI	4.000
356	FLLETAAYL	4.000

Table XVIII – 109P1D4v.1-B7 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
626	LPSTNPGTV	4.000
843	VTLDLPIDL	4.000
542	NSAVTSLIL	4.000
234	NIARRLFHL	4.000
40	IPRDEHCFY	4.000
100	LPAAVDPDV	4.000
515	YNFYVPENL	4.000
717	TNATLINEL	4.000
247	GLITIKEPL	4.000
110	INGVQNYEL	4.000
757	AVAGTITVV	3.000
639	IAVDNDTGM	3.000
415	IPENNSPGI	2.400
203	PVGTSVTQL	2.000
906	LPLDNTFVA	2.000
946	SVHTRPVGI	2.000
296	DIRYIVNPV	2.000
287	DVNDNVPSI	2.000
350	PVFSNQFLL	2.000
754	LVAAVAGTI	2.000
456	DCRTGMLTV	2.000
493	NVTVFVSII	2.000
487	VPPLTSNVT	2.000
51	EVAILPDEI	2.000
948	HTRPVGIVQ	2.000
847	LPIDLEEQT	2.000
591	VSRSSSAKV	2.000
882	ASPOPAFQI	1.800
756	AAVAGTITV	1.800
837	DSDGNRVTL	1.800
272	GGLMPARAM	1.500
453	FSLDCRTGM	1.500
678	KCDVTDLGL	1.200
243	NATTGLITI	1.200
105	DPDVGINGV	1.200
698	QPDSLFSVV	1.200

Table XVIII – 109P1D4v.1-B7 9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
539	YGDNSAVTL	1.200
667	DQETGNITL	1.200
454	SLDCRTGML	1.200
55	LPDEIFRLV	1.200
284	NVTDVNDNV	1.000
633	TVVFQVIAV	1.000
280	MVLNVNTDV	1.000
750	YVKILVAHV	1.000
766	VVIFITAVV	1.000
930	SVSDCGYPV	1.000
486	GVPLTSNV	1.000
765	VVIFITAV	1.000
300	IVNPVNDTV	1.000
598	KVTINVVDV	1.000
423	IQLTKVSAM	1.000
267	VLASDGGML	1.000
704	SVVIVNLFV	1.000
273	GLMPARAMV	0.900
278	RAMVLVNV	0.900

Table XIX – 109P1D4v.1-B7 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
202	APVGSVTQL	240.000
773	VVRCrQAPHL	200.000
615	VPPSnCSYEL	80.000
436	GPNakINYLL	80.000
349	RPVFsNQFLL	80.000
523	LPRHgTVGLI	80.000

Table XIX – 109P1D4v.1-B7 10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
138	MPQLIVQKEL	80.000
383	KPPLnQSAML	80.000
166	FPQRsTAIL	80.000
745	SPTsdyVKIL	80.000
446	GPDAPeFSL	36.000
132	TPEGdKMPQL	24.000
842	RVTLDLPIDL	20.000
307	TVVLsENIPL	20.000
7	LPIDIEEQTM	20.000
5	LVYKiGDVPL	20.000
481	LAKDnGVPP	12.000
53	AILPdeIFRL	12.000
377	LAADaGKPPL	12.000
459	TGMLiVVKKL	12.000

Table XX – 109P1D4v.1- B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
40	IPRDEHCFY	360.000
383	KPPLnQSAM	80.000
523	LPRHGTVGL	60.000
817	SPKNLLLNf	60.000
796	TPNPENRQM	60.000
507	SPVFTHNEY	40.000
349	RPVFSNQFL	40.000
302	NPVNDTVVL	30.000
871	DSPDLARHY	20.000
314	IPLNTKIAL	20.000
260	TPNHKLLVL	20.000
453	FSLDCRTGM	20.000
436	GPNAKINYL	20.000

Table XX – 109P1D4v.1- B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
344	IPFRLRPVF	20.000
28	GARIDREKL	13.500
745	SPTSDYVKI	12.000
798	NPENRQMIM	12.000
292	VPSIDIRYI	12.000
639	IAVDNDTGM	12.000
880	KSASPQPAF	10.000
921	CSSSSSDPY	10.000
158	KVKVEDGGF	9.000
894	TPLNSKHII	8.000
732	APVTPNTEI	8.000
76	APLFPATVI	8.000
186	HPVFKETEI	8.000
166	FPQRSSTAI	8.000
735	TPNTEIADV	6.000
368	STKEYAIKL	6.000
232	VSNIARRLF	5.000
703	FSWIVNLF	5.000
542	NSAVTSLIL	5.000
906	LPLDNTFVA	4.000
630	NPGTVVFQV	4.000
626	LPSTNPGTV	4.000
610	KPVFIVPPS	4.000
593	RSSSAKVTI	4.000
420	SPGIQLTKV	4.000
449	APPEFSLDC	4.000
847	LPIDLEEQT	4.000
100	LPAAVDPDV	4.000
950	RPVGIVQSN	4.000
403	APVFTQSFV	4.000
275	MPARAMVLV	4.000
54	ILPDEIFRL	3.000
92	SAINSKYTL	3.000
510	FTHNEYNFY	3.000
591	VSRSSSAKV	3.000
402	NAPVFTQSF	3.000

Table XX – 109P1D4v.1- B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
548	SILDENDDF	3.000
52	VAILPDEIF	3.000
267	VLASDGGLM	3.000
86	ISIPENSAI	3.000
415	IPENNSPGI	2.400
64	KIRFLIEDI	2.400
55	LPDEIFRLV	2.400
102	AAVDPDVGI	2.400
291	NVPSIDIRY	2.000
223	KIHFSFSNL	2.000
742	DVSSPTSDY	2.000
71	DINDNAPLF	2.000
356	FLETAAYL	2.000
843	VTLDLPIDL	2.000
487	VPPLTSNVT	2.000
614	IVPPSNCSY	2.000
435	SGPNAKINY	2.000
272	GGLMPARAM	2.000
882	ASPQPAFQI	2.000
616	PPSNCSYEL	2.000
714	ESVTNATLI	2.000
169	RSSTAILQV	2.000
384	PPLnQSAML	2.000
502	DQNDNSPVF	2.000
531	LITVTDPDY	2.000
423	IQLTKVSAM	2.000
645	TGMNAEVRY	2.000
605	DVNDNKPVF	2.000
445	LGPDAPPEF	2.000
864	TPTTFKPDS	2.000
688	RVLVKANDL	2.000
79	FPATVINIS	2.000
108	VGINGVQNY	2.000
181	DTNDNHPVF	2.000
90	ENSAINSKY	2.000
147	LDRECKDTY	1.800

Table XX – 109P1D4v.1 – B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
470	REKEDKYL	1.800
395	KVKDENDNA	1.800
596	SAKVTINVV	1.800
837	DSDGNRVTL	1.500
95	NSKYTLPA	1.500
923	SSSSDPYSV	1.500
308	VVLSENIPL	1.500
918	ISKCSSSSS	1.500
39	GIPRDEHCF	1.500
196	VSIPENAPV	1.500
571	FDREKQESY	1.200
468	LDREKEDKY	1.200
698	QPDLSFSV	1.200
243	NATTGLITI	1.200
105	DPDVGINGV	1.200

Table XXI – 109P1D4v.1 – B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
847	LPIDIEEQTM	120.000
383	KPPLnQSAML	40.000
927	DPYSvSDCGY	40.000
349	RPVFsnQFLL	40.000
523	LPRHgTVGLI	24.000
436	GPNAkINYLL	20.000
138	MPQLIVQKEL	20.000

Table XXI – 109P1D4v.1 – B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
202	APVGSVTQL	20.000
745	SPTSdYVKIL	20.000
166	FPQRsSTAIL	20.000
615	VPPSnCSYEL	20.000
481	LAKDnGVPL	18.000
897	NSKHhIQEL	15.000
798	NPENrQMIMM	12.000
817	SPKNILLNFV	12.000
453	FSLdRTGML	10.000
434	DSGPnAKINY	10.000
506	NSPVTHNEY	10.000
796	TPNPnRQMI	8.000
79	FPATvINISI	8.000
314	IPLNiKIALI	8.000
630	NPGTvVFQVI	8.000
894	TPLNsKHHII	8.000
547	LSILdENDDF	7.500
368	STKeyAIKLL	6.000
446	GPDAPeFESL	6.000
377	LAADaGKPP	6.000
347	RLRPvFSNQF	6.000
132	TPEGdKMPQL	6.000
253	EPLDrEETPN	6.000
816	HSPKnLLLNF	5.000
91	NSAInSKYTL	5.000
367	ESTKeyAIKL	5.000
936	YPVTiFEVPV	4.000
292	VPSIdIRYIV	4.000
920	KCSSsSSDPY	4.000

Table XXI – 109P1D4v.1 – B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
943	VPVSvHTRPV	4.000
610	KPVFiVPPSN	4.000
950	RPVGiQVSNT	4.000
487	VPPLISNVTV	4.000
626	LPSTnPGTVV	4.000
906	LPLDnTFVAC	4.000
664	FAIDqETGNI	3.600
744	SSPTsDYVKI	3.000
354	NQFLiETAAY	3.000
118	LIKSqNIFGL	3.000
266	LVLAsDGGLM	3.000
773	VVRCrQAPHL	3.000
39	GIPRdEHCFY	3.000
95	NSKYlPAAV	3.000
795	ATPNpENRQM	3.000
698	QPDsIFSVVI	2.400
885	QPAFqIQPET	2.000
226	FSFSnLVSNi	2.000
842	RVTldLPIDL	2.000
638	VIAVdNDTGM	2.000
120	KSQNIFGLDV	2.000
12	VPLiIEEDT	2.000
613	FIVPpSNCSY	2.000
76	APLFpATVIN	2.000
420	SPGLqLTKVS	2.000
384	PPLNqSAMLf	2.000
945	VSVHrPVGi	2.000
530	GLITvTDPDY	2.000
290	DNVPsDIRY	2.000
507	SPVFtHNEYN	2.000
422	GIQLiKVSAM	2.000
344	IPFRIRPVFS	2.000
275	MPARaMVLVN	2.000
728	KSTeAPVTPN	2.000
302	NPVNdTVVLS	2.000
644	DTGMnAEVRY	2.000
217	DIGEnAKIHf	2.000

Table XXI – 109P1D4v.1 – B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
107	DVGInGVQNY	2.000
779	APHLkAAQKN	2.000
260	TPNHkLLVLA	2.000
735	TPNtElADVS	2.000
271	DGGLmPARAM	2.000
491	TSNVlVFVSI	2.000
403	APVfIQSFVT	2.000
488	PPLTsNVTVF	2.000
732	APVTpNTEIA	2.000
536	DPDYgDNSAV	1.800
8	KTGDvPLIRI	1.600
569	ISFDrEKQES	1.500
53	AILPdElFRL	1.500
307	TVVLsENIPL	1.500
785	AQKNkQNSEW	1.500
922	SSSSsDPYSV	1.500
301	VNPVnDTVVL	1.500
591	VSRSSsAKVT	1.500
38	AGIPrDEHCF	1.500
27	TGARiDREKL	1.500
866	TTFKpDSPDL	1.500
840	GNRVLDLPI	1.200
40	IPRDeHCFYE	1.200
692	KANDIGQPDS	1.200
16	RIEEtTGEIF	1.200
467	KLDReKEDKY	1.200
573	REKQeSYTFY	1.200

Table IX – 109P1D4v.1 – A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
357	LLEtAYLDY	225.0

Table IX – 109P1D4v.1 – A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
		00
850	DLEEqTMGKY	45.000
434	DSGPnAKINY	37.500
310	LSENIPLNTK	27.000
363	YLDYeSTKEY	25.000
103	AVDPdVGING	25.000
160	KVEDgGFPQR	18.000
584	KAEDgGRVSR	18.000
269	ASDGgLMPPAR	15.000
55	LPDEIFRLVK	12.500
534	VTDPdYGDNS	12.500
557	TIDSqTGVIR	10.000
16	RIEEtTGEIF	9.000
925	SSDPySVSDC	7.500
339	FTDHeIPFRL	6.250
290	DNVPsIDIRY	6.250
743	VSSPtSDYVK	6.000
575	KQESyTFYVK	5.400
613	FIVPpSNCSY	5.000
729	STEAptVPNT	4.500
648	NAEVrYSIVG	4.500
88	IPENsAINSK	4.500
747	TSDYvKILVA	3.750
418	NNSPgQLTK	2.500
146	ELDReEKD TY	2.500
644	DTGMnAEVRY	2.500
549	ILDEnDDFTI	2.500
454	SLDCrTGMLT	2.500
285	VTDVnDNVPS	2.500

Table IX – 109P1D4v.1 – A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
467	KLDReKEDKY	2.500
640	AVDNdTGMNA	2.500
669	ETGNtLMEK	2.500
21	TGEIfTTGAR	2.250
444	LLGPdAPPEF	2.000
931	VSDCgYPVTT	1.500
903	IQELpLDNTF	1.350
213	ATDAdIGENA	1.250
179	VTDTnDNHPV	1.250
681	VTDLgLHRVL	1.250
798	NPENrQMIMM	1.125
191	ETElEVSIPe	1.125
181	DTNDnHPVFK	1.000
378	AADAgKPPLN	1.000
432	DADSGpNAKI	1.000
215	DADlgENAKI	1.000
126	GLDVIEtPEG	1.000
683	DLGLhRVLVK	1.000
458	RTGMITVVKK	1.000
719	ATLInELVRK	1.000
530	GLITvTDPDY	1.000
329	DADHnGRVTC	1.000
397	KDENdNAPVF	0.900
827	TIEEtKADDV	0.900
129	VIETpEGDKM	0.900
193	EIEVsIPENA	0.900
506	NSPVtHNEY	0.750
228	FSNLvSNIAR	0.750
288	VNDNvPSIDI	0.625
606	VNDNkPVFIV	0.625
399	ENDNaPVFTQ	0.625
72	INDNaPLFPA	0.625
503	QNDNsPVFTH	0.625
446	GPDApPEFSL	0.625
914	ACDSiSKCSS	0.500
678	KCDViDLGLH	0.500
718	NATLInELVR	0.500

Table IX – 109P1D4v.1 – A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
217	DIGEnAKIHF	0.500
53	AILPdEIFRL	0.500
628	STNPgTVVFQ	0.500
248	LITiKEPLDR	0.500
151	EKDTyVMKVK	0.500
430	AMDAdSGPNA	0.500
832	KADDvDSDGN	0.500
273	GLMPaRAMVL	0.500
889	QIQPeTPLNS	0.500
564	VIRPnISFDR	0.500
461	MLTVvKKLDR	0.500
337	TCFTdHEIPF	0.500
500	IIDQnDNSPV	0.500
448	DAPPeFSLDC	0.500
140	QLIVqKELDR	0.500
107	DVGInGVQNY	0.500
52	VAILpDEIFR	0.500
760	GTITvVVVIF	0.500
920	KCSSsSSDPY	0.500
881	SASPqPAFQI	0.500
603	VVDVnDNKPV	0.500
26	TTGAhDREK	0.500
835	DVDSdGNRVT	0.500
665	AIDQeTGNIT	0.500
132	TPEGdKMPQL	0.450
251	IKEPIDREET	0.450
712	VNESvTNATL	0.450
778	QAPHIAAQK	0.400
196	VSIPeNAPVG	0.300
388	QSAMIFIKVK	0.300
871	DSPDIARHYK	0.300
86	ISIPeNSAIN	0.300
872	SPDLaRHYKS	0.250
833	ADDVdSDGNR	0.250

Table VIII – 109P1D4v.2
C' Terminal-A1-9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
12	RTSTIEICS	0.125
8	PTDSRTSTI	0.125
14	STIEICSEI	0.025
5	HTRPTDSRT	0.025
3	SVHTRPTDS	0.010
10	DSRTSTIEI	0.008
2	VSVHTRPTD	0.003
7	RPTDSRTST	0.003
13	TSTIEICSE	0.002
1	PVSVHTRPT	0.001
4	VHTRPTDSR	0.001
11	SRTSTIEIC	0.001
6	TRPTDSRTS	0.001
9	TDSRTSTIE	0.000

Table VIII – 109P1D4v.2- N' terminal - A1-9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
29	GMDLLSGTY	12.500
2	RTERQWVLI	0.450
25	TSVPGMDLL	0.150
24	VTSPGMDL	0.125
26	SVPGMDLLS	0.050
14	QVLCGLIQQ	0.050
22	QTVTSVPGM	0.050
7	WVLIQIFQV	0.050
18	GLIQQTVTS	0.020
9	LIQIFQVLC	0.020
27	VPGMDLLSG	0.013
19	LIQQTVTSV	0.010
8	VLIQIFQVL	0.010
11	QIFQVLCGL	0.010
15	VLCGLIQQT	0.010

Table VIII – 109P1D4v.2- N' terminal - A1-9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
16	LCGLIQQTV	0.010
10	IQIFQVLCG	0.007
13	FQVLCGLIQ	0.007
21	QQTVTSPVG	0.003
6	QWVLIQIFQ	0.003
4	ERQWVLIQI	0.003
17	CGLIQQTVT	0.003
5	RQWVLIQIF	0.002
23	TVTSVPGMD	0.001
1	MRTERQWVL	0.001
12	IFQVLCGLI	0.001
3	TERQWVLIQ	0.000
28	PGMDLLSGT	0.000
20	IQQTVTSVP	0.000

Table VIII – 109P1D4v.3 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
37	KSEGVVAGK	54.000
106	NSDPESTFI	7.500
78	TSHGLPLGY	3.750
145	HSDACWMPA	3.750
111	STFIPGLKK	2.500
135	NCTQECLY	2.500
234	SAQASALCY	2.500
29	WIHPQPQRK	2.000
108	DPESTFIPG	1.125
128	TVEEASDNC	0.900
120	AAEITVQPT	0.900
132	ASDNCTQEC	0.750
62	SSDGGLGDH	0.750
288	SVDQGVQGS	0.500
154	SLDHSSSSQ	0.500

Table VIII – 109P1D4v.3 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
25	TMEIWIHPQ	0.450
3	SVHTRPPMK	0.400
110	ESTFIPGLK	0.300
137	TQECLYGH	0.270
84	LGYPQEEYF	0.250
20	MKESTMEI	0.225
54	LPEGSQESS	0.225
100	RTEGDGNSD	0.225
254	HSSPLPQVI	0.150
230	HSPPSAQAS	0.150
218	HSPPLVQAT	0.150
177	ASTQHHSR	0.150
194	HSPPVTQTI	0.150
206	HSPPPIQVS	0.150
170	HSPPLSQAS	0.150
242	YSPPLAQAA	0.150
58	SQESSSDGG	0.135
186	VTQTIALCH	0.125
136	CTQECLYIG	0.125
67	LGDHDAGSL	0.125
294	QGSATSQFY	0.125
256	SPLPQVIAL	0.125
86	YPQEEYFDR	0.125
69	DHDAGSLTS	0.125
198	VTQTIALCH	0.125
258	LPQVIALHR	0.125
333	RGDSPMEEH	0.125
16	SCTPMKEST	0.100
316	KVIPLTTFT	0.100
307	RLHPSDDSI	0.100
124	TVQPTVEEA	0.100
41	KVAGKSQRR	0.100
310	PSDDSIKVI	0.075
76	TSTSHGLPL	0.075
22	ESTTMEIWI	0.075
295	GSATSQFYT	0.075
252	ISHSSPLPQ	0.075

Table VIII – 109P1D4v.3 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
222	LVQATALHH	0.050
77	STSHGLPLG	0.050
240	LCYSPPLAQ	0.050
168	LCHSPPLSQ	0.050
7	RPPMKEVVR	0.050
80	HGLPLGY PQ	0.050
178	STQHHSPRV	0.050
246	LAQAAAISH	0.050
162	QAQASALCH	0.050
322	TFTPRQQAR	0.050
83	PLGYPQEEY	0.050
282	GADGLCSVD	0.050
207	SPPPIQVSA	0.050
10	MKEVVR SCT	0.045
88	QEEYFDRAT	0.045
129	VEEASDNCT	0.045
13	VVR SCTPMK	0.040
287	CSVDQGVQG	0.030
157	HSSSSQAQA	0.030
255	SSPLPQVIA	0.030
159	SSSQAQASA	0.030
2	VSVHTRPPM	0.030
304	MSERLHPSD	0.027
318	IPLTTFTPR	0.025
297	ATSQFYTMS	0.025
149	CWMPASLDH	0.025
5	HTRPPMKEV	0.025
105	GNSDPESTF	0.025
95	ATPSNRTEG	0.025
205	CHSPPIQV	0.025
23	STTMEIWIH	0.025
17	CTPMKESTT	0.025
320	LTTFTPRQQ	0.025
321	TFTFTPRQA	0.025
50	VTFHLPEGS	0.025
215	ALHHSPLLV	0.020
167	ALCHSPPLS	0.020

Table VIII – 109P1D4v.3 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
214	SALHHSPL	0.020
190	IALCHSPPV	0.020
238	SALCYSPL	0.020
49	RVTFHLPEG	0.020
226	TALHHSPPS	0.020
274	SLQQGWVQG	0.020
192	LCHSPPVQT	0.020
204	LCHSPPIQ	0.020
66	GLGDHDAGS	0.020
185	RVTQTIALC	0.020
147	DACWMPASL	0.020

Table VIII -109P1D4v.4 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	HPQPQSQR	0.250
2	WIHPQPQS	0.100
3	IHPQPQSQR	0.005
7	PQSQR RVTF	0.003
6	QPQSQR RV	0.003
8	QSQR RVTFH	0.002
1	IWIHPQPQS	0.001
5	PQPQSQR RV	0.000

Table IX – 109P1D4v.4 A1-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	WIHPQPQSQR	1.000
7	QPQSQR RVTF	0.050

Table IX – 109P1D4v.4 A1-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
5	HPQPqSQRRV	0.025
9	QSQRrVTFHL	0.008
4	IHPQpQSQRR	0.005
1	EIWlhPQPQS	0.002
2	IWIHpQPQSQ	0.001
6	PQPQsQRRVT	0.000
8	PQSQRrVTFH	0.000

Table X – 109P1D4v.4 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	PQPQsQRRV	0.031
2	WIHPQPQSQ	0.009
8	QSQRrVTFH	0.006
6	QPQsQRRVT	0.004
7	PQSQRrVTF	0.000
3	IHPQPQSQR	0.000
1	IWIHPQPQS	0.000
4	HPQPQSQRR	0.000

Table XI – 109P1D4v.4 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	QSQRrVTFHL	0.809
3	WIHPqPQSQR	0.009
1	EIWlhPQPQS	0.006
5	HPQPqSQRRV	0.003
8	PQSQRrVTFH	0.002
6	PQPQsQRRVT	0.001

Table XI – 109P1D4v.4 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
7	QPQsQRRVTF	0.000
4	IHPQpQSQRR	0.000
2	IWIHpQPQSQ	0.000

Table XII – 109P1D4v.4 A3-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	HPQPQSQRR	0.060
3	IHPQPQSQR	0.006
7	PQSQRrVTF	0.006
2	WIHPQPQSQ	0.003
8	QSQRrVTFH	0.003
6	QPQsQRRVT	0.000
1	IWIHPQPQS	0.000
5	PQPQsQRRV	0.000

Table XIII – 109P1D4v.4 A3-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	WIHPqPQSQR	0.900
7	QPQsQRRVTF	0.020
9	QSQRrVTFHL	0.013
1	EIWlhPQPQS	0.009
4	IHPQpQSQRR	0.004
8	PQSQRrVTFH	0.002
5	HPQPqSQRRV	0.000
6	PQPQsQRRVT	0.000
2	IWIHpQPQSQ	0.000

Table XIV – 109P1D4v.4 A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	HPQPQSQRR	0.040
3	IHPQPQSQR	0.004
7	PQSQRrVTF	0.001
2	WIHPQPQSQ	0.000
8	QSQRrVTFH	0.000
5	PQPQsQRRV	0.000
1	IWIHPQPQS	0.000
6	QPQsQRRVT	0.000

Table XV – 109P1D4v.4 A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	WIHPqPQSQR	0.080
4	IHPQpQSQRR	0.004
7	QPQsQRRVTF	0.002
8	PQSQRrVTFH	0.001
9	QSQRrVTFHL	0.001
1	EIWlhPQPQS	0.000
5	HPQPqSQRRV	0.000
2	IWIHpQPQSQ	0.000
6	PQPQsQRRVT	0.000

Table XVI – 109P1D4v.4 A24-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	PQSQRrVTF	0.200
6	QPQsQRRVT	0.150
1	IWIHPQPQS	0.150
4	HPQPQSQRR	0.022

Table XVI – 109P1D4v.4 A24-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
8	QSQRRTVFH	0.015
5	PQPQSRRV	0.015
2	WIHPQPSQ	0.014
3	IHPQPSQR	0.002

Table XVII – 109P1D4v.4 A24-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	QSQRrVTFHL	8.400
7	QPQSRRVTF	3.000
5	HPQPqSRRV	0.180
1	EIWihPQPQS	0.100
2	IWIHpQPQSQ	0.018
6	PQPQSRRVT	0.015
3	WIHPqPSQR	0.012
4	IHPqPSQRR	0.002
8	PQSQRVTFH	0.001

Table XVIII – 109P1D4v.4 B7-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
6	QPQSRRVT	3.000
4	HPQPQSRR	0.200
5	PQPQSRRV	0.020
8	QSQRRTVFH	0.010
2	WIHPQPSQ	0.010
7	PQSRRVTF	0.003
1	IWIHPQPS	0.003
3	IHPQPSQR	0.002

Table XIX – 109P1D4v.4 B7-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	QSQRrVTFHL	4.000
5	HPQPqSRRV	4.000
7	QPQSRRVTF	0.600
1	EIWihPQPQS	0.030
3	WIHPqPSQR	0.015
6	PQPQSRRVT	0.015
8	PQSQRVTFH	0.001
2	IWIHpQPQSQ	0.001
4	IHPqPSQRR	0.001

Table XX – 109P1D4v.4 B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
6	QPQSRRVT	2.000
4	HPQPQSRR	0.200
7	PQSRRVTF	0.100
8	QSQRRTVFH	0.050
5	PQPQSRRV	0.020
1	IWIHPQPS	0.010
2	WIHPQPSQ	0.010
3	IHPQPSQR	0.001

Table XXI – 109P1D4v.4 B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	QPQSRRVTF	20.000
9	QSQRrVTFHL	5.000

Table XXI – 109P1D4v.4 B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HPQPqSRRV	4.000
1	EIWihPQPQS	0.100
6	PQPQSRRVT	0.010
3	WIHPqPSQR	0.010
8	PQSQRVTFH	0.001
2	IWIHpQPQSQ	0.001
4	IHPqPSQRR	0.001

Table VIII-109P1D4v.5 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	SVHTRPSQR	0.100
7	RPSRRVTF	0.050
2	VSVHTRPSQ	0.030
5	HTRPSRRV	0.025
1	PVSVHTRPS	0.001
4	VHTRPSQRR	0.001
6	TRPSRRVT	0.001
8	PSRRVTFH	0.000

Table IX-109P1D4v.5 A1-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	VSVHTRPSQR	0.150
4	SVHTRPSQRR	0.100
6	HTRPSRRV T	0.025
7	TRPSRRVTF	0.010
1	VPVSvHTRPS	0.003

Table IX-109P1D4v.5 A1-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
8	RPSQRrVTFH	0.003
2	PVSvhTRPS Q	0.002
9	PSQRrVTFHL	0.001
5	VHTRpSQRR V	0.000

Table X-109P1D4v.5 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	SVHTRPSQR	0.001
5	HTRPSQRRV	0.000
7	RPSQRRVTF	0.000
2	VSVHTRPSQ	0.000
8	PSQRRVTFH	0.000
6	TRPSQRRVT	0.000
1	PVSvhTRPS	0.000
4	VHTRPSQRR	0.000

Table XI-109P1D4v.5 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	PSQRrVTFHL	0.018
5	VHTRpSQRRV	0.016
8	RPSQRrVTFH	0.006
4	SVHTrPSQRR	0.001
1	VPVSvhTRPS	0.000
3	VSVHrPSQR	0.000
2	PVSvhTRPSQ	0.000

Table XI-109P1D4v.5 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	HTRPsQRRVT	0.000
7	TRPSqRRVTF	0.000

Table XII-109P1D4v.5 A3-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	SVHTRPSQR	0.400
7	RPSQRRVTF	0.020
4	VHTRPSQRR	0.006
5	HTRPSQRRV	0.002
8	PSQRRVTFH	0.000
2	VSVHTRPSQ	0.000
1	PVSvhTRPS	0.000
6	TRPSQRRVT	0.000

Table XIV-109P1D4v.5 A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	SVHTrPSQRR	0.600
3	VSVHrPSQR	0.030
8	RPSQRrVTFH	0.006
7	TRPSqRRVTF	0.002
9	PSQRrVTFHL	0.001
6	HTRPsQRRVT	0.001
2	PVSvhTRPSQ	0.000
1	VPVSvhTRPS	0.000
5	VHTRpSQRRV	0.000

Table XV-109P1D4v.5 A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	SVHTrPSQRR	0.400
3	VSVHrPSQR	0.006
8	RPSQRrVTFH	0.006
7	TRPSqRRVTF	0.000
2	PVSvhTRPSQ	0.000
6	HTRPsQRRVT	0.000
9	PSQRrVTFHL	0.000
1	VPVSvhTRPS	0.000
5	VHTRpSQRRV	0.000

Table XVI-109P1D4v.5 A24-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	RPSQRRVTF	4.000
5	HTRPSQRRV	0.120
6	TRPSQRRVT	0.015
2	VSVHTRPSQ	0.015
1	PVSvhTRPS	0.010
3	SVHTRPSQR	0.010
8	PSQRRVTFH	0.002
4	VHTRPSQRR	0.001

Table XVII-109P1D4v.5 A24-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	PSQRrVTFHL	0.840
7	TRPSqRRVTF	0.300
1	VPVSvhTRPS	0.150
6	HTRPsQRRVT	0.120

Table XVII-109P1D4v.5 A24-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
8	RPSQRVTFH	0.020
3	VSVHIRPSQR	0.015
4	SVHTRPSQRR	0.012
5	VHTRpSQRRV	0.010
2	PVSVhTRPSQ	0.001

Table XVIII-109P1D4v.5 B7-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HTRPSQRRV	2.000
7	RPSQRRVTF	0.600
3	SVHTRPSQR	0.050
2	VSVHTRPSQ	0.015
6	TRPSQRRVT	0.015
1	PVSVHTRPS	0.010
4	VHTRPSQRR	0.002
8	PSQRRVTFH	0.001

Table XIX-109P1D4v.5 B7-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	HTRPsQRRVT	1.500
9	PSQRvTFHL	0.400
1	VPVSVHTRPS	0.400
8	RPSQRVTFH	0.200
4	SVHTRPSQRR	0.075
5	VHTRpSQRRV	0.020
3	VSVHIRPSQR	0.010
2	PVSVhTRPSQ	0.008

Table XIX-109P1D4v.5 B7-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
7	TRPSqRRVTF	0.003

Table XX-109P1D4v.5 B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	RPSQRRVTF	40.000
5	HTRPSQRRV	0.600
2	VSVHTRPSQ	0.050
6	TRPSQRRVT	0.010
1	PVSVHTRPS	0.010
3	SVHTRPSQR	0.010
8	PSQRRVTFH	0.005
4	VHTRPSQRR	0.001

Table XXI-109P1D4v.5 B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
1	VPVSVHTRPS	2.000
9	PSQRvTFHL	0.500
8	RPSQRVTFH	0.400
6	HTRPsQRRVT	0.300
7	TRPSqRRVTF	0.100
3	VSVHIRPSQR	0.050
5	VHTRpSQRRV	0.020
4	SVHTRPSQRR	0.010
2	PVSVhTRPSQ	0.001

Table VIII-109P1D4v.6 C' terminal-A1-9-mers		
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Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HTRPTDSRT	0.025
3	SVHTRPTDS	0.010
2	VSVHTRPTD	0.003
1	PVSVHTRPT	0.001
4	VHTRPTDSR	0.001

Table IX-109P1D4v.6 C' terminal-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	SVHTrPTDSR	0.100
3	VSVHIRPTDS	0.015
1	VPVSVHTRPT	0.003
2	PVSVhTRPTD	0.000
5	VHTRpTDSRT	0.000

Table X-109P1D4v.6 C' terminal-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	SVHTRPTDS	0.007
1	PVSVHTRPT	0.003
5	HTRPTDSRT	0.000
2	VSVHTRPTD	0.000
4	VHTRPTDSR	0.000

Table XI-109P1D4v.6 C' terminal-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		

Pos	Subsequence	Score
1	VPVSvHTRPT	0.017
5	VHTRpTDSRT	0.009
3	VSVHrPTDS	0.001
4	SVHTrPTDSR	0.001
2	PVSvHTRPTD	0.000

Table XII-109P1D4v.6 C' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HTRPTDSRT	0.007
4	VHTRPTDSR	0.006
3	SVHTRPTDS	0.004
2	VSVHTRPTD	0.000
1	PVSvHTRPT	0.000

Table XIII-109P1D4v.6 C' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	SVHTrPTDSR	0.600
3	VSVHrPTDS	0.000
2	PVSvHTRPTD	0.000
1	VPVSvHTRPT	0.000
5	VHTRpTDSRT	0.000

Table XIV-109P1D4v.6 C' terminal-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	VHTRPTDSR	0.004
3	SVHTRPTDS	0.002
5	HTRPTDSRT	0.001
2	VSVHTRPTD	0.000

Table XIV-109P1D4v.6 C' terminal-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
1	PVSvHTRPT	0.000

Table XV-109P1D4v.6 C' terminal-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	SVHTrPTDSR	0.400
2	PVSvHTRPTD	0.000
3	VSVHrPTDS	0.000
1	VPVSvHTRPT	0.000
5	VHTRpTDSRT	0.000

Table XVI-109P1D4v.6 C' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HTRPTDSRT	0.120
3	SVHTRPTDS	0.100
2	VSVHTRPTD	0.015
1	PVSvHTRPT	0.010
4	VHTRPTDSR	0.001

Table XVII-109P1D4v.6 C' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	VSVHrPTDS	0.150

Table XVII-109P1D4v.6 C' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
1	VPVSvHTRPT	0.150
4	SVHTrPTDSR	0.010
5	VHTRpTDSRT	0.010
2	PVSvHTRPTD	0.001

Table XVIII-109P1D4v.6 C' terminal-B7-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	HTRPTDSRT	1.000
3	SVHTRPTDS	0.100
1	PVSvHTRPT	0.050
2	VSVHTRPTD	0.015
4	VHTRPTDSR	0.002

Table XIX-109P1D4v.6 C' terminal-B7-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
1	VPVSvHTRPT	2.000
4	SVHTrPTDSR	0.075
3	VSVHrPTDS	0.020
5	VHTRpTDSRT	0.010
2	PVSvHTRPTD	0.008

Table XX-109P1D4v.6 C' terminal-B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		

Pos	Subsequence	Score
5	HTRPTDSRT	0.300
3	SVHTRPTDS	0.100
2	VSVHTRPTD	0.050
1	PVSVHTRPT	0.010
4	VHTRPTDSR	0.001

Table XXI-109P1D4v.6 C' terminal-B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
1	VPVSVHTRPT	2.000
3	VSVHTRPTDS	0.500
4	SVHTRPTDSR	0.010
5	VHTRPTDSRT	0.010
2	PVSVHTRPTD	0.001

Table VIII-109P1D4v.6 N' terminal-A1-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
6	NSDISSVVR	15.000
23	CLLSGTYIF	0.200
14	RVNTTNCHK	0.200
9	ISSVVRVNT	0.030
16	NTTNCHKCL	0.025
1	MTVGFNSDI	0.025
21	HKCLLSGT	0.025
17	TTNCHKCLL	0.025
10	SSVVRVNTT	0.015
3	VGFNSDISS	0.013
18	TNCHKCLLS	0.013
2	TVGFNSDIS	0.010
22	KCLLSGTIY	0.010
8	DISSVVRVN	0.010
19	NCHKCLLSG	0.005
5	FNSDISSVV	0.003
15	VNTTNCHKC	0.003

Table VIII-109P1D4v.6 N' terminal-A1-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	SDISSVVRV	0.001
11	SVVRVNTTN	0.001
12	VVRVNTTNC	0.001
4	GFNSDISSV	0.001
13	VRVNTTNCH	0.001
20	CHKCLLSGT	0.000

Table IX-109P1D4v.6 N' terminal-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	NSDISSVVRV	1.500
22	KCLLSGTIYF	0.200
17	TTNCHKCLLS	0.125
5	FNSDISSVVR	0.050
2	TVGFNSDISS	0.050
23	CLLSgTYIFA	0.050
16	NTTNCHKCLL	0.025
1	MTVG/NSDIS	0.025
8	DISSVVRVNT	0.020
10	SSVVRVNTTN	0.015
9	ISSVVRVNTT	0.015
18	TNCHKCLLSG	0.013
13	VRVNTTNCHK	0.010
14	RVNTTNCHKC	0.010
20	CHKCLLSGT	0.003
15	VNTTNCHKCL	0.003
3	VGFNsDISSV	0.003
19	NCHKCLLSGT	0.001
12	VVRVNTTNCH	0.001
11	SVVRVNTTNC	0.001
7	SDISSVVRVN	0.001
21	HKCLLSGTIY	0.001
4	GFNSdISSVV	0.001

Table X-109P1D4v.6 N' terminal-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
22	KCLLSGTIY	4.851
5	FNSDISSVV	3.511
1	MTVGFNSDI	0.936
16	NTTNCHKCL	0.297
17	TTNCHKCLL	0.297
7	SDISSVVRV	0.222
23	CLLSGTIYF	0.113
10	SSVVRVNTT	0.112
4	GFNSDISSV	0.111
9	ISSVVRVNT	0.083
12	VVRVNTTNC	0.056
15	VNTTNCHKC	0.055
11	SVVRVNTTN	0.007
3	VGFNSDISS	0.003
2	TVGFNSDIS	0.001
14	RVNTTNCHK	0.001
19	NCHKCLLSG	0.001
18	TNCHKCLLS	0.000
20	CHKCLLSGT	0.000
8	DISSVVRVN	0.000
13	VRVNTTNCH	0.000
6	NSDISSVVR	0.000
21	HKCLLSGT	0.000

Table XI-109P1D4v.6 N' terminal-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
23	CLLSgTYIFA	151.648
3	VGFNsDISSV	6.568
14	RVNTTNCHKC	0.435
11	SVVRVNTTNC	0.435
6	NSDISSVVRV	0.418

Table XI-109P1D4v.6 N' terminal-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
16	NTTNcHKCLL	0.297
15	VNTTnCHKCL	0.237
9	ISSVvRVNTT	0.190
19	NCHKcLLSGT	0.112
8	DISSvVRVNT	0.077
4	GFNSdISSVV	0.020
2	TVGFnSDISS	0.007
21	HKCLISGTYI	0.003
22	KCLLSgTYIF	0.003
18	TNCHKCLLSG	0.001
17	TTNChKCLLS	0.001
12	VVRVnTTNCH	0.001
5	FNSDISSVVR	0.001
10	SSVVRVNTTN	0.000
1	MTVGfNSDIS	0.000
7	SDISSvVRVN	0.000
13	VRVNtTNCHK	0.000
20	CHKCILSGTY	0.000

Table XII-109P1D4v.6 N' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
23	CLLSgTYIF	9.000
14	RVNTTNCHK	2.000
1	MTVGfNSDI	0.203
17	TTNCHKCLL	0.030
22	KCLLSgTYI	0.027
6	NSDISSVVR	0.020
12	VVRVnTTNC	0.020
16	NTTNCHKCL	0.015
11	SVVRVNTTN	0.005
2	TVGFNSDIS	0.004
10	SSVVRVNTT	0.002

Table XII-109P1D4v.6 N' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
21	HKCLLSGTY	0.001
7	SDISSVVRV	0.001
4	GFNSDISSV	0.001
9	ISSVVRVNT	0.001
19	NCHKCLLSG	0.001
5	FNSDISSV	0.001
15	VNTTNCHKC	0.000
3	VGfNSDISS	0.000
13	VRVNTTNCH	0.000
8	DISSVVRVN	0.000
18	TNCHKCLLS	0.000
20	CHKCLLSGT	0.000

Table XIII-109P1D4v.6 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
23	CLLSgTYIFA	0.600
22	KCLLSgTYIF	0.270
13	VRVNtTNCHK	0.030
16	NTTNcHKCLL	0.030
11	SVVRnTTNc	0.030
14	RVNTnCHKC	0.020
12	VVRVnTTNCH	0.020
5	FNSDISSVVR	0.008
2	TVGFnSDISS	0.008
1	MTVGfNSDIS	0.005
8	DISSvVRVNT	0.005
17	TTNChKCLLS	0.004
6	NSDISSVVRV	0.003
3	VGfNsDISSV	0.002
9	ISSVVRVNTT	0.002
19	NCHKcLLSGT	0.002
20	CHKCILSGTY	0.001

Table XIII-109P1D4v.6 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	GFNSdISSVV	0.001
15	VNTTnCHKCL	0.001
21	HKCLISGTYI	0.001
10	SSVVRVNTTN	0.000
18	TNCHKCLLSG	0.000
7	SDISSvVRVN	0.000

Table XIV-109P1D4v.6 N' terminal-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
14	RVNTTNCHK	6.000
1	MTVGfNSDI	0.015
23	CLLSgTYIF	0.012
17	TTNCHKCLL	0.010
22	KCLLSgTYI	0.009
4	GFNSDISSV	0.006
16	NTTNCHKCL	0.005
6	NSDISSVVR	0.004
11	SVVRVNTTN	0.003
12	VVRVnTTNC	0.002
2	TVGFNSDIS	0.002
19	NCHKCLLSG	0.000
5	FNSDISSVV	0.000
7	SDISSVVRV	0.000
13	VRVNTTNCH	0.000
21	HKCLLSGTY	0.000
3	VGfNSDISS	0.000
18	TNCHKCLLS	0.000
15	VNTTNCHKC	0.000
10	SSVVRVNTT	0.000
9	ISSVVRVNT	0.000
20	CHKCLLSGT	0.000
8	DISSVVRVN	0.000

Table XV-109P1D4v.6 N' terminal-A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
13	VRVNITNCHK	0.030
12	VVRVnTTNCH	0.020
22	KCLLSgTYIF	0.018
23	CLLSgTYIFA	0.012
16	NTTNcHKCLL	0.010
5	FNSDISSVVR	0.008
14	RVNTINCHKC	0.006
4	GFNSdISSVV	0.006
2	TVGFnSDISS	0.004
11	SVVRvNTTNC	0.003
17	TTNcHKCLS	0.002
1	MTVGfNSDIS	0.002
3	VGFnSDISSV	0.000
19	NCHKcLLSGT	0.000
6	NSDISSVVRV	0.000
20	CHKCILSGTY	0.000
15	VNTTnCHKCL	0.000
21	HKCLISGTYI	0.000
8	DISSVRVNT	0.000
18	TNcHKCLLSG	0.000
10	SSVVRVNTTN	0.000
9	ISSVRVNTT	0.000
7	SDISSVVRVN	0.000

Table XVI-109P1D4v.6 N' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
17	TTNcHKCLL	6.000
16	NTTNcHKCL	4.000
23	CLLSgTYIF	3.000
22	KCLLSgTYI	3.000
1	MTVGfNSDI	1.500

Table XVI-109P1D4v.6 N' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
4	GFNSDISSV	0.750
11	SVVRVNTTN	0.210
10	SSVRVNTT	0.180
5	FNSDISSV	0.168
8	DISSVRVN	0.140
9	ISSVRVNT	0.140
15	VNTTNCHKC	0.110
2	TVGFNSDIS	0.100
18	TNcHKCLS	0.100
3	VGfNSDIS	0.100
12	VVRVNTTNC	0.100
14	RVNTTNCHK	0.030
7	SDISSVVRV	0.015
21	HKCLLSGTY	0.012
20	CHKCLLSGT	0.012
6	NSDISSVVR	0.010
19	NCHKCLLSG	0.010
13	VRVNTTNCH	0.002

Table XVII-109P1D4v.6 N' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
22	KCLLSgTYIF	6.000
16	NTTNcHKCLL	4.000
15	VNTTNCHKCL	4.000
4	GFNSdISSVV	1.050
14	RVNTINCHKC	0.330
10	SSVVRVNTTN	0.210
17	TTNcHKCLS	0.150
1	MTVGfNSDIS	0.150
11	SVVRvNTTNC	0.150
23	CLLSgTYIFA	0.150

Table XVII-109P1D4v.6 N' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
8	DISSVRVNT	0.140
9	ISSVRVNTT	0.120
19	NCHKcLLSGT	0.120
21	HKCLISGTYI	0.100
2	TVGFnSDISS	0.100
6	NSDISSVVRV	0.100
3	VGFnSDISSV	0.100
7	SDISSVVRVN	0.021
20	CHKCILSGTY	0.012
5	FNSDISSVVR	0.012
12	VVRVnTTNCH	0.012
18	TNcHKCLLSG	0.010
13	VRVNITNCHK	0.002

Table XVIII-109P1D4v.6 N' terminal-B7-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
12	VVRVNTTNC	5.000
16	NTTNcHKCL	4.000
17	TTNcHKCLL	4.000
1	MTVGfNSDI	0.400
22	KCLLSgTYI	0.400
5	FNSDISSV	0.200
9	ISSVRVNT	0.150
10	SSVRVNTT	0.100
11	SVVRVNTTN	0.100
2	TVGFNSDIS	0.100
15	VNTTNCHKC	0.100
14	RVNTTNCHK	0.050
8	DISSVRVN	0.020
4	GFNSDISSV	0.020
18	TNcHKCLS	0.020
7	SDISSVVRV	0.020

Table XVIII-109P1D4v.6 N' terminal-B7-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
23	CLLSGTYIF	0.020
3	VGFNDSISS	0.020
20	CHKCLSGT	0.010
19	NCHKCLSG	0.010
6	NSDISSVVR	0.003
21	HKCLSGTY	0.002
13	VRVNTTNCH	0.001

Table XIX-109P1D4v.6 N' terminal-B7-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
16	NTTNCHKCLL	4.000
15	VNTTNCHKCL	4.000
11	SVVRvNTTNC	0.500
14	RVNTTNCHKC	0.500
12	VVRVnTTNCH	0.500
3	VGFNsDISSV	0.200
8	DISSvRVNT	0.150
19	NCHKcLLSGT	0.100
9	ISSVrVNTT	0.100
23	CLLSgTYIFA	0.100
2	TVGFnSDISS	0.100
6	NSDIssVVRV	0.060
21	HKCLISGTYI	0.040
4	GFNSdISSV	0.020
22	KCLLSgTYIF	0.020
10	SSVrVNTTN	0.020
1	MTVGnSDIS	0.020
17	TTNChKCLLS	0.020
18	TNChkCLLSG	0.010
5	FNSDISSVVR	0.010
7	SDISsVVRVN	0.002
20	CHKCILSGTY	0.002

Table XIX-109P1D4v.6 N' terminal-B7-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
13	VRVNITNCHK	0.001

Table XX-109P1D4v.6 N' terminal-B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
16	NTTNCHKCL	1.000
23	CLLSGTYIF	1.000
17	TTNCHKCLL	1.000
22	KCLLSGTYI	0.800
9	ISSVVRNT	0.500
10	SSVVRVNTT	0.500
1	MTVGFNsDI	0.400
5	FNSDISSV	0.400
12	VVRVNTTNC	0.300
21	HKCLSGTY	0.200
2	TVGFNSDIS	0.100
8	DISSVVRVN	0.100
18	TNCHKCLLS	0.100
15	VNTTNCHKC	0.100
3	VGFNDSISS	0.100
11	SVVRVNTTN	0.100
20	CHKCLSGT	0.030
4	GFNSDISSV	0.030
7	SDISSVVRV	0.020
14	RVNTTNCHK	0.020
6	NSDISSVVR	0.015
19	NCHKCLSG	0.010
13	VRVNTTNCH	0.001

Table XXI-109P1D4v.6 N' terminal-B3501-10-mers		
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Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
22	KCLLSgTYIF	2.000
16	NTTNcHKCLL	1.000
15	VNTTNCHKCL	1.000
20	CHKCILSGTY	0.600
9	ISSVrVNTT	0.500
10	SSVrVNTTN	0.500
6	NSDIssVVRV	0.300
3	VGFNsDISSV	0.300
14	RVNTTNCHKC	0.200
19	NCHKcLLSGT	0.100
2	TVGFnSDISS	0.100
8	DISSvRVNT	0.100
1	MTVGnSDIS	0.100
23	CLLSgTYIFA	0.100
17	TTNChKCLLS	0.100
11	SVVRvNTTNC	0.100
21	HKCLISGTYI	0.040
12	VVRVnTTNCH	0.030
4	GFNSdISSV	0.020
5	FNSDISSVVR	0.020
18	TNChkCLLSG	0.010
7	SDISsVVRVN	0.010
13	VRVNITNCHK	0.001

Table VIII-109P1D4v.7 N' terminal-A1-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
14	SLSPLLLVS	0.500
12	SSLSPLLL	0.075
13	SSLSPLLV	0.075
3	RVGFLISS	0.050
15	LSPLLLVSV	0.030
11	SSSSLSPLL	0.030
17	PLLLVSVVR	0.020
18	LLLVSVRV	0.020

Table VIII-109P1D4v.7 N' terminal-A1-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
20	LVSvVRVNT	0.020
10	SSSSSLSP	0.015
21	VSVVRVNTT	0.015
19	LLSVVRVN	0.010
8	LISSSSLS	0.010
6	FLISSSSS	0.010
7	LISSSSSL	0.010
9	ISSSSSLSP	0.007
4	VGFLISSS	0.003
2	FRVGFLIIS	0.003
16	SPLLLSVV	0.003
5	GFLISSSS	0.001
1	MFRVGFLII	0.000

Table IX-109P1D4v.7 N' terminal-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
14	SLSPILLVSV	0.200
12	SSSLsPILLV	0.075
11	SSSSSPLL	0.075
13	SSLSpLLLVS	0.075
16	SPLLIVSVR	0.050
10	SSSSSLPILL	0.030
19	LLSVVRVNT	0.020
15	LSPLLVSvV	0.015
21	VSVVRVNTTN	0.015
9	ISSSSLSPL	0.015
6	FLIIsSSSSL	0.010
18	LLLVSVVRVN	0.010
20	LVSvVRVNTT	0.010
3	RVGFIISSS	0.010
7	LISSSSLS	0.010
8	IISSSSLSP	0.005

Table IX-109P1D4v.7 N' terminal-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	VGFLISSSS	0.003
2	FRVGFLIIS	0.003
17	PILLvSVVRV	0.002
5	GFLIIsSSSS	0.001
1	MFRVgFLIIS	0.000

Table X-109P1D4v.7 N' terminal-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
18	LLLVSvVRV	1006.209
7	LISSSSSL	4.993
13	SSSLPILLV	3.864
15	LSPLLVSv	1.775
16	SPLLVSvV	1.584
20	LVSvVRVNT	1.108
6	FLISSSSS	0.343
10	SSSSLSPL	0.321
21	VSVVRVNTT	0.190
11	SSSSLPILL	0.139
12	SSSLPILL	0.139
14	SLSPILLVS	0.070
19	LLSVVRVN	0.024
8	IISSSSLs	0.017
3	RVGFIIIS	0.015
4	VGFLISSS	0.007
1	MFRVGFLII	0.001
17	PILLSVVR	0.000
5	GFLISSSS	0.000
2	FRVGFLIIS	0.000
9	ISSSSSLSP	0.000

Table XI-109P1D4v.7 N' terminal-A0201-10-mers		
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Table XII-109P1D4v.7 N' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
17	PILLVSvVR	0.900
18	LLLVSvVRV	0.900
14	SLSPILLVS	0.180
7	LISSSSSL	0.090
6	FLISSSSS	0.060
20	LVSvVRVNT	0.015
19	LLSVVRVN	0.013
3	RVGFIIIS	0.012
16	SPLLVSvV	0.009
13	SSLPILLV	0.007

Table XII-109P1D4v.7 N' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
14	SLSPILLVS	0.180
7	LISSSSSL	0.090
6	FLISSSSS	0.060
20	LVSvVRVNT	0.015
19	LLSVVRVN	0.013
3	RVGFIIIS	0.012
16	SPLLVSvV	0.009
13	SSLPILLV	0.007

Table XII-109P1D4v.7 N' terminal-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
12	SSSLSPLLL	0.006
10	SSSSLSPL	0.005
8	IISSSSLS	0.004
1	MFRVGFLII	0.004
11	SSSLSPLL	0.003
21	VSVVRVNTT	0.002
15	LSPLLVS	0.002
2	FRVGFLIIS	0.001
4	VGFLIISSS	0.000
5	GFLIISSSS	0.000
9	ISSSSSLSP	0.000

Table XIII-109P1D4v.7 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	FLIISSSSL	0.900
14	SLSPILLVSV	0.450
19	LLVSvVRVNT	0.225
16	SPLLIVSVVR	0.090
17	PLLLvSVVRV	0.090
20	LVSVvRVNTT	0.030
18	LLLVsVVRVN	0.013
3	RVGFIISSS	0.009
7	LIISsSSSLS	0.006
11	SSSSISPLLL	0.006
12	SSSLsPPLL	0.005
9	ISSSsLSPL	0.005
8	IISsSSLSP	0.004
10	SSSSsLSPLL	0.003
15	LSPLLVS	0.003
13	SSLSpLLLVS	0.001
1	MFRVgFLIIS	0.000
4	VGFLIISSSS	0.000

Table XIII-109P1D4v.7 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
2	FRVGFLIIS	0.000
21	VSVVRVNTT	0.000
5	GFLIISSSS	0.000

Table XIV-109P1D4v.7 N' terminal-A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
17	PLLLVS	0.012
3	RVGFLIIS	0.012
18	LLLVSVVRV	0.006
7	LIISSSSL	0.006
1	MFRVGFLII	0.004
16	SPLLVS	0.003
20	LVSVRVNT	0.002
5	GFLIISSS	0.001
14	SLSPLLLVS	0.001
13	SSSLPPLL	0.001
6	FLIISSSS	0.001
8	IISSSSLS	0.000
12	SSSLPPLL	0.000
10	SSSSLSPL	0.000
11	SSSLSPLL	0.000
15	LSPLLVS	0.000
2	FRVGFLIIS	0.000
19	LLSVVRVN	0.000
9	ISSSSSLSP	0.000
4	VGFLIISSS	0.000
21	VSVVRVNTT	0.000

Table XV-109P1D4v.7 N' terminal-A1101-10-mers		
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Table XVI-109P1D4v.7 N' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
16	SPLLIVSVVR	0.060
6	FLIISSSSL	0.006
3	RVGFIISSS	0.006
14	SLSPILLVSV	0.004
20	LVSVVRVNTT	0.002
5	GFLIISSSS	0.001
8	IISsSSLSP	0.001
17	PLLLvSVVRV	0.001
7	LIISsSSSLS	0.001
19	LLVSvVRVNT	0.001
11	SSSSISPLLL	0.000
1	MFRVgFLIIS	0.000
12	SSSLsPPLL	0.000
10	SSSSsLSPLL	0.000
15	LSPLLVS	0.000
9	ISSSsLSPL	0.000
18	LLLVsVVRVN	0.000
13	SSLSpLLLVS	0.000
2	FRVGFLIIS	0.000
4	VGFLIISSSS	0.000
21	VSVVRVNTT	0.000

Table XVI-109P1D4v.7 N' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	LIISSSSL	6.000
1	MFRVGFLII	6.000
11	SSSLSPLL	4.800
12	SSSLPPLL	4.000
10	SSSSLSPL	4.000
5	GFLIISSSS	1.050
3	RVGFLIIS	0.240
19	LLSVVRVN	0.210
15	LSPLLVS	0.180
16	SPLLIVSV	0.180

Table XVI-109P1D4v.7 N' terminal-A24-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
21	VSVVRVNTT	0.180
18	LLVSVVRV	0.150
13	SSLSPLLLV	0.150
6	FLIISSSSS	0.150
14	SLSPILLVS	0.144
20	LVSVRVNT	0.140
4	VGFLIISSS	0.140
8	LISSSSSL	0.100
2	FRVGFLIIS	0.015
9	ISSSSSLSP	0.010
17	PLLLVSVVR	0.002

Table XVII-109P1D4v.7 N' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	FLIISSSSL	6.000
10	SSSSsLSPLL	4.800
11	SSSSISPLLL	4.000
9	ISSSSLSPL	4.000
5	GFLIISSSSS	0.750
1	MFRVgFLIIS	0.500
3	RVGFIISSS	0.280
19	LLVSVRVNT	0.210
21	VSVVRVNTTN	0.210
18	LLVsVVRVN	0.210
15	LSPLILVSVV	0.180
13	SSLSpLLLV	0.180
7	LIISsSSSL	0.150
14	SLSPILLVS	0.144
4	VGFLIISSS	0.140
20	LVSVRVNTT	0.120
12	SSSLsPLLLV	0.100
16	SPLLIVSVR	0.021

Table XVII-109P1D4v.7 N' terminal-A24-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
2	FRVGFLIIS	0.018
17	PLLLVSVVRV	0.015
8	LISSsSSLSP	0.010

Table XVIII-109P1D4v.7 N' terminal-B7-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
16	SPLLIVSVV	4.000
11	SSSSLSPLL	4.000
12	SSSLSPLLL	4.000
7	LIISSSSL	4.000
10	SSSSLSPL	4.000
20	LVSVRVNT	0.750
1	MFRVGFLII	0.400
13	SSLSPLLLV	0.300
15	LSPLLIVSV	0.200
18	LLVSVVRV	0.200
21	VSVVRVNTT	0.100
3	RVGFIISS	0.100
14	SLSPILLVS	0.020
19	LLVSVVRVN	0.020
4	VGFLIISSS	0.020
8	LISSSSSL	0.020
6	FLIISSSS	0.020
9	ISSSSSLSP	0.010
5	GFLIISSSS	0.002
2	FRVGFLIIS	0.002
17	PLLLVSVVR	0.001

Table XIX-109P1D4v.7 N' terminal-B7-10-mers		
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Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	ISSSSLSPL	4.000
11	SSSSISPLLL	4.000
10	SSSSsLSPLL	4.000
6	FLIISSSSL	4.000
20	LVSVRVNTT	0.500
12	SSSLsPLLLV	0.300
15	LSPLLIVSVV	0.200
16	SPLLIVSVR	0.200
14	SLSPILLVS	0.200
19	LLVSVRVNT	0.150
3	RVGFIISSS	0.100
18	LLVsVVRVN	0.020
13	SSLSpLLLV	0.020
4	VGFLIISSS	0.020
21	VSVVRVNTTN	0.020
7	LIISsSSSL	0.020
17	PLLLVSVVRV	0.020
1	MFRVgFLIIS	0.020
8	LISSsSSLSP	0.010
2	FRVGFLIIS	0.002
5	GFLIISSSS	0.002

Table XX-109P1D4v.7 N' terminal-B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
12	SSSLSPLLL	5.000
11	SSSSLSPLL	5.000
10	SSSSLSPL	5.000
16	SPLLIVSVV	4.000
7	LIISSSSL	1.000
15	LSPLLIVSV	1.000
13	SSLSPLLLV	1.000
21	VSVVRVNTT	0.500
3	RVGFIISS	0.200
18	LLVSVVRV	0.200

Table XX-109P1D4v.7 N' terminal-B3501-9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
1	MFRVGFLII	0.120
19	LLVSVVRVN	0.100
14	SLSPLLLVS	0.100
20	LVSVVRVNT	0.100
8	IISSSSLS	0.100
6	FLIISSSS	0.100
4	VGFLIIS	0.100
9	ISSSSSLSP	0.050
5	GFLIISSS	0.010
2	FRVGFLIIS	0.010
17	PLLLSVVR	0.001

Table XXI-109P1D4v.7 N' terminal-B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
9	ISSSSLSPL	5.000
11	SSSSISPLL	5.000
10	SSSSLSPLL	5.000
15	LSPLIVSVV	1.000
6	FLIISSSSL	1.000
12	SSSLsPLLLV	1.000
21	VSVVRVNTTN	0.500
13	SSLSPLLLVS	0.500
16	SPLLIVSVVR	0.200
14	SLSPILLVSV	0.200
3	RVGFIIS	0.200
18	LLLVsVVRVN	0.100
19	LLVSVVRVNT	0.100
20	LVSvRVNTT	0.100
4	VGFLIISSS	0.100
7	LISSSSLS	0.100
1	MFRVgFLIIS	0.030
17	PLLLSVVRV	0.020

Table XXI-109P1D4v.7 N' terminal-B3501-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
2	FRVGFLIIS	0.010
8	IISSSSLSP	0.010
5	GFLIISSSS	0.010

Table VIII-109P1D4v.8 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	KKEITVQPT	0.045
2	FIPGLKKEI	0.010
3	IPGLKKEIT	0.003
8	KEITVQPTV	0.001
1	TFIPGLKKE	0.001
4	PGLKKEITV	0.000
5	GLKKEITVQ	0.000
6	LKKEITVQP	0.000

Table IX-109P1D4v.8 A1-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
8	KKEITVQPTV	0.090
4	IPGLKKEITV	0.013
3	FIPGIKKEIT	0.010
2	TFIPgLKKEI	0.005
1	STFIPGLKKE	0.003
7	LKKEITVQPT	0.000
9	KEITvQPTVE	0.000
5	PGLKKEITVQ	0.000
6	GLKKeITVQP	0.000

Table X-109P1D4v.8 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
2	FIPGLKKEI	6.599
8	KEITVQPTV	4.733
4	PGLKKEITV	0.037
3	IPGLKKEIT	0.017
7	KKEITVQPT	0.005
5	GLKKEITVQ	0.000
1	TFIPGLKKE	0.000
6	LKKEITVQP	0.000

Table XI-109P1D4v.8 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
3	FIPGIKKEIT	0.947
4	IPGLKKEITV	0.772
8	KKEITVQPTV	0.022
2	TFIPgLKKEI	0.007
7	LKKEITVQPT	0.006
1	STFIPGLKKE	0.002
6	GLKKeITVQP	0.001
9	KEITvQPTVE	0.000
5	PGLKKEITVQ	0.000

Table XII-109P1D4v.8 A3-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
5	GLKKEITVQ	0.090
2	FIPGLKKEI	0.045
8	KEITVQPTV	0.004
3	IPGLKKEIT	0.001

Table XII-109P1D4v.8 A3-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
7	KKEITVQPT	0.001
4	PGLKKEITV	0.000
6	LKKEITVQP	0.000
1	TFIPGLKKE	0.000

Table XIII-109P1D4v.8 A3-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	GLKKEITVQP	0.090
3	FIPGIKKEIT	0.015
4	IPGLKKEITV	0.004
1	STFIPGLKKE	0.004
8	KKEIVQPTV	0.001
2	TFIPGLKKEI	0.001
7	LKKEITVQPT	0.000
9	KEITVQPTVE	0.000
5	PGLKKEITVQ	0.000

Table XIV-109P1D4v.8 A1101-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
8	KEITVQPTV	0.003
2	FIPGLKKEI	0.002
5	GLKKEITVQ	0.001
3	IPGLKKEIT	0.000
1	TFIPGLKKE	0.000
4	PGLKKEITV	0.000
7	KKEITVQPT	0.000
6	LKKEITVQP	0.000

Table XV-109P1D4v.8 A1101-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	IPGLKKEITV	0.004
2	TFIPGLKKEI	0.002
6	GLKKEITVQP	0.001
1	STFIPGLKKE	0.001
8	KKEIVQPTV	0.001
3	FIPGIKKEIT	0.000
9	KEITVQPTVE	0.000
7	LKKEITVQPT	0.000
5	PGLKKEITVQ	0.000

Table XVI-109P1D4v.8 A24-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
2	FIPGLKKEI	1.980
3	IPGLKKEIT	0.100
1	TFIPGLKKE	0.099
8	KEITVQPTV	0.042
7	KKEITVQPT	0.036
4	PGLKKEITV	0.015
5	GLKKEITVQ	0.010
6	LKKEITVQP	0.002

Table XVII-109P1D4v.8 A24-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
2	TFIPGLKKEI	11.880
3	FIPGIKKEIT	0.150

Table XVII-109P1D4v.8 A24-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	IPGLKKEITV	0.100
8	KKEIVQPTV	0.042
7	LKKEITVQPT	0.014
6	GLKKEITVQP	0.014
1	STFIPGLKKE	0.011
9	KEITVQPTVE	0.003
5	PGLKKEITVQ	0.002

Table XVIII-109P1D4v.8 B7-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	IPGLKKEIT	2.000
2	FIPGLKKEI	0.400
8	KEITVQPTV	0.020
4	PGLKKEITV	0.020
5	GLKKEITVQ	0.010
7	KKEITVQPT	0.003
6	LKKEITVQP	0.001
1	TFIPGLKKE	0.001

Table XIX-109P1D4v.8 B7-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	IPGLKKEITV	4.000
3	FIPGIKKEIT	0.100
2	TFIPGLKKEI	0.040
7	LKKEITVQPT	0.010
1	STFIPGLKKE	0.010

Table XIX-109P1D4v.8 B7-10-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
6	GLKKeITVQP	0.010
8	KKEITVQPTV	0.006
9	KEITvQPTVE	0.001
5	PGLKkeITVQ	0.001

Table XX-109P1D4v.8 B3501-9-mers		
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Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	Subsequence	Score
3	IPGLKKEIT	2.000
2	FIPGLKKEI	0.400
5	GLKKEITVQ	0.045
8	KEITVQPTV	0.040
4	PGLKKEITV	0.020
6	LKKEITVQP	0.006
7	KKEITVQPT	0.006
1	TFIPGLKKE	0.001

Table XXI-109P1D4V.8 B3501-10-mers		
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Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	Subsequence	Score
4	IPGLKKEITV	4.000
3	FIPGIKKEIT	0.100
7	LKKEITVQPT	0.060
2	TFIPgLKKEI	0.040
6	GLKKeITVQP	0.030
8	KKEITVQPTV	0.012
1	STFIpGLKKE	0.010
9	KEITvQPTVE	0.002
5	PGLKkeITVQ	0.002

Tables XXII – XLIX:

Table XXII -109P1D4v.1 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
911	LEEQTMGKY	27
59	TAMQFKLVY	22
570	FIHNEYNFY	22
807	TSDYVKILV	22
20	HSGAQEKNY	21
418	LETAAYLDY	21
495	SGPNAKINY	21
594	VTDPDYGDN	21
985	SSDPYSVSD	21
364	VNDTVVLSE	20
370	LSENIPLNT	20
674	IVPPSNCSY	20
789	STEAPVTPN	20
168	VGINGVQNY	19
351	NVPSIDIRY	19
741	VTDLGLHRV	19
931	DSPDLARHY	19
981	CSSSSSDPY	19
116	PDEIFRLVK	18
150	ENSAINSKY	18
329	ASDGGLMPA	18
345	VIDVNDNVP	18
991	VSDCGYPVT	18
221	VEDGGFPQR	17
239	VIDTNDNHP	17
251	ETEIEVSIP	17
273	ATDADIGEN	17
354	SIDIRYIVN	17
385	VIDKDADHN	17
399	FIDHEIPFR	17
528	LDREKEDKY	17
567	SPVFTHNEY	17
727	DQETGNITL	17
929	KPDSPDLAR	17

Table XXII -109P1D4v.1 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
1008	HTRPVGIQV	17
34	MPENVLIGD	16
78	EEDTGEIFT	16
90	RIDREKLCA	16
109	EVEVAILPD	16
132	INDNAPLFP	16
163	AVDPDVGIN	16
401	DHEIPFRLR	16
531	EKEOKYLFT	16
631	FDREKQESY	16
738	KCDVTDLGL	16
797	NTEIADVSS	16
802	DVSSPTSDY	16
897	DSGNGRVTL	16
69	TGDVPLIRI	15
100	IPRDEHCFY	15
115	LPDEIFRLV	15
207	LDREEKDTY	15
415	QELLETAAY	15
423	YLDYESTKE	15
424	LDYESTKEY	15
428	STKEYAIKL	15
591	LITVTDPDY	15
634	EKQESYIFY	15
645	AEDGGRVSR	15
688	SINPGTVVF	15
705	TGMNAEVRY	15
988	PYSVSDCGY	15
68	KTGDVPLIR	14
148	IPENSAINS	14
211	EKDTYVMKV	14
278	IGENAKIHF	14
311	IKEPLDREE	14

Table XXII -109P1D4v.1 A1-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
317	REETPNHKL	14
319	ETPNHKLIV	14
411	VFSNQFLL	14
514	SLDCRTGML	14
542	AKDNGVPPL	14
572	HNEYNFYVP	14
612	ENDDFTIDS	14
644	KAEDGGRVS	14
668	DNKPVFIVP	14
681	SYELVLPST	14
720	TRDLFAIDQ	14
758	QPDLSFSVV	14
779	ATLINELVR	14
851	NSEWATPNP	14
904	TLDLPIDLE	14
967	PLDNTFVAC	14

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
114	ILPDEIFRL	27
416	FLLETAAYL	27
43	LLKDLNLSL	26
333	GLMPARAMV	26
520	GMLTVVKKL	26
39	LIGDLLKDL	25
294	NIARRLFHL	24
514	SLDCRTGML	24

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
817	AVAGTITVV	24
880	NLLNFVTI	24
64	KLVTYKTDV	23
231	STAILQVSV	23
307	GLITIKEPL	23
375	PLNTKIALI	23
539	TILAKDNGV	23
745	GLHRVLVKA	23
810	YVKILVAHV	23
813	ILVAHVAGT	23
38	VLIGDLLKD	22
741	VTDLGLHRV	22
816	AAVAGITIV	22
9	IFAVLLACV	21
76	RIEEDTGEI	21
124	KIRFLIEDI	21
152	SAINSKYTL	21
301	HLNATTGLI	21
356	DIRYIVNPV	21
360	IVNPVNDTV	21
536	YLFTILAKD	21
743	DLGLHRVLV	21
820	GTITVWVI	21
825	VVIFITAV	21
999	TTFEVPVSV	21
50	SLIPNKSLT	20
127	FLIEDINDN	20
234	ILQVSVTDT	20
270	QLHATDADI	20
298	RLFHLNATT	20
334	LMPARAMVL	20
337	ARAMVLVNV	20
340	MVLVNVTDV	20
347	DVNDNVPSI	20
359	YIVNPVNDT	20
428	STKEYAIKL	20

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
546	GVPPLTSNV	20
550	LTSNVTVFV	20
656	SAKVTINVV	20
658	KVTINVVDV	20
715	IVGGNTRDL	20
725	AIDQETGNI	20
777	TNATLINEL	20
781	LINELVRKS	20
826	VVIFITAVV	20
6	GTYIFAVLL	19
12	VLLACVVFH	19
22	GAQEKNYTI	19
135	NAPLFPATV	19
162	AAVDPDVGI	19
303	NATTGLITI	19
326	LVLASDGGL	19
377	NTKIALITV	19
438	AADAGKPPL	19
503	YLLGPDAPP	19
542	AKDNGVPPL	19
583	LPRHGTVGL	19
616	FTIDSQTGV	19
818	VAGTITVVV	19
881	LLNFTVIE	19
903	VTDLPLIDL	19
914	QTMGKYNWV	19
3	LLSGTYIFA	18
4	LSGTYIFAV	18
13	LLACVVFHS	18
51	LIPNKSLTT	18
95	KLCAGIPRD	18
120	FRLVKIRFL	18
121	RLVKIRFLI	18
213	DTYVMKVKV	18
276	ADIGENAKI	18
283	KIHFSFSNL	18

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
369	VLSENIPLN	18
381	ALITVIDKD	18
403	EIPFRLRPV	18
480	SPGIQLTKV	18
496	GPNAKINYL	18
609	ILDENDFFT	18
617	TIDSQTGVI	18
693	TVVFQVIAV	18
733	ITLMEKCDV	18
734	TLMEKCDVT	18
748	RVLVKANDL	18
757	GQPDLSFSV	18
762	LFSVIVNVL	18
780	TLINELVRK	18
814	LVAHVAGTI	18
822	ITVVVIFI	18
955	PLNSKHII	18
958	SKHHIIQEL	18
990	SVSDCGYPV	18
8	YIFAVLLAC	17
57	LTTAMQFKL	17
88	GARIDREKL	17
143	VINISIPEN	17
156	SKYTLPAHV	17
165	DPDVGINGV	17
179	IKSQNIFGL	17
256	VSIPENAPV	17
320	TPNHKLLVL	17
327	VLASDGGLM	17
368	VVLSENIPL	17
379	KIALITVTD	17
482	GIQLTKVSA	17
493	ADSGPNAKI	17
586	HGTVGLITV	17
685	VLPSTNPGT	17
761	SLFSVIVNV	17

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
764	SVVIVNLFV	17
795	TPNTEIADV	17
819	AGTITVVVV	17
965	ELPLDNTFV	17
1006	SVHTRPVGI	17
2	DLLSGTYIF	16
10	FAVLLACVV	16
42	DLLKDLNLS	16
49	LSLIPNKSL	16
60	AMQFKLVYK	16
67	YKTGDVPLI	16
83	EIFTTGARI	16
107	FYEVEVAIL	16
117	DEIFRLVKI	16
145	NISIPENSA	16
197	KMPQLIVQK	16
233	AILQVSVTD	16
290	NLVSNIARR	16
291	LVSNIARRL	16
300	FHLNATTGL	16
432	YAIKLLAAD	16
433	AIKLLAADA	16
435	KLLAADAGK	16
436	LLAADAGKP	16
532	KEDKYLFTI	16
553	NVTVFVSII	16
587	GTVGLITVT	16
599	YGDNSAVTL	16
602	NSAVTL_SIL	16
655	SSAKVTINV	16
667	NDNKPVFIV	16
722	DLFAIDQET	16
754	NDLGQPDLS	16
760	DSLFSVVIV	16
771	FVNESVTNA	16
806	PTSDYVKIL	16

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
882	LLNFVTIEE	16
934	DLARHYKSA	16
1008	HTRPVGIQV	16
41	GDLLKDLNL	15
58	TTAMQFKLV	15
146	ISIPENSAI	15
160	LPAAVDPDV	15
170	INGVQNYEL	15
181	SNIFGLDV	15
182	QNIFGLDVI	15
229	RSSTAILQV	15
263	PVGTSVTQL	15
284	IHFSSNLV	15
287	SFSNLVSNI	15
338	RAMVLNVVT	15
374	IPLNTKIAL	15
396	VTCFTDHEI	15
448	QSAMLFIKV	15
450	AMLFIKVKD	15
451	MLFIKVKDE	15
504	LLGPDAPPE	15
517	CRTGMLTVV	15
590	GLITVDPD	15
624	VIRPNJSFD	15
643	VKAEDGGRV	15
651	VSRSSSAKV	15
688	STNPGTVVF	15
703	NDTGMNAEV	15
707	MNAEVRYSI	15
742	TDLGLHRVL	15
767	IVNLFVNES	15
769	NLFVNESVT	15
875	KHSPKNLLL	15
897	DSDGNRVTL	15
904	TLDLPIDLE	15
906	DLPIDLEEQ	15

Table XXIII 109P1D4v.1 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
961	HIIQELPLD	15
970	NTFVACDSI	15
983	SSSSDPYSV	15
995	GYPVTIFEV	15
44	LKDLNLSLI	14
46	DLNLSLIPN	14
66	VYKTGDVPL	14
106	CFYEVEVAI	14
111	EVAILPDEI	14
113	AILPDEIFR	14
115	LPDEIFRLV	14
128	LIEDINDNA	14
137	PLFPATVIN	14
138	LFPATVINI	14
147	SIPENSAIN	14
159	TLPAAVDPD	14
183	NIFGLDVIE	14
211	EKDTYVMKV	14
232	TAILQVSVT	14
248	VFKETEIEV	14
250	KETEIEVSI	14
310	TIKEPLDRE	14
324	KLLVLASDG	14
329	ASDGGLMPA	14
335	MPARAMVLV	14
339	AMVLNVNVT	14
344	NVTDVNDNV	14
362	NPVNDIVVL	14
388	KDADHNGRV	14
412	FSNQFLLET	14
465	VFTQSEVTV	14
483	IQLTKVSAM	14
500	KINYLLGPD	14
507	PDAPPEFSL	14
516	DCRTGMLTV	14
540	ILAKDNGVP	14

Table XXIII 109P1D4v.1
A0201-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

552	SNVTVEVSI	14
571	THNEYNFYV	14
678	SNCSYELVL	14
686	LPSTNPGTV	14
690	NPGTVVVFQV	14
706	GMNAEVRYS	14
714	SIVGGNTRD	14
768	VNLFVNESV	14
773	NESVTNATL	14
784	ELVRKSTEA	14
812	KILVAAVAG	14
878	PKNLLNFV	14
895	DVDSGDGNRV	14
948	FQIQPETPL	14
962	IIQELPLDN	14

Table XXIV
109P1D4v.1
A0203-9-mers

No Results Found.

Table XXV-
109P1D4v.1-A3-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

650	RVSRSSSAK	31
435	KLLAADAGK	30
11	AVLLACVVF	28
37	NVLIGDLLK	28

Table XXV-
109P1D4v.1-A3-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

780	TLINELVRK	28
527	KLDREKEDK	26
172	GVQNYELIK	24
407	RLRPVFSNQ	24
827	VFITAVVR	24
839	APHLKAAQK	24
422	AYLDYESTK	23
674	IVPPSNCSY	23
841	HLKAAQKNK	23
972	FVACDSISK	23
12	VLLACVVFH	22
233	AILQVSVTD	22
518	RTGMLTVVK	22
623	GVIRPNISF	22
662	NVVDVNDNK	22
814	LVAAVAGTI	22
833	VVRCROAPH	22
910	DLEEQTMGK	22
56	SLITAMQFK	21
65	LVYKTGDVP	21
167	DVGINGVQN	21
298	RLFHLNATT	21
324	KLLVLASDG	21
379	KIALITVTD	21
524	VVKLDREK	21
582	NLPRHGTVG	21
740	DVTDLGLHR	21
744	LGLHRVLVK	21
812	KILVAAVAG	21
817	AVAGTITVV	21
880	NLLNFVTI	21
921	WVITPITFK	21
50	SLIPNKS LT	20
113	AILPDEIFR	20
197	KMPQLIVQK	20

Table XXV-
109P1D4v.1-A3-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

360	IVNPVNDTV	20
748	RVLVKANDL	20
826	VVIFITAVV	20
17	VVFHSGAQE	19
116	PDEIFRLVK	19
189	VIETPEGDK	19
218	KVKVEDGGF	19
220	KVEDGGGFPQ	19
384	TVTDKADADH	19
416	FILETAAYL	19
433	AIKLLAADA	19
479	NSPGIQLTK	19
535	KYLFITLAK	19
549	PLTSNVTVF	19
588	TVGLITVTD	19
665	DVNDNKPVF	19
802	DVSSPTS DY	19
864	MIMMKKKKK	19
2	DLLSGTYIF	18
38	VLI GDLLKD	18
60	AMQFKLVYK	18
90	RIDREKLCA	18
212	KDIYVMKVK	18
267	SVTQLHATD	18
333	GLMPARAMV	18
445	PLNQSAML F	18
487	KVSAMDADS	18
540	ILAKDNGVP	18
642	YVKAEDGGR	18
645	AEDGGRVSR	18
658	KVTINVVDV	18
688	STNPGTVVF	18
694	VVEQVIADV	18
697	QVI AVDNDT	18
745	GLHRVLVKA	18

Table XXV- 109P1D4v.1-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
832	AVVRCRQAP	18
835	RCRQAPHLK	18
871	KKKKKHSPK	18
1002	EVPVSVHTR	18
1006	SVHTRPVG	18
43	LLKDLNLSL	17
51	LIPNKS_LTT	17
95	KLCAGIPRD	17
122	LVKIRFLIE	17
137	PLFPATVIN	17
163	AVDPDVGIN	17
177	ELIKSQNIF	17
210	EKDTYVMK	17
257	SIPENAPVG	17
270	QLHATDADI	17
290	NLYSNIARR	17
381	ALITVTDKD	17
436	LLAADAGKP	17
484	QLTKVSAMD	17
503	YLLGPDAPP	17
604	AVTLSILDE	17
624	VIRPNISFD	17
710	EVRYISVGG	17
755	DLGQPDSLF	17
765	VVIVNLFVN	17
769	NLFVNESVT	17
779	ATLINELVR	17
813	ILVAAGVAGT	17
821	TITVVVIF	17
1013	GIQVSNTTF	17
55	KSLTTAMQF	16
73	PLIRIEEDT	16
74	LIRIEEDTG	16
131	DINDNAPLF	16
201	LIVQKELDR	16

Table XXV- 109P1D4v.1-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
238	SVTDNDNH	16
242	TNDNHPVFK	16
277	DIGENAKIH	16
293	SNJARRLFH	16
304	ATTGLITIK	16
341	VLNVTDVN	16
351	NVPSIDIRY	16
354	SIDIRYIVN	16
371	SENIPLNTK	16
380	IALITVTDK	16
449	SAMLFIVK	16
504	LLGPDAPPE	16
546	GVPPLTSNV	16
608	SILDENDDF	16
636	QESYTFYVK	16
700	AVDNDTGMN	16
713	YSIVGGNTR	16
734	TLMEKCDVT	16
743	DLGLHRVLV	16
750	LVKANDLGQ	16
761	SLFSVIVN	16
764	SVIVNLFV	16
810	YVKILVAIV	16
934	DLARHYKSA	16
967	PLDNTFVAC	16

Table XXVI- 109P1D4v.1 A26-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		

802	DVSSPTSDY	30
665	DVNDNKPVF	28
241	DTNDNHPVF	26
36	ENVLIGDLL	25
109	EVEVAILPD	25
347	DVNDNVPSI	25
1002	EVPVSVHTR	25
150	ENSAINSKY	24
188	DVIETPEGD	24
351	NVPSIDIRY	24
410	PVFSNQFLL	24
623	GVIRPNISF	24
710	EVRYISVGG	24
118	EIFRLVKIR	23
251	ETEIEVSIP	23
263	PVGTSVTQL	23
740	DVTDLGLHR	23
130	EDINDNAPL	22
131	DINDNAPLF	22
177	ELIKSQNIF	22
419	ETAAYLDYE	22
477	ENNSPGIQL	22
634	EKQESYTFY	22
674	IVPPSNCSY	22
729	ETGNITLME	22
71	DVPLIRIEE	21
80	DTGEIFTTG	21
111	EVAILPDEI	21
167	DVGINGVQN	21
191	ETPEGDKMP	21
255	EVSIPENAP	21
280	ENAKIHFSF	21
318	EETPNHKLL	21
366	DTVVLSENI	21
428	STKEYAIKL	21
693	TVVFQVIAV	21
806	PTSDYVKIL	21
993	DCGYPVITF	21
291	LVSNIARRL	20
368	VVLSENIPL	20
391	DHNGRVTCF	20
523	TVVKKLDRE	20
555	TVFVSIIDQ	20
895	DVDSGDGNRV	20

Table XXVI- 109P1D4v.1 A26-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
931	DSPDLARHY	20
83	EIFTTGARI	19
218	KVKVEDGGF	19
319	ETPNHKLLV	19
326	LVLASDGGL	19
533	EDKYLFTIL	19
715	IVGGNTRDL	19
748	RVLVKANDL	19
765	VVIVNLFVN	19
809	DYVKILVAA	19
823	TVVVVIFIT	19
825	VVVFITAV	19
903	VTLDLPIDL	19
953	ETPLNSKHH	19
11	AVLLACVVF	18
33	EMPENVLIG	18
39	LIGDLLKDL	18
57	LTTAMQFKL	18
141	ATVINISIP	18
142	TVINISIPE	18
168	VGINGVQNY	18
253	EIEVSIPEN	18
356	DIRYIVNPV	18
403	EIPFRLRPV	18
458	DENDNAPVF	18
562	DQNDNSPVF	18
570	FTHNEYNFY	18
688	STNPGTVVF	18
694	VVFQVIAVD	18
727	DQETGNITL	18
763	FSVVIVNLF	18
821	TITVVVVF	18
824	VVVVIFITA	18
890	ETKADDVDS	18

Table XXVI- 109P1D4v.1 A26-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
897	DSDGNRVTL	18
2	DLLSGTYIF	17
117	DEIFRLVKI	17
213	DTYVMKVKV	17
350	DNVPSIDIR	17
372	ENIPLNTKI	17
431	EYAIKLLAA	17
578	YVPENLPRH	17
587	GTVGLITVT	17
704	DTGMNAEVR	17
755	DLGQPDSLF	17
822	ITVVVIFI	17
899	DGNRVTLDL	17
6	GTIFYAVLL	16
16	CVVFHSGAQ	16
17	VVFHSGAQE	16
79	EDTGEIFTT	16
163	AVDPDVGIN	16
294	NIARRLFHL	16
529	DREKEDKYL	16
553	NVTVFVSII	16
604	AVTLSILDE	16
614	DDFTIDSQT	16
658	KVTINVVDV	16
659	VTINVVDVN	16
764	SVVIVNLFV	16
771	FVNESVTNA	16
799	EIADVSSPT	16
810	YVKILVAAV	16
820	GTITVVVVI	16
826	VVVFITAVV	16
976	DSISKCSSS	16
999	TTFEVPVSV	16
211	EKDTYVMKV	15

Table XXVI- 109P1D4v.1 A26-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
277	DIGENAKIH	15
320	TPNHKLLVL	15
340	MVLNVVTDV	15
363	PVNDTVVLS	15
367	TVVLSENIP	15
470	FVTVSIPEN	15
471	VTVSIPENN	15
549	PLTSNVTVF	15
567	SPVFTHNEY	15
591	LITVTDPDY	15
605	VTLSILDEN	15
646	EDGGRVSR	15
662	NVVDVNDNK	15
671	PVFIVPPSN	15
774	ESVTNATLI	15
784	ELVRKSTEA	15
832	AVVRCRQAP	15
860	ENRQMIMMK	15
877	SPKNLLNLF	15
886	VTIEETKAD	15
902	RVTLDLPID	15
958	SKHHIIQEL	15
1011	PVGIQVSNT	15

Table XXVII-109P1D4 v.1-B0702-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
583	LPRHGTVGL	25

Table XXVII-109P1D4 v.1-B0702-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
362	NPVNDTVVL	24
136	APLFPATVI	23
320	TPNHKLLVL	23
374	IPLNTKIAL	22
409	RPVFSNQFL	22
676	PPSNCSYEL	22
792	APVTPNTEI	22
444	PPLNQSAML	21
496	GPNAKINYL	21
404	IPFRLRPVF	20
52	IPNKSLLTA	19
160	LPAAVDPDV	19
258	IPENAPVGT	19
335	MPARAMVLV	19
463	APVFTQSFV	19
758	QPDLSFSVV	19
115	LPDEIFRLV	18
226	FPQRSSTAI	18
352	VPSIDIRYI	18
443	KPPLNQSAM	18
475	IPENNSPGI	18
480	SPGIQLTKV	18
548	PPLTSNVT	18
686	LPSTNPGTV	18
690	NPGTVVFQV	18
805	SPTSDYVKI	18
877	SPKNLLNF	18
929	KPDSPLAR	18
966	LPLDNTFVA	18
165	DPDVGINGV	17
246	HPVFKETEI	17
547	VPPLTSNVT	17
596	DPDYGDNDA	17
795	TPNTEIADV	17
856	TPNPENRQM	17

Table XXVII-109P1D4 v.1-B0702-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
262	APVGTSVTQ	16
438	AADAGKPPL	16
493	ADSGPNAKI	16
506	GPDAPPEFS	16
542	AKDNGVPPL	16
858	NPENRQMIM	16
875	KHSPKNLLL	16
897	DSDGNRVTL	16
907	LPIDLEEQT	16
954	TPLNSKHHI	16
31	REEMPENVL	15
477	ENNSPGIQL	15
507	PDAPPEFSL	15
715	IVGGNTRDL	15
948	FQIQPETPL	15
1010	RPVGIQVSN	15
100	IPRDEHCFY	14
154	INSKYTLPA	14
227	PQRSSTAIL	14
317	REETPNHKL	14
509	APPEFSLDC	14
670	KPVFIVPPS	14
738	KCDVTDLGL	14
762	LFSWVIVNL	14
874	KKHSPKNLL	14
5	SGTYIFAVL	13
49	LSLIPNKS	13
66	VYKTGDVPL	13
88	GARIDREKL	13
130	EDINDNAPL	13
162	AAVDPDVGI	13
179	IKSQNIFGL	13
192	TPEGDKMPQ	13
263	PVGTSVTQL	13
533	EDKYLFTIL	13

Table XXVII-109P1D4 v.1-B0702-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
599	YGDNSAVTL	13
678	SNCSYELVL	13
742	TDLGLHRVL	13
773	NESVTNATL	13
806	PTSDYVKIL	13
817	AVAGTITVV	13
839	APHLKAAQK	13
899	DGNRVTLDL	13
940	KSASPQPAF	13
951	QPETPLNSK	13
960	HHIIQELPL	13

Table XXVIII-109P1D4 v.1-B08-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
496	GPNAKINYL	28
43	LLKDLNLSL	27
320	TPNHKLLVL	26
453	FIKVKDEND	26
514	SLDCRTGML	26
22	GAQEKNYTI	24
246	HPVFKETEI	24
428	STKEYAIKL	24
877	SPKNLLNF	24
120	FRLVKIRFL	23
216	VMKVKVEDG	23
375	PLNTKIALI	23
533	EDKYLFTIL	23
583	LPRHGTVGL	23

Table XXVIII-109P1D4 v.1-B08-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
41	GDLLKDLNL	22
66	VYKTGDVPL	22
294	NIARRLFHL	22
955	PLNSKHIII	22
88	GARIDREKL	21
736	MEKCDVTDL	21
748	RVLVKANDL	21
866	MMKKKKKKK	21
867	MKKKKKKKK	21
868	KKKKKKKKH	21
869	KKKKKKKHS	21
873	KKKHSPKNL	21
875	KHSPKNLLL	21
91	IDREKLCAG	20
193	PEGDKMPQL	20
845	AQKNKQNSE	20
870	KKKKKKHSP	20
871	KKKKKHSPK	20
927	TFKPDSPDL	20
416	FLLETAAYL	19
631	FDREKQESY	19
784	ELVRKSTEA	19
114	ILPDEIFRL	18
122	LVKIRFLIE	18
334	LMPARAMVL	18
374	IPLNTKIAL	18
451	MLFIKVKDE	18
528	LDREKEDKY	18
530	REKEDKYLF	18
656	SAKVTINVV	18
666	VNDNKPVFI	18
734	TLMEKCDVT	18
841	HLKAAQKNK	18
64	KLVTGTGDV	17
72	VPLIRIEED	17

Table XXVIII-109P1D4 v.1-B08-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
124	KIRFLIEDI	17
218	KVKVEDGGF	17
307	GLITKEPL	17
362	NPVNDTVVL	17
409	RPVFSNQFL	17
426	YESTKEYAI	17
676	PPSNCSEYL	17
839	APHLKAAQK	17
1006	SVHTRPVGI	17
152	SAINSKYTL	16
176	YELIKSQNI	16
227	PQRSSTAIL	16
310	TIKEPLDRE	16
313	EPLDREETP	16
405	PFRLRPVFS	16
444	PPLNQSAML	16
633	REKQESYTF	16
843	KAAQKNKQN	16
39	LIGDLLKDL	15
117	DEIFRLVKI	15
178	LIKSQNI FG	15
391	DHNGRVT CF	15
433	AIKLLAADA	15
541	LAKDNGVPP	15
805	SPTSDYVKI	15
833	VVRCRQAPH	15
864	MIMMKKKKK	15
51	LIPNKSLTT	14
119	IFRLVKIRF	14
153	AINSKYTLP	14
170	INGVQNYEL	14
177	ELIKSQNIF	14
201	LIVQKELDR	14
203	VQKELDREE	14
226	FPQRSSTAI	14

Table XXVIII-109P1D4 v.1-B08-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
248	VFKETEIEV	14
281	NAKIHFSFS	14
283	KIHFSFSNL	14
308	LITIKEPLD	14
352	VPSIDIRYI	14
354	SIDIRYIVN	14
403	EIPFRLRPV	14
438	AADAGKPPL	14
498	NAKINYLLG	14
539	TILAKDNGV	14
792	APVTPNTEI	14
808	SDYVKILVA	14
858	NPENRQMIM	14
880	NLLLNFTVI	14
958	SKHHIIQEL	14

Table XXIX-109P1D4 v.1-B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
875	KHSPKNLLL	23
300	FHLNATTGL	20
960	HHIIQELPL	20
391	DHNGRVT CF	18
114	ILPDEIFRL	16
179	IKSQNIFGL	16
715	IVGGNTRDL	16
742	TDLGLHRVL	16
897	DSDGNRVTL	16
291	LVSNIARRL	15

Table XXIX-109P1D4 v.1-B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
400	TDHEIPFRL	15
762	LFSWIVNL	15
31	REEMPENVL	14
104	EHC FYEVEV	14
120	FRLVKIRFL	14
170	INGVQNYEL	14
318	EETPNHKLL	14
362	NPVNDTVVL	14
374	IPLNTKIAL	14
401	DHEIPFRLR	14
507	PDAPPEFSL	14
599	YGDNSAVTL	14
777	TNATLINEL	14
927	TFKPDSPDL	14
6	GTYIFAVLL	13
66	VYKTGDVPL	13
107	FYEVEVAIL	13
193	PEGDKMPQL	13
245	NHPVFKETE	13
320	TPNHKLLVL	13
429	TKEYAIKLL	13
438	AADAGKPPL	13
542	AKDNGVPPL	13
583	LPRHGTVGL	13
688	STNPGTVVF	13
727	DQETGNITL	13
746	LHRVLVKAN	13
773	NESVTNATL	13
806	PTSDYVKIL	13
5	SGTYIFAVL	12
19	FHSGAQEKN	12
35	PENVLIGDL	12
88	GARIDREKL	12
152	SAINSKYTL	12
284	IHFSFSNLV	12

Table XXIX-109P1D4 v.1-B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
307	GLITIKEPL	12
317	REETPNHKL	12
322	NHKLLVLAS	12
334	LMPARAMVL	12
404	IPFRLRPVF	12
477	ENNSPGIQL	12
496	GPNAKINYL	12
497	PNAKINYLL	12
520	GMLTVVKKL	12
529	DREKEDKYL	12
571	THNEYNFYV	12
575	YNFYVPENL	12
602	NSAVTSLIL	12
665	DVNDNKPVF	12
676	PPSNCSYEL	12
678	SNCSYELVL	12
754	NDLGQPDLS	12
874	KKHSPKNLL	12
903	VTLDLPIDL	12
948	FQIQPETPL	12
958	SKHHIIQEL	12
1007	VHTRPVGIL	12

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
120	FRLVKIRFL	26

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
394	GRVTCFTDH	24
529	DREKEDKYL	24
861	NRQMIMMKK	24
408	LRPVFSNQF	23
625	IRPNISFDR	23
316	DREETPNHK	22
834	VRCRQAPHL	22
41	GDLLKDLNL	21
92	DREKLCAGI	20
197	KMPQLIVQK	20
633	REKQESYTF	20
901	NRVTLDLPI	20
47	LNLSLIPNK	19
304	ATTGLITIK	19
520	GMLTVVKKL	19
584	PRHGTVGLI	19
623	GVIRPNISF	19
748	RVLVKANDL	19
75	IRIEEDTGE	18
177	ELIKSQNIF	18
297	RRLFHLNAT	18
317	REETPNHKL	18
496	GPNAKINYL	18
535	KYLFTILAK	18
1013	GIQVSNTTF	18
6	GTYIFAVLL	17
31	REEMPENVL	17
55	KSLTTAMQF	17
114	ILPDEIFRL	17
119	IFRLVKIRF	17
290	NLVSNIARR	17
307	GLITIKEPL	17
309	ITIKEPLDR	17
357	IRYIVNPVN	17

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
404	IPFRLRPVF	17
409	RPVFSNQFL	17
479	NSPGIQLTK	17
518	RTGMLTVVK	17
530	REKEDKYLF	17
645	AEDGGRVSR	17
649	GRVSRSSSA	17
650	RVSRSSSAK	17
747	HRVLVKAND	17
762	LFSVVIVNL	17
780	TLINELVRK	17
865	IMMKKKKKK	17
948	FQIQPETPL	17
964	QELPLDNTF	17
11	AVLLACVVF	16
37	NVLIGDLLK	16
125	IRFLIEDIN	16
152	SAINSKYTL	16
179	IKSQNIFGL	16
199	PQLIVQKEL	16
209	REEKDTYVM	16
221	VEDGGFPQR	16
276	ADIGENAKI	16
283	KIHFSFSNL	16
337	ARAMVLNV	16
350	DNVPSIDIR	16
380	IALITVTDK	16
435	KLLAADAGK	16
517	CRTGMLTVV	16
575	YNFYVPENL	16
713	YSIVGGNTR	16
742	TDLGLHRVL	16
777	TNATLINEL	16
827	VIFITAVVR	16

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
835	RCRQAPHLK	16
839	APHLKAAQK	16
860	ENRQMIMMK	16
862	RQMIMMKKK	16
866	MMKKKKKKK	16
867	MKKKKKKKK	16
868	KKKKKKKKH	16
871	KKKKKHSPK	16
875	KHSPKNLLL	16
940	KSASPQPAF	16
1009	TRPVGIQVS	16
2	DLLSGTYIF	15
23	AQEKNYTIR	15
49	LSLIPNKS	15
82	GEIFTTGAR	15
88	GARIDREKL	15
112	VAILPDEIF	15
113	AILPDEIFR	15
118	EIFRLVKIR	15
149	PENSAINSK	15
168	VGINGVQNY	15
201	LIVQKELDR	15
208	DREEKDTYV	15
263	PVGTSVTQL	15
289	SNLVSNIAR	15
296	ARRLFHLNA	15
332	GGLMPARAM	15
368	VVLSENIPL	15
372	ENIPLNTKI	15
374	IPLNTKIAL	15
391	DHNGRVTCF	15
399	FTDHEIPFR	15
406	FRLRPVFSN	15
410	PVFSNQFLL	15

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
416	FLLETAAYL	15
422	AYLDYESTK	15
428	STKEYAIKL	15
438	AADAGKPPL	15
445	PLNQSAMLF	15
449	SAMLFIVVK	15
497	PNAKINYLL	15
519	TGMLTVVKK	15
524	VVKLDREK	15
542	AKDNGVPPL	15
577	FYVPENLPR	15
662	NVVDVNDNK	15
688	STNPGTVVF	15
727	DQETGNITL	15
728	QETGNITLM	15
744	LGLHRVLVK	15
754	NDLGQPDLS	15
755	DLGQPDLSL	15
779	ATLINELVR	15
820	GTITVVVVI	15
863	QMIMMKKKK	15
873	KKKHSPKNL	15
874	KKHSPKNLL	15
877	SPKNLLNLF	15
894	DDVSDSGNR	15
929	KPDSPDLAR	15
936	ARHYKSASP	15
958	SKHHIIQEL	15
993	DCGYPVTTF	15
18	VFHSGAQEK	14
22	GAQEKNYTI	14
26	KNYTIREEM	14
30	IREEMPENV	14
35	PENVLIGDL	14

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
43	LLKDLNLSL	14
57	LTTAMQFKL	14
60	AMQFKLVYK	14
66	VYKTGDVPL	14
68	KTGDVPLIR	14
121	RLVKIRFLI	14
130	EDINDNAPL	14
136	APLFPATVI	14
170	INGVQNYEL	14
172	GVQNYELIK	14
212	KDTYVMKVK	14
218	KVKVEDGGF	14
280	ENAKIHFSF	14
291	LVSNIARRL	14
300	FHLNATTGL	14
320	TPNHKLLVL	14
326	LVLASDGGI	14
330	SDGGLMPAR	14
371	SENIPLNTK	14
400	TDHEIPFRL	14
427	ESTKEYAIK	14
443	KPPLNQSAM	14
444	PPLNQSAML	14
483	IQLTKVSAM	14
493	ADSGPNAKI	14
522	LTVVKKLDR	14
527	KLDREKEDK	14
549	PLTSNVTVF	14
599	YGDNSAVTL	14
608	SILDENDDF	14
618	IDSQTGVIR	14
627	PNISFDREK	14
711	VRYSIVGGN	14
738	KCDVTDLGL	14

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
763	FSVVIVNLF	14
804	SSPTSDYVK	14
836	CRQAPHLKA	14
841	HLKAAQKNK	14
864	MIMMKKKKK	14
897	DSDGNRVTL	14
903	VTLDPIDL	14
920	NWVTPPTTF	14
951	QPETPLNSK	14
952	PETPLNSKH	14
5	SGTYIFAVL	13
36	ENVLIGDLL	13
59	TAMQFKLVY	13
85	FTTGARIDR	13
87	TGARIDREK	13
89	ARIDREKLC	13
94	EKLCAGIPR	13
99	GIPRDEHCF	13
107	FYEVEVAIL	13
146	ISIPENSAI	13
150	ENSAINSKY	13
190	IETPEGDKM	13
193	PEGDKMPQL	13
275	DADIGENAK	13
278	IGENAKIHF	13
315	LDREETPNH	13
334	LMPARAMVL	13
351	NVPSIDIRY	13
362	NPVNDTVVL	13
415	QFLLETAAY	13
424	LDYESTKEY	13
429	TKEYAIKLL	13
458	DENDNAPVF	13
477	ENNSPGIQL	13

Table XXX- 109P1D4v.1- B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
492	DADSGPNAK	13
507	PDAPPEFSL	13
533	EDKYLFTIL	13
562	DQNDNSPVF	13
569	VFTHNEYNF	13
578	YVPENLPRH	13
583	LPRHGTVGL	13
587	GTVGLITVT	13
631	FDREKQESY	13
632	DREKQESYT	13
652	SRSSSAKVT	13
653	RSSSAKVTI	13
665	DVNDNKPVF	13
674	IVPPSNCSY	13
676	PPSNCSYEL	13
699	IAVDNDTGM	13
715	IVGGNTRDL	13
720	TRDLFAIDQ	13
730	TGNITLMEK	13
736	MEKCDVTDL	13
773	NESVTNATL	13
792	APVTPNTEI	13
821	TITVWVIF	13
854	WATPNPENR	13
884	NFVTIEETK	13
921	WVTPPTTFK	13
927	TFKPDSDDL	13
930	PDSPDLARH	13
960	HHIQELPL	13
972	FVACDSISK	13
1002	EVVSVHTR	13

Table XXXI-109P1D4v.1
B2709-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
120	FRLVKIRFL	22
834	VRCRQAPHL	22
337	ARAMVLVNV	21
30	IREEMPENV	20
529	DREKEDKYL	20
901	NRVTLDLP	20
408	LRPVFSNQF	19
517	CRTGMLTVV	19
584	PRHGTVGLI	19
786	VRKSTEAPV	19
92	DREKLCAGI	18
208	DREEKDTYV	18
6	GTYIFAVLL	17
41	GDLLKDLNL	17
748	RVLVKANDL	17
297	RRLFHLNAT	16
520	GMLTVVKKL	16
307	GLITIKEPL	15
409	RPVFSNQFL	15
649	GRVSRSSSA	15
711	VRYSIVGGN	15
31	REEMPENVL	14
55	KSLTTAMQF	14
88	GARIDREKL	14
121	RLVKIRFLI	14
125	IRFLIEDIN	14
209	REEKDTYVM	14
229	RSSTAILQV	14
317	REETPNHKL	14
332	GGLMPARAM	14
357	IRYIVNPVN	14
394	GRVTCFTDH	14
530	REKEDKYLF	14
653	RSSSAKVTI	14
820	GTITVVVVI	14
875	KHSPKNLLL	14
26	KNYTIREEM	13

Table XXXI-109P1D4v.1 B2709-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
76	RIEEDTGEI	13
102	RDEHCFYEV	13
250	KETEIEVSI	13
283	KIHFSFSNL	13
291	LVSNIARRL	13
296	ARRLFHLNA	13
362	NPVNDTVVL	13
368	VVLSENIPL	13
374	IPLNTKIAL	13
406	FRLRPVFSN	13
410	PVFSNQFLL	13
416	FLLETAAYL	13
496	GPNAKINYL	13
542	AKDNGVPPL	13
546	GVPPLTSNV	13
575	YNFYVPENL	13
633	REKQESYTF	13
658	KVTINVVDV	13
718	GNTRDLFAI	13
738	KCDVTDLGL	13
873	KKKHSPKNL	13
874	KKHSPKNLL	13
927	TFKPDSPDL	13
2	DLLSGTYIF	12
5	SGTYIFAVL	12
11	AVLLACVVF	12
22	GAQEKNYTI	12
36	ENVLIGDLL	12
49	LSLIPNKS	12
67	YKTGDVPLI	12
75	IRIEEDTGE	12
89	ARIDREKLC	12
99	GIPRDEHCF	12
114	ILPDEIFRL	12
130	EDINDNAPL	12

Table XXXI-109P1D4v.1 B2709-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
136	APLFPATVI	12
152	SAINSKYTL	12
170	INGVQNYEL	12
193	PEGDKMPQL	12
195	GDKMPQLIV	12
199	PQLIVQKEL	12
228	QRSSTAILQ	12
263	PVGTSVTQL	12
284	IHFSSFNLV	12
300	FHLNATTGL	12
318	EETPNHKL	12
326	LVLSDGGL	12
333	GLMPARAMV	12
400	TDHEIPFRL	12
404	IPFRLRPVF	12
438	AADAGKPPL	12
444	PPLNQSAML	12
477	ENNSPGIQL	12
483	IQLTKVSAM	12
497	PNAKINYLL	12
599	YGDNSAVTL	12
623	GVIRPNISF	12
625	IRPNISFDR	12
652	SRSSSAKVT	12
678	SNCSYELVL	12
736	MEKCDVTDL	12
742	TDLGLHRVL	12
747	HRVLVKAND	12
754	NDLGQPDLS	12
760	DSLFSVIV	12
762	LFSVIVNL	12
805	SPTSDYVKI	12
819	AGTITVVVV	12
903	VTLDLPIDL	12
940	KSASPQPAF	12

Table XXXI-109P1D4v.1
B2709-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

960	HHIIQELPL	12
43	LLKDLNLSL	11
57	LTTAMQFKL	11
64	KLVYKTGDV	11
66	VYKTGDVPL	11
83	EIFTTGARI	11
106	CFYEVEVAI	11
107	FYEVEVAIL	11
146	ISIPENSAI	11
162	AAVDPDVGI	11
176	YELIKSQNI	11
179	IKSQNIFGL	11
190	IETPEGDKM	11
213	DTYVMKVKV	11
227	PQRSSTAIL	11
320	TPNHKLLVL	11
334	LMPARAMVL	11
340	MVLVNVTDV	11
353	PSIDIRYIV	11
388	KDADHNGRV	11
428	STKEYAIKL	11
457	KDENDNAPV	11
507	PDAPPEFSL	11
548	PPLTSNVTV	11
549	PLTSNVTVF	11
569	VFTHNEYNF	11
581	ENLPRHGTV	11
583	LPRHGTVGL	11
597	PDYGDNSAV	11
621	QTGVIRPNI	11
635	KQESYTFYV	11
676	PPSNCSYEL	11
715	IVGGNTRDL	11
720	TRDLFAIDQ	11
733	ITLMEKCDV	11

Table XXXI-109P1D4v.1
B2709-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

757	GQPDSLFSV	11
763	FSVIVNLF	11
806	PTSDYVKIL	11
821	TITVVVIF	11
822	ITVVVVIFI	11
836	CRQAPHLKA	11
861	NRQMIMMKK	11
880	NLLNFVTI	11
895	DVSDSGNRV	11
897	DSDGNRVTL	11
899	DGNRVTLDL	11
936	ARHYKSASP	11
942	ASPQPAFQI	11
948	FQIQPETPL	11
958	SKHHIIQEL	11
964	QELPLDNTF	11
983	SSSSDPYSV	11
995	GYPTTTEV	11
999	TTFEVPVSV	11
1013	GIQVSNTTF	11

Table XXXII-109P1D4
v.1-B4402-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

318	EETPNHKLL	29
32	EEMPENVL	26
964	QELPLDNTF	26
117	DEIFRLVKI	25
458	DENDNAPVF	24

Table XXXII-109P1D4
v.1-B4402-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

35	PENVLIGDL	23
317	REETPNHKL	23
773	NESVTNATL	23
31	REEMPENVL	22
193	PEGDKMPQL	22
426	YESTKEYAI	22
532	KEDKYLFTI	22
77	IEEDTGEIF	21
250	KETEIEVSI	21
418	LETAAYLDY	21
530	REKEDKYL	21
633	REKQESYTF	21
736	MEKCDVTDL	21
911	LEEQTMGKY	21
176	YELIKSQNI	19
402	HEIPFRLRP	18
11	AVLLACVWF	17
372	ENIPLNTKI	17
645	AEDGGRVSR	17
688	STNPGTVWF	17
875	KHSPKNLLL	17
82	GEIFTTGAR	16
130	EDINDNAPL	16
146	ISIPENSAI	16
152	SAINSKYTL	16
177	ELIKSQNIF	16
276	ADIGENAKI	16
429	TKEYAIKLL	16
520	GMLTVVKKL	16
542	AKDNGVPPL	16
709	AEVRYSIG	16
728	QETGNITLM	16
897	DSDGNRVTL	16
36	ENVLIGDLL	15
55	KSLTTAMQF	15

Table XXXII-109P1D4
v.1-B4402-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

78	EEDTGEIFT	15
114	ILPDEIFRL	15
120	FRLVKIRFL	15
129	IEDINDNAP	15
150	ENSAINSKY	15
168	VGINGVQNY	15
179	IKSQNIFGL	15
205	KELDREEKD	15
291	LVSNIARRL	15
307	GLITIKEPL	15
362	NPVNDTVVL	15
374	IPLNTKIAL	15
404	IPFRLRPVF	15
415	QFLLETAAY	15
599	YGDNSAVTL	15
623	GVRPNISF	15
762	LFSVVIVNL	15
777	TNATLINEL	15
806	PTSDYVKIL	15
820	GTITVVVVI	15
880	NLLNFVTI	15
912	EEQTMGKYN	15
958	SKHHIIQEL	15

Table XXXIII-109P1D4
v.1-B5101-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

136	APLFPATVI	27
22	GAQEKNYTI	26

Table XXXIII-109P1D4
v.1-B5101-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

303	NATTGLITI	26
548	PPLTSNVT	26
954	TPLNSKHII	25
115	LPDEIFRLV	24
165	DPDVGINGV	24
656	SAKVITINV	24
686	LPSTNPGTV	24
690	NPGTVVFQV	24
818	VAGTITVVV	24
10	FAVLLACVV	23
135	NAPLFPATV	23
160	LPAAVDPDV	23
226	FPQRSSTAI	23
320	TPNHKLLVL	23
352	VPSIDIRYI	23
792	APVTPNTEI	23
805	SPTS DYVKI	23
140	PATVINISI	22
162	AAVDPDVGI	22
246	HPVFKETEI	22
374	IPLNTKIAL	22
475	IPENNSPGI	22
480	SPGIQLTKV	22
691	PGTVVFQVI	22
758	QPDSLFSVV	22
816	AAVAGTITV	22
362	NPVNDTVVL	21
795	TPNTEIADV	21
819	AGTITVVVV	21
69	TGDVPLIRI	20
213	DTYVMKVKV	20
335	MPARAMVLV	20
496	GPNAKINYL	20
778	NATLINELV	20
987	DPYSVSDCG	20

Table XXXIII-109P1D4
v.1-B5101-9-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

106	CFYEVEVAI	19
152	SAINSKYTL	19
194	EGDKMPQLI	19
463	APVFTQSFV	19
583	LPRHGTVGL	19
599	YGDNSAVTL	19
708	NAEVRYIV	19
820	GTITVVVVI	19
899	DGNRVTLDL	19
52	IPNKSLTTA	18
88	GARIDREKL	18
117	DEIFRLVKI	18
138	LFPATVINI	18
336	PARAMVLVN	18
380	IALITVTDK	18
389	DADHNGRVT	18
409	RPVFSNQFL	18
444	PPLNQSAML	18
586	HGTVGLITV	18
601	DNSAVTLSI	18
760	DSLFSVVIV	18
814	LVA AVAGTI	18
966	LPLDNTFVA	18
996	YPVTTFEVP	18
171	NGVQNYELI	17
347	DVNDNVPSI	17
438	AADAGKPPL	17
440	DAGKPPLNQ	17
547	VPPLTSNVT	17
822	ITVVVIFI	17
880	NLLNFVTI	17
5	SGTYIFAVL	16
139	FPATVINIS	16
208	DREEKDTYV	16
232	TAILQVSVT	16

Table XXXIII-109P1D4 v.1-B5101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
338	RAMVLNVT	16
404	IPFRLRPVF	16
492	DADSGPNAK	16
508	DAPPEFSLD	16
516	DCRTGMLTV	16
520	GMLTVVKKL	16
676	PPSNCSYEL	16
744	LGLHRVLVK	16
791	EAPVTPNTE	16
973	VACDSISKC	16
999	TTFEVPVSV	16
1	MDLLSGTYI	15
14	LACVVFHSG	15
34	MPENVLIGD	15
59	TAMQFKLVY	15
67	YKTGDVPLI	15
92	DREKLCAGI	15
148	IPENSAINS	15
176	YELIKSQNI	15
185	FGLDVIETP	15
198	MPQLIVQKE	15
261	NAPVGTSVT	15
262	APVGTSVTQ	15
275	DADIGENAK	15
313	EPLDREETP	15
356	DIRYIVNPV	15
360	IVNPVNDTV	15
449	SAMLFIVK	15
517	CRTGMLTVV	15
532	KEDKYLFTI	15
552	SNVTVFVSI	15
596	DPDYGDNSA	15
644	KAEDGGRVS	15
707	MNAEVRYSI	15
727	DQETGNITL	15

Table XXXIII-109P1D4 v.1-B5101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
800	IADVSSPTS	15
817	AVAGTITVV	15
1003	VPVSVHTRP	15
30	IREEMPENV	14
72	VPLIRIIED	14
83	EIFTTGARI	14
156	SKYTLPAAV	14
161	PAAVDPDVG	14
182	QNIIFGLDVI	14
211	EKDTYVMKV	14
258	IPENAPVGT	14
276	ADIGENAKI	14
328	LASDGLMP	14
334	LMPARAMVL	14
340	MVLNVNTDV	14
361	VNPVNDTVV	14
366	DTVVLSENI	14
372	ENIPLNTKI	14
421	AAYLDYEST	14
426	YESTKEYAI	14
432	YAIKLLAAD	14
437	LAADAGKPP	14
465	VFTQSFVTV	14
467	TQSFVTVSI	14
493	ADSGPNAKI	14
509	APPEFSLDC	14
539	TILAKDNGV	14
541	LAKDNGVPP	14
579	VPENLPRHG	14
584	PRHGTVGLI	14
597	PDYGDNSAV	14
610	LDENDDFTI	14
617	TIDSQTGVI	14
666	VNDNKPVI	14
699	IADVNDTGM	14

Table XXXIII-109P1D4 v.1-B5101-9-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
742	TDLGLHRVL	14
759	PDSLFSVVI	14
768	VNLVFNESV	14
895	DVSDGNGRV	14
897	DSGNGRVTL	14

Table XXXIV-109P1D4 v.1-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
417	LLETAAYLDY	32
58	TIAMQFKLVY	28
423	YLDYESTKEY	28
527	KLDREKEDKY	28
910	DLEEQTMGKY	28
494	DSGPNAKINY	27
630	SFDREKQESY	27
206	ELDREKEDTY	26
350	DNVPSIDIRY	23
594	VIDPDYGDNS	22
673	FIVPPSNCSY	21
704	DIGMNAEVRY	21
807	TSDYVKILVA	21
985	SSDPYSVSDC	21
163	AVDPDVGING	20
251	ETEIEVSIPE	20
566	NSPVFTHNEY	19
930	PDSPDLARHY	19
115	LPDEIFRLVK	18
149	PENSAINISKY	18

Table XXXIV-109P1D4 v.1-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
239	VTDNDNHPV	18
273	ATDADIGENA	18
345	VTDVNDNVPS	18
429	TKEYAIKLLA	18
741	VIDLGLHRVL	18
789	STEAPVTPNT	18
897	DSDGNRVTLT	18
19	FHSGAQEKY	17
107	FYEVEVAILP	17
385	VTDKDAQHNG	17
399	FIDHEIPFRL	17
401	DHEIPFRLRP	17
797	NTEIADVSSP	17
904	TLDLPIDLEE	17
40	IGDLLKDLNL	16
44	LKDLNLSLIP	16
167	DVGINGVQNY	16
194	EGDKMPQLIV	16
329	ASDGGLMPAR	16
514	SLDCRTGMLT	16
569	VFTHNEYNFY	16
590	GLITVTDPDY	16
801	ADVSSPISDY	16

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
3	LLSGTYIFAV	29
761	SLFSVVIVNL	29

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
38	VLIGDLLKDL	28
113	AILPDEIFRL	28
8	YIFAVLLACV	27
169	GINGVQNYEL	25
42	DLLKDLNLSL	24
43	LLKDLNLSLI	24
178	LIKSNIFGL	24
333	GLMPARAMVL	24
339	AMVLNVTDV	24
609	ILDENDFTI	24
50	SLIPNLSLTT	23
56	SLTTAMQFKL	23
114	ILPDEIFRLV	23
325	LLVLASDGGI	23
582	NLPRHGTVGL	23
685	VLPSTNPGTV	23
735	LMEKCDVTDL	23
776	VTNATLINEI	23
137	PLFPATVINI	22
334	LMPARAMVLV	22
359	YIVNPVNDTV	22
474	SIPENNSPGI	22
714	SIVGGNTRDL	22
812	KILVAAVAGT	22
813	ILVAAVAGTI	22
817	AVAGTITVVV	22
882	LLNFVTIEET	22
48	NLSLIPNKSL	21
159	TLPAAVDPDV	21
183	NIFGLDVIET	21
541	LAKDNGVPPL	21
706	GMNAEVRYSI	21
794	VTPNTEIADV	21
818	VAGTITVVVV	21
29	TIREEMPENV	20

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
51	LIPNKSLTTA	20
60	AMQFKLVYKT	20
233	AILQVSVTDT	20
290	NLVSNIARRL	20
428	STKEYAIKLL	20
437	LAADAGKPPL	20
560	IIDQNDNSPV	20
692	GTVVFQVIIV	20
756	LGQPDLSFSV	20
816	AAVAGTITTV	20
824	VVVVIFITAV	20
962	IIQELPLDNT	20
65	LVYKTGDVPL	19
106	CFYEVEVAIL	19
127	FLIEDINDNA	19
257	SIPENAPVGT	19
283	KIHFSFSNLV	19
355	IDIRYIVNPV	19
360	IVNPVNDTVV	19
373	NIPLNTKIAL	19
538	FTILAKDNGV	19
655	SSAKVTINNV	19
767	IVNLFVNESV	19
815	VAVAGTITTV	19
821	TITVVVIFII	19
887	TIEETKADDV	19
68	KTGDVPLIRI	18
164	VDPDVGINGV	18
262	APVGTSVTQL	18
293	SNIARRLFHL	18
302	LNATTGLITI	18
369	VLSENIPLNT	18
374	IPLNTKIALI	18
402	HEIPFRLRPV	18
479	NSPGIQLTKV	18

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
482	GIQLTKVSAM	18
549	PLTSNVTVFV	18
650	RVSRSSSAKV	18
657	AKVTINVVDV	18
740	DVTDLGLHRV	18
780	TLINELVRKS	18
781	LINELVRKST	18
785	LVRKSTEAPV	18
12	VLLACVVFHS	17
13	LLACVVFHSG	17
134	DNAPLFPATV	17
145	NISIPENSAI	17
336	PARAMLVNV	17
376	LNTKIALITV	17
381	ALITVIDKDA	17
445	PLNQSAMLF	17
466	FTQSFVTVSI	17
495	SGPNAKINYL	17
503	YLLGPDAPPE	17
504	LLGPDAPPEF	17
608	SILDENDDFT	17
732	NITLMEKCDV	17
734	TLMEKCDVTD	17
825	VVVFITAVV	17
998	VTTFEVPVSV	17
75	IRIEEDTGEI	16
119	IFRLVKIRFL	16
153	AINSKYTLPA	16
231	STAILQVSVT	16
239	VTDNDNHPV	16
301	HLNATTGLIT	16
319	ETPNHKLLVL	16
351	NVPSIDIRYI	16
354	SIDIRYIVNP	16
416	FLLETAAYLD	16

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
464	PVFTQSFVTV	16
514	SLDCRTGMLT	16
519	TGMLTVVKKL	16
540	ILAKDNGVPP	16
559	SIIDQNDNSP	16
585	RHGTVGLITV	16
616	FTIDSQTGVI	16
684	LVLPTNPGT	16
689	TNPGTVVFQV	16
698	VIAVDNDTGM	16
724	FAIDQETGNI	16
726	IDQETGNITL	16
742	TDLGLHRVLV	16
744	LGLHRVLVKA	16
766	VIVNLFVNES	16
809	DYVKILVAHV	16
827	VIFITAVVRC	16
833	VVRCRQAPHL	16
877	SPKNLLNLFV	16
880	NLLNLFVTIE	16
881	LLNLFVTIEE	16
896	VDSGDNRVTL	16
915	TMGKYNWVTT	16
926	TTFKPDSPDL	16
941	SASPQPAFQI	16
2	DLLSGTYIFA	15
6	GTIFYAVLLA	15
21	SGAQEKNYTI	15
46	DLNLSLIPNK	15
91	IDREKLCAIG	15
123	VKIRFLIEDI	15
151	NSAINSKYTL	15
181	SNIFGLDVI	15
197	KMPQLVQKE	15
228	QRSSTAILQV	15

Table XXXV-109P1D4 v.1-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
230	SSTAILQVSV	15
265	GTSVTQLHAT	15
275	DADIGENAKI	15
328	LASDGGLMPA	15
332	GGLMPARAMV	15
346	TDVNDNVPSI	15
379	KIALITVTDK	15
399	FTDHEIPFRL	15
435	KLLAADAGKP	15
456	VKDENDNAPV	15
490	AMDADSGPNA	15
492	DADSGPNAKI	15
515	LDCRTGMLTV	15
547	VPPLTSNVTV	15
570	FTHNEYNFYV	15
642	YVKAEDGGRV	15
665	DVNDNKPVFI	15
666	VNDNKPVFIV	15
688	STNPGTVVFQ	15
717	GGNTRDLFAI	15
725	AIDQETGNIT	15
741	VTDLGLHRVL	15
745	GLHRVLVKAN	15
769	NLFVNESVTN	15
819	AGTITVWVVI	15
879	KNLLNFVTI	15
957	NSKHIIQEL	15
982	SSSSSDPYSV	15
994	CGYPVITFEV	15

Table XXXVI-109P1D4
v.1-A0203-10-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

154	INSKYTLPA	19
413	SNQFLLETA	19
430	KEYAIKLLAA	19
808	SDYVKILVAA	19
836	CRQAPHLKAA	19
330	SDGGLMPARA	18
432	YAIKLLAADA	18
810	YVKILVAAVA	18
155	NSKYTLPAAV	17
414	NQFLLETAAY	17
431	EYAIKLLAAD	17
809	DYVKILVAAV	17
837	RQAPHLKAAQ	17
2	DLLSGTYIFA	10
6	GIYIFAVLLA	10
14	LACVVFHSGA	10
51	LIPNKSLLTA	10
80	DTGEIFTTGA	10
89	ARIDREKLCA	10
104	EHCFYEVEVA	10
127	FLIEDINDNA	10
132	INDNAPLFPA	10
144	INISIPENSA	10
153	AINSKYTLPA	10
224	GGFPQRSSTA	10
253	EIEVSIPENA	10
264	VGTSVTQLHA	10
267	SVTQLHATDA	10
273	ATDADIGENA	10
287	SFENLVSNIA	10
295	IARRLFHLNA	10
320	TPNHKLLVLA	10
328	LASDGGGLMPA	10
372	ENIPLNTKIA	10
381	ALITVTDKDA	10
412	FSNQFLLETA	10
424	LDYESTKEYA	10

Table XXXVI-109P1D4
v.1-A0203-10-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

429	TKEYAIKLLA	10
441	AGKPPLNQSA	10
454	IKVKDENDNA	10
481	PGIQLTKVSA	10
484	QLTKVSAMDAD	10
490	AMDADSGPNA	10
500	KINYLLGPDAD	10
533	EDKYLFITLA	10
595	TDPDYGDNSA	10
636	QESYTFYVKA	10
648	GGRVSRSSSA	10
691	PGTVVFQVIA	10
700	AVDNDTGMNA	10
716	VGGNTRDLFA	10
744	LGLHRVLVKA	10
770	LFVNESVTNA	10
783	NELVRKSTEA	10
792	APVTPNTEIA	10
807	TSYVKILVA	10
823	TVVVVFITA	10
830	ITAVVRCRQA	10
835	RCRQAPHLKA	10
846	QKNKQNSEWA	10
884	NEVTIEETKA	10
927	TEKPDSPDLA	10
933	PDLARHYKSA	10
938	HYKSASPQPA	10
965	ELPLDNTFVA	10
3	LLSGTYIFAV	9
7	TYIFAVLLAC	9
15	ACVVFHSGAQ	9
52	IPNKSLLTAM	9
81	TGEIFTTIGAR	9
90	RIDREKLCAQ	9
105	HCFYEVEVAI	9

Table XXXVI-109P1D4
v.1-A0203-10-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

128	LIEDINDNAP	9
133	NDNAPLFPAT	9
145	NISIPENSAI	9
225	GFPQRSSTAI	9
254	IEVSIPENAP	9
265	GTSVTQLHAT	9
268	VTQLHATDAD	9
274	TDADIGENAK	9
288	FSNLVSNIAI	9
296	ARRLFHLNAT	9
321	PNHKLLVLAS	9
329	ASDGGGLMPAR	9
331	DGGGLMPARAM	9
373	NIPLNTKIAL	9
382	LITVTDKQDAD	9
425	DYESTKEYAI	9
433	AIKLLAADAG	9
442	GKPPLNQSAM	9
455	KVKDENDNAP	9
482	GQLTKVSAM	9
485	LTKVSAMDAD	9
491	MDADSGPNAK	9
501	INYLLGPDAP	9
534	DKYLFITLAK	9
596	DPDYGDNSAV	9
637	ESYTFYVKA	9
649	GRVSRSSSAK	9
692	GTVVVFQVIAV	9
701	VDNDTGMNAE	9
717	GGNTRDLFAI	9
745	GLHRVLVKAN	9
771	FVNESVTNAT	9
784	ELVRKSTEAP	9
793	PVTPNTEIAD	9
811	VKILVAAVAG	9

Table XXXVI-109P1D4 v.1-A0203-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
824	VVVIFITAV	9
831	TAVVRCRQAP	9
847	KNKQNSEWAT	9
885	FVTIEETKAD	9
928	FKPDSPDLAR	9
934	DLARHYKSAS	9
939	YKSASPQPAF	9
966	LPLDNTFVAC	9

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
743	DLGLHRVLVK	28
826	VVIFITAVVR	28
407	RLRPVFSNQF	27
188	DVJETPEGDK	25
421	AAYLDYESTK	25
11	AVLLACVVFH	24
50	SLIPNKSLTT	24
379	KIALITVTDK	24
817	AVAGTITVVV	24
17	VVFHSGAQEK	23
206	ELDREKPTY	23
832	AVVRCRQAPH	23
200	QLIVQKELDR	22
298	RLFHLNATTG	22
527	KLDREKEDKY	22
810	YVKILVAAVA	22
813	ILVAAVAGTI	22

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
46	DLNLSLIPNK	21
220	KVEDGGFPQR	21
333	GLMPARAMVL	21
435	KLLAADAGKP	21
697	QVIAVDNDTG	21
838	QAPHLKAAQK	21
64	KL VYKTGDVP	20
73	PLRIEEDTG	20
76	RIEEDTGEIF	20
196	DKMPQLIVQK	20
360	IVNPVNDTVV	20
478	NNSPGQLTK	20
487	KVSAMDADSG	20
517	CRTGMLTVVK	20
523	TVVKKLDRK	20
540	ILAKDNGVPP	20
650	RVSRSSSAKV	20
779	ATLINELVRK	20
16	CVVFHSGAQE	19
115	LPDEIFRLVK	19
163	AVDPDVGING	19
209	REEKDTYVMK	19
417	LLETAAYLDY	19
534	DKYLFILAK	19
590	GLITVTDPDY	19
617	TIDSQTGVIR	19
623	GVIRPNISFD	19
673	FVPPSNCSY	19
715	IVGGNTRDLF	19
734	TLMEKCDVTD	19
65	LVYKTGDVPL	18
218	KVKVEDGGFP	18
301	HLNATTGLIT	18
326	VLASDGGGLM	18
327	VLASDGGGLMP	18
434	IKLLAADAGK	18

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
464	PVFTQSFVTV	18
504	LLGPDAPPEF	18
518	RTGMLTVVKK	18
624	VIRPNISFDR	18
658	KVTINVVDVN	18
674	IVPPSNCSYE	18
700	AVDNDTGMNA	18
769	NLFVNESVTN	18
825	VVIFITAVV	18
864	MIMMKKKKKK	18
910	DLEEQTMGKY	18
934	DLARHYKSAS	18
42	DLLKDLNLSL	17
99	GIPRDEHCFY	17
121	RLVKIRFLIE	17
167	DVGINGVQNY	17
270	QLHATDADIG	17
308	LITIKEPLDR	17
314	PLDREETPNH	17
403	EIPFRLRPVF	17
433	AIKLLAADAG	17
448	QSAMLFIVK	17
503	YLLGPDAPPE	17
521	MLTVVKKLDR	17
539	TILAKDNGVP	17
546	GVPLTNSVT	17
582	NLPRHGTVGL	17
609	ILDENDDFTI	17
635	KQESYTFYVK	17
642	YVKAEDGGRV	17
693	TVVFQVIADV	17
694	VVFQVIAVDN	17
750	LVKANDLGQP	17
765	VVIVNLFVNE	17
803	VSSPTSDYVK	17
814	LVAAVAGTIT	17

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
870	KKKKKKHSPK	17
949	QIQPETPLNS	17
37	NVLIGDLLKD	16
90	RIDREKLCAG	16
95	KLCAGIPRDE	16
111	EVAILPDEIF	16
113	AILPDEIFRL	16
234	ILQVSVTDN	16
241	DTNDNHPVFK	16
291	LVSNIARRLF	16
340	MVLNVNVDVN	16
363	PVNDTVLSE	16
375	PLNTKIALIT	16
381	ALITVTDKDA	16
416	FLLETAAYLD	16
423	YLDYESTKEY	16
436	LLAADAGKPP	16
455	KVKDENONAP	16
484	QLTKVSAMDA	16
526	KKLDREKEDK	16
665	DVNDNKPVFI	16
685	VLPSTNPGTV	16
712	RYSIVGGNTR	16
722	DLFAIDQETG	16
748	RVLVKANDLG	16
764	SVVIVNLFVN	16
785	LVRKSTEAPV	16
812	KILVAAVAGT	16
833	VVRCRQAPHL	16
902	RVTLDLPIDL	16
909	IDLEEQTMGK	16
990	SVSDCGYPVT	16
38	VLIGDLLKDL	15
43	LLKDLNLSLI	15
55	KSLTTAMQFK	15
118	EIFRLVKIRF	15

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
148	IPENSAINSK	15
156	SKYTLPAAVD	15
257	SIPENAPVGT	15
267	SVTQLHATDA	15
276	ADIGENAKIH	15
315	LDREETPNHK	15
324	KLLVLASDGG	15
341	VLNVNVDVND	15
344	NVTDVNDNVP	15
347	DVNDNVPSID	15
356	DIRIVNPNVN	15
369	VLSENIPLNT	15
370	LSENIPLNTK	15
457	KDENDNAPVF	15
514	SLDCRTGMLT	15
559	SIIDQNDNSP	15
626	RPNISFDREK	15
644	KAEDGGRVSR	15
671	PVEIVPPSNC	15
684	LVLPTNPGT	15
761	SLFSVIVNVL	15
767	IVNLFVNESV	15
859	PENRQMIMMK	15
862	ROMIMMKKKK	15
863	QMIMMKKKKK	15
950	IQPETPLNSK	15
961	HIQELPLDN	15
965	ELPLDNFVA	15
1004	PVSVHTRPVG	15
1011	PVGIVQSNTT	15
12	VLLACVVFHS	14
36	ENVLIGDLLK	14
51	LIPNKSLTTA	14
58	TTAMQFKLVY	14
59	TAMQFKLVYK	14
124	KIRFLIEDIN	14

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
127	FLIEDINDNA	14
142	TVINISIPEN	14
153	AINSKYTLPA	14
211	EKDTYVMKVK	14
233	AILQVSVTDT	14
255	EVSIPENAPV	14
263	PVGTSVTQLH	14
354	SIDIRYIVNP	14
384	TVTDKADAHN	14
395	RVICFTDHEI	14
491	MDADSGPNAK	14
500	KINYLLGPDA	14
549	PLTSNVTVFV	14
568	PVETHNEYNF	14
604	AVTLSILDEN	14
649	GRVSRSSSAK	14
710	EVRYSIGGN	14
725	AIDQETGNIT	14
745	GLHRVLVKAN	14
780	TLINELVRKS	14
784	ELVRKSTEAP	14
793	PVTPNTEIAD	14
799	EIADVSSPTS	14
823	TVVVIFITA	14
834	VRCRQAPHLK	14
860	ENRQMIMMKK	14
879	KNLLNFEVTI	14
880	NLLNFEVTIE	14
883	LNFEVTIEETK	14
895	DVDSGNGRVT	14
904	TDLPIDLEE	14
906	DLPIDLEEQT	14
967	PLDNFVACD	14
971	TFVACDSISK	14
972	FVACDSISKC	14
977	SISKCSSSSS	14

Table XXXVII-109P1D4 v.1-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
997	PVITFEVPVS	14

Table XXXVIII-109P1D4 v.1-A26-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
167	DVGINGVQNY	32
319	ETPNHKLLVL	31
111	EVAIPDEIF	28
118	EIFRLVKIRF	27
704	DTGMNAEVRY	26
188	DVIETPEGDK	25
710	EVRYIVGGN	25
109	EVEVAILPDE	24
350	DNVPSIDIRY	24
367	TVLSENIPL	24
740	DVTDLGLHRV	24
820	GTITVVVIF	24
277	DIGENAKIHF	23
428	STKEYAIKLL	23
890	ETKADDVDS	23
71	DVPLIRIEED	22
130	EDINDNAPLF	22
403	EIPFRLRPVF	22
568	PVFTHNEYNF	22
729	ETGNITLMEK	22
910	DLEEQTMGKY	22
206	ELDREEDTY	21
427	ESTKEYAIKL	21
601	DNSAVTSL	21
926	TTFKPDSPDL	21

Table XXXVIII-109P1D4 v.1-A26-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
58	TTAMQFKLVY	20
191	ETPEGDKMPQ	20
213	DTYVMKVKVE	20
255	EVSIPENAPV	20
347	DVNDNVPSID	20
366	DTVLSSENIPL	20
494	DSGPNKAKINY	20
555	TVFVSIIDQN	20
673	FIVPPSNCYSY	20
737	EKCDVTDLGL	20
776	VTNATLINE	20
902	RVTLDLPIDL	20
999	TFEVPVSVH	20
1002	EVPSVHTRP	20
142	TVINISIPEN	19
251	ETEIEVSIPE	19
316	DREETPNHKL	19
623	GVIRPNISFD	19
665	DVNDNKPVFI	19
693	TVVFQVIAVD	19
764	SVIVNLFVN	19
802	DVSSPTSDYV	19
824	VVVVIFITAV	19
895	DVDSGDNRT	19
987	DPYSVSDCGY	19
42	DLKDLNLSL	18
65	LVYKTGDVPL	18
80	DTGEIFTTGA	18
83	EIFTTGARID	18
291	LVSNIARRLF	18
419	ETAAYLDYES	18
461	DNAPVFTQSF	18
574	EYNFYVPENL	18
598	DYGDNSAVTL	18
692	GTVVFQVIAV	18
715	IVGGNTRDLF	18

Table XXXVIII-109P1D4 v.1-A26-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
761	SLFSVIVNL	18
833	VVRCRQAPHL	18
953	ETPLNSKHHL	18
33	EMPENVLIGD	17
113	AILPDEIFRL	17
178	LIKSQNIIFGL	17
241	DTNDNHPVFK	17
262	APVGTSVTQL	17
293	SNIARRLFHL	17
363	PVNDTVLSE	17
554	VTVFVSIIDQ	17
632	DREKQESYTF	17
714	SIVGGNTRDL	17
775	SVTNATLINE	17
809	DYVKILVAAV	17
823	TVVVIFITA	17
16	CVVFHSGAQE	16
32	EEMPENVLIG	16
37	NVLIGDLLKD	16
38	VLIGDLLKDL	16
117	DEIFRLVKIR	16
172	GVQNYELIKS	16
210	EKEDTYVMKV	16
309	ITIKEPLDRE	16
399	FTDHEIPFRL	16
410	PVFSNQFLL	16
522	LTVVKKLDRE	16
529	DREKEDKYL	16
531	EKEDKYLFTI	16
612	ENDDFTIDSQ	16
662	NVVDVNDNKP	16
741	VTDLGLHRL	16
750	LVKANDLGQP	16
799	EIADVSSPTS	16
801	ADVSSPTS	16
822	ITVVVIFIT	16

Table XXXVIII-109P1D4 v.1-A26-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
972	FVACDSISKC	16
1006	SVHTRPVGIQ	16

Table XXXIX-109P1D4 v.1-B0702-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
262	APVGTSVTQL	26
192	TPEGDKMPQL	23
226	FPQRSSTAIL	22
443	KPPLNQSAML	22
506	GPDAPPEFSL	22
52	IPNKSLTTAM	21
409	RPVFSNQFLL	21
496	GPNAKINYLL	21
805	SPTSDYVKIL	21
34	MPENVLIGDL	20
198	MPQLIVQKEL	20
675	VPPSNCSEYL	20
686	LPSTNPGTVV	20
758	QPDLSLFSVI	20
1010	RPVGIVQSNT	20
352	VPSIDIRYIV	19
463	APVFTQSFVT	19
548	PPLTSNVTVF	19
583	LPRHGTVGLI	19
690	NPGTVVFQVI	19
792	APVTPNTEIA	19
996	YPVTTFEVPV	19
320	TPNHKLLVLA	18
374	IPLNTKIALI	18

Table XXXIX-109P1D4 v.1-B0702-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
547	VPPLTSNVTV	18
596	DPDYGDNSAV	18
676	PPSNCSEYELV	18
856	TPNPENRQMI	18
945	QPAFQIQPET	18
1003	VPVSVHTRPV	18
139	FPATVINISI	17
579	VPENLPRHGT	17
877	SPKNLLLNFEV	17
72	VPLRIEEDT	16
444	PPLNQSAMLF	16
510	PPEFSLDCRT	16
858	NPENRQMIMM	16
907	LPIDLEEQT	16
954	TPLSKHHII	16
115	LPDEIFRLVK	15
136	APLFPATVIN	15
335	MPARAMVLVN	15
532	KEDKYLFTIL	15
817	AVAGTITVVV	15
896	VDSGDNRVTL	15
4	LSGTIFYAVL	14
40	IGDLLKDLNL	14
65	LVYKTGDVPL	14
119	IFRLVKIRFL	14
129	IEDINDNAPL	14
319	ETPNHKLVL	14
361	VNPVNDTVVL	14
404	IPFRLRPVFS	14
898	SDGNRVTLDL	14
947	AFQIQPETPL	14
959	KHHIQELPL	14
966	LPLDNTFVAC	14
42	DLLKDLNLSL	13
100	IPRDEHCFYE	13
113	AILPDEIFRL	13

Table XXXIX-109P1D4 v.1-B0702-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
160	LPAAVDPDVG	13
282	AKIHFSFSNL	13
313	EPLDREETPN	13
333	GLMPARAMVL	13
362	NPVNDTVLS	13
437	LAADAGKPPL	13
480	SPGIQLTKVS	13
541	LAKDNGVPPL	13
582	NLPRHGTVGL	13
598	DYGDNSAVTL	13
601	DNSAVTSL	13
677	PSNCSEYLV	13
714	SIVGGNTRDL	13
735	LMEKCDVTDL	13
737	EKCDVTDLGL	13
753	ANDLGQPDLS	13
833	VVRCRQAPHL	13
874	KKHSPKNLLL	13
929	KPDSPDLARH	13

Table XL- 109P1D4 v.1-B08- 10-mers
No Results Found.

Table XLI- 109P1D4 v.1-B1510- 10-mers
No Results

Found.

Table
XLII-
109P1D4
v.1-
B2705-
10-mersNo
Results
Found.Table
XLIII-
109P1D4
v.1-
B2709-
10-mersNo
Results
Found.

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
317	REETPNHKLL	24
476	PENNSPGIQL	23
532	KEDKYLFTIL	23
912	EEQTMGKYNW	23
176	YELIKSQNIF	22
773	NESVTNATLI	22
35	PENVLIGDLL	21
82	GEIFTTGARI	21
129	IEDINDNAPL	21
149	PENSAINSKY	21
193	PEGDKMPQLI	21
31	REEMPENVLI	20
98	AGIPRDEHCF	20
113	AILPDEIFRL	20
279	GENAKIHFSF	20
371	SENIPLNTKI	20

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
633	REKQESYTFY	20
110	VEVAILPDEI	19
32	EEMPENVLIG	18
78	EEDTGEIFTT	18
130	EDINDNAPLF	18
402	HEIPFRLRPV	18
709	AEVRYSIGGG	18
38	VLIGDLLKDL	17
282	AKIHFSFSNL	17
318	EETPNHKLLV	17
319	ETPNHKLLVL	17
414	NQFLLETAAY	17
428	STKEYAIKLL	17
495	SGPNAKINYL	17
761	SLFSVVIVNL	17
117	DEIFRLVKIR	16
118	EIFRLVKIRF	16
252	TEIEVSIPEN	16
262	APVGTSVTQL	16
333	GLMPARAMVL	16
373	NIPLNTKIAL	16
519	TGMLTVVKKL	16
645	AEDGGRVSR	16
753	ANDLGQPDLS	16
790	TEAPVTPNTE	16
820	GTITVVVIF	16
930	PDSPDLARHY	16
1001	FEVPVSVHTR	16
24	QEKNYTIREE	15
48	NLSLIPNKSL	15
54	NKSLTTAMQF	15
119	IFRLVKIRFL	15
123	VKIRFLIEDI	15
137	PLFPATVINI	15
190	IETPEGDKMP	15
205	KELDREKDT	15

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
206	ELDREKDTY	15
210	EEKDTYVMKV	15
291	LVSNIARRLF	15
293	SNIARRLFHL	15
390	ADHNGRVTCF	15
403	EIPFRLRPVF	15
407	RLRPVFSNQF	15
427	ESTKEYAIKL	15
430	KEYAIKLLAA	15
582	NLPRHGTVGL	15
896	VDSGDGNRVTL	15
941	SASPQPAFQI	15
952	PETPLNSKHH	15
5	SGTYIFAVLL	14
19	FHSGAQEKNY	14
34	MPENVLIGDL	14
108	YEVEVAILPD	14
312	KEPLDREETP	14
350	DNVPSIDIRY	14
351	NVPSIDIRYI	14
361	VNPVNDTVVL	14
374	IPLNTKIALI	14
397	TCFTDHEIPF	14
423	YLDYESTKEY	14
444	PPLNQSAMLF	14
457	KDENDNAPVF	14
461	DNAPVFTQSF	14
494	DSGPNAKINY	14
504	LLGPDAPPEF	14
511	PEFSLDCRTG	14
527	KLDREKEDKY	14
548	PPLTSNVTVF	14
590	GLITVTDPOY	14
598	DYGDNSAVTL	14
607	LSILDENDDF	14
616	FTIDSQTGVI	14

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
687	PSTNPGTVVF	14
714	SIVGGNTRDL	14
737	EKCDVTDLGL	14
741	VTDLGLHRVL	14
754	NDLGQPDSLF	14
762	LFSVIVNLF	14
776	VTNATLINEL	14
801	ADVSSPTS DY	14
805	SPTS DYVKIL	14
819	AGTITVVVVI	14
845	AQKNKQNSEW	14
859	PENRQMIMMK	14
872	KKKKHSPKNL	14
879	KNLLNFVTI	14
898	SDGNRVTLDL	14
957	NSKHIIQEL	14
964	QELPLDNTFV	14
992	SDCGYPVTTF	14
1012	VGIQVSNNTF	14
1	MDLLSGTYIF	13
4	LSGTYIFAVL	13
10	FAVLLACVVF	13
40	IGDLLKDLNL	13
56	SLTTAMQFKL	13
87	TGARIDREKL	13
105	HCFYEVEVAI	13
135	NAPLFPATVI	13
178	LIKSNIFGL	13
198	MPQLIVQKEL	13
221	VEDGGFPQRS	13
254	IEVSIPENAP	13
290	NLVSNIARRL	13
415	QFLLETAAYL	13
443	KPPLNQSAML	13
458	DENDNAPVFT	13
513	FSLDCRTGML	13

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
531	EKEDKYLFTI	13
566	NSPVFTHNEY	13
568	PVFTHNEYNF	13
573	NEYNFYVPEN	13
574	EYNFYVPENL	13
611	DENDDFTIDS	13
630	SFDREKQESY	13
636	QESYTFYVKA	13
673	FIVPPSNCSY	13
715	IVGGNTRDLF	13
724	FAIDQETGNI	13
728	QETGNITLME	13
747	HRVLVKANDL	13
798	TEIADVSSPT	13
804	SSPTS DYVKI	13
873	KKKHSPKNLL	13
874	KKHSPKNLLL	13
876	HSPKNLLNF	13
889	EETKADDVDS	13
902	RVTLDLPIDL	13
939	YKSASPQPAF	13
947	AFQIQPETPL	13
953	ETPLNSKHII	13
963	IQELPLDNTF	13
30	IREEMPENVL	12
42	DLLKDLNLSL	12
58	TTAMQFKLVY	12
68	KTGDVPLIRI	12
75	IRIEEDTGEI	12
77	IEEDTGEIFT	12
93	REKLCAGIPR	12
99	GIPRDEHCFY	12
111	EVAILPDEIF	12
145	NISIPENSAI	12
151	NSAINSKYTL	12
192	TPEGDKMPQL	12

Table XLIV-109P1D4 v.1-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
226	FPQRSSTAIL	12
240	TDNDNHPVF	12
250	KETEIEVSIP	12
299	LFHLNATTGL	12
300	FHLNATTGLI	12
302	LNATTGLITI	12
316	DREETPNHKL	12
367	TVVLSENIPL	12
399	FTDHEIPFRL	12
417	LLETAAYLDY	12
426	YESTKEYAIK	12
528	LDREKEDKYL	12
541	LAKDNGVPPL	12
561	IDQNDNSPVF	12
580	PENLPRHGTV	12
601	DNSAVTSLIL	12
652	SRSSSAKVTI	12
664	VDVNDNKPVF	12
677	PSNCSYELVL	12
690	NPQTVVFQVI	12
717	GGNTRDLFAI	12
726	IDQETGNITL	12
736	MEKCDVTDLG	12
783	NELVRKSTEA	12
856	TPNPENRQMI	12
888	IEETKADDVD	12
911	LEEQTMGKYN	12
919	YNWVTTPTTF	12
926	TTFKPDSPDL	12
959	KHHIIQELPL	12
980	KCSSSSSDPY	12

Table
XLV-
109P1D4
v.1-
B5101-

10-mers
No Results Found.

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
808	SDYVKILVAAGVTI	36
7	TYIFAVLLACVVFHS	34
265	GTSVTQLHATDADIG	34
482	GIQLTKVSAMDADSG	33
498	NAKINYLLGPDAPPE	33
285	HFSFSNLVSNIRRL	32
173	VQNYELIKSQNIFGL	31
405	PFRLRPVFSNQFLE	30
117	DEIFRLVKIRFLIED	28
155	NSKYTLPAAVDPDVG	28
297	RRLFHLNATTGLITI	28
710	EVRYSIGGNTRDLF	28
797	NTEIADVSSPTS DYV	28
882	LLNFVTIEETKADDV	28
945	QPAFQIQPETPLNSK	28
109	EVEVAILPDEIFRLV	27
413	SNQFLETAAYLDYE	27
807	TSDYVKILVAAGVT	27
90	RIDREKLCAGIPRDE	26
105	HCFYEVEVAILPDEI	26
141	ATVINISIPENSAIN	26
187	LDVIETPEGDKMPQL	26
288	FSNLVSNIRRLFHL	26
430	KEYAIKLLAADAGKP	26
431	EYAIKLLAADAGKPP	26
538	FTILAKDNGVPPLTS	26
572	HNEYNFYVPENLPRH	26
596	DPDYGDN SAVTLSIL	26
738	KCDVTDLGLHRVLVK	26
823	TVVVFITAVVRCR	26
831	TAVVRCRQAPHLKAA	26
33	EMPENVLIGDLLKDL	25

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
41	GDLLKDLNLSLIPNK	25
62	QFKLVYKTGDVPLIR	25
104	EHC FYEVEVAILPDE	25
176	YELIKSQNIFGLDVI	25
216	VMKVKVEDGGFPQRS	25
223	DGGFPQRSSTAILQV	25
296	ARRLFHLNATTGLIT	25
325	LLVLASDGGMLPARA	25
337	ARAMVLVNVTDVNDN	25
433	AIKLLAADAGKPLN	25
434	IKLLAADAGKPLNQ	25
580	PENLPRHGTVGLITV	25
613	NDDFTIDSQTGVIRP	25
640	TFYVKAEDGGVRVRS	25
730	TGNITLMEKCDVTDL	25
764	SVVIVNLFVNESVTN	25
811	VKILVAAGVAGTITVV	25
925	PTTFKPDSPDLARHY	25
936	ARHYKSASPQAFQI	25
27	NYTIREEMPENVLIG	24
46	DLNLSLIPNKSLTTA	24
74	LIRIEEDTGEIFTTG	24
116	PDEIFRLVKIRFLIE	24
145	NISIPENSAINSKYT	24
322	NHKLVLASDGGMLMP	24
324	KLLVLASDGGMLPAR	24
329	ASDGGMLPARAMVLV	24
331	DGGLMPARAMVLVNV	24
358	RYIVNPVNDTVLSE	24
472	TVSIPENNPGIQLT	24
478	NNSPGIQLTKVSAMD	24
488	VSAMDADSGPNAKIN	24
499	AKINYLLGPDAPPEF	24
586	HGTVGLITVTDPDYG	24
660	TINVVDVNDNKPVFI	24
670	KPVFIVPPSNCSYEL	24
698	VIAVDNDTG MNAEVR	24

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
712	RYSIVGGNTRDLFAI	24
745	GLHRVLVKANDLGQP	24
760	DSLFSVVIVNLFVNE	24
822	ITVVVFITAVVRC	24
885	FVTIEETKADDVDS	24
900	GNRVTLDLPIDLEE	24
919	YNWVTPTTFKPDSP	24
975	CDSISKCSSSSSDPY	24
3	LLSGTYIFAVLLACV	23
45	KDLNLSLIPNKSLTT	23
78	EEDTGEIFTTGARID	23
129	IEDINDNAPLFPATV	23
151	NSAINSKYTLPAAVD	23
167	DVGINGVQNYELIKS	23
281	NAKIHFSFSNLVSNI	23
289	SNLVSNIRRLFHLN	23
342	LVNVTDVNDNVPSID	23
349	NDNVPSIDIRYIVNP	23
370	LSENIPLNTKIALIT	23
379	KIALITVTDKADHNN	23
531	EKEDKYLFTILAKDN	23
534	DKYLFILAKDNGVP	23
547	VPPLTSNVTVFVSII	23
630	SFOREKQESYTFYVK	23
648	GGVRVSRSSSAKV TIN	23
663	VVDVNDNKPVFIVPP	23
669	NKPVFIVPPSNCSYE	23
679	NCSYELVLPSTNPGT	23
680	CSYELVLPSTNPGTV	23
782	INELVRKSTEAPVTP	23
812	KILVAAGVAGTITVV	23
819	AGTITVVVFITAV	23
821	TITVVVFITAVVR	23
824	VVVVFITAVVRCRQ	23
844	AAQKNKQNSEWATPN	23
916	MGKYNWVTPTTFKP	23
963	IQELPLDNTFVACDS	23

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
6	GTYIFAVLLACVVFH	22
126	RFLIEDINDNAPLFP	22
132	INDNAPLFPATVINI	22
178	LIKSNIFGLDVIET	22
251	ETEIEVSIPENAPVG	22
328	LASDGGMLPARAMVL	22
402	HEIPFRLRPVFSNQF	22
442	GKPPLNQSAMLFIV	22
462	NAPVFTQSFVTVSIP	22
485	LTKVSAMDADSGPNA	22
502	NYLLGPDAPPEFSLD	22
510	PPEFSLDCRTGMLTV	22
535	KYLFTILAKDNGVPP	22
544	DNGVPPLTSNVTVFV	22
557	FVSIIDQNDNSPVFT	22
615	DFTIDSQTGVIRPNI	22
683	ELVLPSTNPGTVVFQ	22
692	GTVVFQVIADVNDTG	22
753	ANDLGQPDLSFVVI	22
756	LGQPDLSFVIVNL	22
759	PDSLSFVIVNLFVN	22
800	IADVSSPTSDYVKIL	22
815	VAAVAGTITVVVIF	22
939	YKSASQPAPFQIQPE	22
947	AFQIQPETPLNSKHH	22
1001	FEVPVSVHTRPVGIG	22
60	AMQFKLVYKTGDVPL	21
108	YEVEVAILPDEIFRL	21
184	IFGLDVIETPEGDKM	21
363	PVNDTVLSENIPLN	21
541	LAKDNGVPPLTSNVT	21
722	DLFAIDQETGNITLM	21
143	VINISIPENSAINSK	20
215	YVMKVKVEDGGFPQR	20
222	EDGGFPQRSSTAILQ	20
246	HPVFKETEIEVSIPE	20
253	EIEVSIPENAPVGTS	20

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
323	HKLLVLASDGGMLPA	20
346	TDVNDNVPSIDIRYI	20
425	DYESTKEYAIKLLAA	20
459	ENDNAPVFTQSFVTV	20
463	APVFTQSFVTVSIPE	20
470	FVTVSIPENNSPGIQ	20
522	LTVVKLDREKEDKY	20
619	DSQTGVIRPNISFDR	20
768	VNLFVNESVTNATLI	20
783	NELVRKSTEAPVTPN	20
883	LNFVTIEETKADDVD	20
944	PQPAFQIQPETPLNS	20
992	SDCGYPVTTFEVPVS	20
63	FKLVYKTGDVPLIRI	19
64	KLVYKTGDVPLIRIE	19
122	LVKIRFLIEDINDNA	19
182	QNIFGLDVIETPEGD	19
306	TGLITIKEPLDREET	19
352	VPSIDIRYIVNPVND	19
365	NDTVVLSENIPLNTK	19
420	TAAYLDYESTKEYAI	19
500	KINYLLGPDAPPEFS	19
604	AVTLSILDENDDFTI	19
696	FQVIADVNDTGMNAE	19
733	ITLMEKCDVTDLGLH	19
8	YIFAVLLACVVFHSG	18
14	LACVVFHSGAQEKNY	18
40	IGDLLKDLNLSLIPN	18
50	SLIPNKSLLTAMQFK	18
54	NKSLTTAMQFKLVYK	18
81	TGEIFTTGARIDREK	18
133	NDNAPLFPATVINIS	18
136	APLFPATVINISIPE	18
170	INGVQNYELIKSQNI	18
245	NHPVFKETEIEVSIP	18
257	SIPENAPVGTSVTQL	18
293	SNIARRFLHNLNATTG	18

Table XLVI -109P1D4v.1-DRB1 0101- 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
319	ETPNHKLVLASDGG	18
411	VFSNQFLLETAAYLD	18
423	YLDYESTKEYAIKLL	18
450	AMLFIVKVDENDNAP	18
641	FYVKAEDGGRVSRSS	18
717	GGNTRDLFAIDQETG	18
750	LVKANDLGQPDLSFS	18
762	LFSVIVNLFVNESV	18
765	VVIVNLFVNESVTNA	18
778	NATLINELVRKSTEA	18
779	ATLINELVRKSTEAP	18
870	KKKKKKHSPKNLLN	18
918	KYNWVTTPTTFKPDS	18
986	SDPYSVSDCGYPVTT	18
993	DCGYPVTTFEVPVSV	18
995	GYPVTTFEVPVSVHT	18

Table XLVII -109P1D4v.1- DRBI 0301 - 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
40	IGDLLKDLNLSLIPN	38
111	EVAILPDEIFRLVKI	32
900	GNRVTLDLPIDLEEQ	31
36	ENVLIGDLLKDLNLS	30
74	LIRIEEDTGEIFTTG	29
97	CAGIPRDEHCFYEVE	29
125	IRFLIEDINDNAPLF	29
502	NYLLGPDAPPEFSLD	29
893	ADDVSDSGNRVTLDL	28
365	NDTVVLSENIPLNTK	27
605	VTLSILDENDDFTID	27
671	PVFIVPPSNCSYELV	27

Table XLVII -109P1D4v.1- DRBI 0301 – 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
904	TLDLPIDLEEQTMGK	27
46	DLNLSLIPNKSLLTA	26
54	NKSLTTAMQFKLVYK	26
371	SENIPLNTKIALITV	26
525	VKKLDREKEDKYLFT	26
613	NDDFTIDSQTGVIRP	26
626	RPNISFDREKQESYT	26
204	QKELDREKEDTYVMK	25
275	DADIGENAKIHFSFS	25
289	SNLVSNIARRLFHLN	25
401	DHEIPFRLRPVFSNQ	25
510	PPEFSLDCRTGMLTV	25
566	NSPVFTHNEYNFYVP	25
662	NVVDVNDNKPVFIVP	25
713	YSIVGGNTRDLFAID	25
116	PDEIFRLVKIRFLIE	24
167	DVGINGVQNYELIKS	24
395	RVTCTDHEIPFRLR	24
721	RDLFAIDQETGNITL	24
325	LLVLASDGGLMPARA	23
628	NISFDREKQESYTFY	23
945	QPAFQIQPETPLNSK	23
161	PAAVDPDVGINGVQN	22
488	VSAMDADSGPNKIN	22
925	PTTFKPDSPDLARHY	22
970	NTFVACDSISKCSSS	22
165	DPDVGINGVQNYELI	21
323	HKLLVLASDGGLMPA	21
405	PFRLRPVFSNQFLE	21
538	FTILAKDNGVPPLTS	21
698	VIAVDNDTGMNAEVR	21
759	PDSLFSVIVNLFVN	21
963	IQELPLDNTFVACDS	21
63	FKLVYKTGDVPLIRI	20
128	LIEDINDNAPLFPAT	20
176	YELIKSQNIFGLDVI	20

Table XLVII -109P1D4v.1- DRBI 0301 – 15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
288	FSNLVSNIARRLFHL	20
413	SNQFLLETAAYLDYE	20
434	IKLLAADAGKPPLNQ	20
580	PENLPRHGTVGLITV	20
696	FQVIADVNDTGMNAE	20
803	VSSPTSDYVKILVAA	20
861	NRQIMMMKKKKKKKK	20
908	PIDLEEQTMGKYNWV	20
928	FKPDSPDLARHYKSA	20
104	EHC FYEVEVAILPDE	19
109	EVEVAILPDEIFRLV	19
117	DEIFRLVKIRFLIED	19
182	QNIFGLDVIETPEGD	19
186	GLDVIETPEGDKMPQ	19
190	IETPEGDKMPQLIVQ	19
198	MPQLIVQKELDREK	19
238	SVTDTNDNHPVKET	19
305	TTGLITIKEPLDREE	19
331	DGGLMPARAMVLNV	19
415	QFLLETAAYLDYEST	19
421	AAYLDYESTKEYAIK	19
452	LFIKVKDENDNAPVF	19
518	RTGMLTVVKKLDREK	19
519	TGMLTVVKKLDREKE	19
567	SPVFTHNEYNFYVPE	19
588	TVGLITVDPDYGDN	19
682	YELVLPSTNPGTVVF	19
712	RYSIVGGNTRDLFAI	19
730	TGNITLMEKCDVTDL	19
746	LHRVLVKANDLGQPD	19
791	EAPVTPNTEIADVSS	19
831	TAVVRCRQAPHLKAA	19
839	APHLKAAQKNKQNSE	19
862	RQMIMMKKKKKKKKH	19
864	MIMMKKKKKKKKHSP	19

Table XLVIII – 109P1D4v.1- DRBI 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
173	VQNYELIKSQNIFGL	28
285	HFSFSNLVSNIARRL	28
510	PPEFSLDCRTGMLTV	28
613	NDDFTIDSQTGVIRP	28
916	MGKYNWVTTPTTFKP	28
40	IGDLLKDLNLSLIPN	26
46	DLNLSLIPNKSLLTA	26
54	NKSLTTAMQFKLVYK	26
125	IRFLIEDINDNAPLF	26
167	DVGINGVQNYELIKS	26
354	SIDIRYVNPVNDTV	26
544	DNGVPPLTSNVTVFV	26
555	TVFVSIIDQNDNSPV	26
704	DTGMNAEVRYSIGG	26
765	VVIVNLFVNESVTNA	26
779	ATLINELVRKSTEAP	26
797	NTEIADVSSPTSDYV	26
823	TVVVIFITAVVRCR	26
827	VIFITAVVRCRQAPH	26
893	ADDVDSGDNRVTLDL	26
963	IQELPLDNTFVACDS	26
7	TYIFAVLLACVVFHS	22
16	CVVFHSGAQEKNYTI	22
104	EHC FYEVEVAILPDE	22
117	DEIFRLVKIRFLIED	22
124	KIRFLIEDINDNAPL	22
297	RRLFHLNATTGLITI	22
413	SNQFLLETAAYLDYE	22
467	TQSFTVSIPENNNSP	22
628	NISFDREKQESYTFY	22
670	KPVFVPPSNCSYEL	22
679	NCSYELVLPSTNPGT	22
721	RDLFAIDQETGNITL	22
768	VNLFVNESVTNATLI	22
807	TSDYVKILVAAVAGT	22
882	LLNFVTIETKADDV	22
918	KYNWVTTPTTFKPS	22

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
925	PTTFKPDSPDLARHY	22
936	ARHYKSASPQPAFQI	22
969	DNTFVACDSISKCSS	22
998	VTFEVPVSVHTRPV	22
6	GTYIFAVLLACVVFH	20
27	NYTIREEMPENVLIG	20
36	ENVLIGDLLKDLNLS	20
37	NVLIGDLLKDLNLSL	20
41	GDLLKDLNLSLIPNK	20
48	NLSLIPNKSLTTAMQ	20
97	CAGIPRDEHCFYEVE	20
111	EVAILPDEIFRLVKI	20
112	VAILPDEIFRLVKIR	20
122	LVKIRFLIEDINDNA	20
135	NAPLFPATVINISIP	20
140	PATVINISIPENSAI	20
143	VINISIPENSAINSK	20
157	KYTLPAAVDPDVGIN	20
181	SQNIFGLDVIETPEG	20
184	IFGLDVIETPEGDKM	20
231	STAILQVSVTDNDN	20
232	TAILQVSVTDNDNH	20
234	ILQVSVTDNDNHPV	20
245	NHPVFKETEIEVSIP	20
253	EIEVSIPENAPVGTS	20
265	GTSVTQLHATDADIG	20
281	NAKIHFSFSNLVSNI	20
289	SNLVSNIARRLFHLN	20
312	KEPLDREETPNHKLL	20
322	NHKLLVLASDGGGLMP	20
323	HKLLVLASDGGGLMPA	20
331	DGGLMPARAMVLVNV	20
337	ARAMVLVNVTDVNDN	20
338	RAMVLVNVTDVNDNV	20
349	NDNVPSIDIRYIVNP	20
357	IRYIVNPVNDTVVLS	20
358	RYIVNPVNDTVVLSE	20

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
365	NDTVVLSENIPLNTK	20
366	DTVVLSENIPLNTKI	20
377	NTKIALITVTDKAD	20
379	KIALITVTDKADAHN	20
393	NGRVTCTFDHEIPFR	20
405	PFRLRPVFSNQFLE	20
421	AAALDYESTKEYAIK	20
472	TVSIPENNSPGIQLT	20
482	GIQLTKVSAMDADSG	20
488	VSAMDADSGPNAKIN	20
498	NAKINYLLGPDAPPE	20
522	LTVVKKLDREKEDKY	20
534	DKYLFTILAKDNGVP	20
547	VPPLTSNVTVFVSII	20
551	TSNVTVFVSIIDQND	20
558	VSIIQNDNSPVFTH	20
580	PENLPRHGTVGLITV	20
606	TLSILDENDDFIDS	20
640	TFYVKAEDGGRVSR	20
648	GGRVSRSSSAKVITN	20
658	KVTINWVDVNDNKPV	20
661	INVVDVNDNKPVFIV	20
682	YELVLPSTNPGTVVF	20
692	GTVVFQVIAVDNDTG	20
695	VFQVIAVDNDTGMNA	20
696	FQVIAVDNDTGMNAE	20
698	VIAVDNDTGMNAEVR	20
712	RYSIVGGNTRDLFAI	20
720	TRDLFAIDQETGNIT	20
723	LFAIDQETGNITLME	20
738	KCDVTDGLHRLVK	20
743	DLGLHRLVKANDLG	20
747	HRVLVKANDLGQPDS	20
753	ANDLGQPDLSFVVI	20
759	PDSLSFVVIIVNLFVN	20
762	LFSVVIIVNLFVNESV	20
764	SVVIIVNLFVNESVTN	20

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
767	IVNLFVNESVTNATL	20
769	NLFVNESVTNATLIN	20
778	NATLINELVRKSTEA	20
800	IADVSSPTSDYVKIL	20
808	SDYVKILVAAGVAGTI	20
810	YVKILVAAGVAGTITV	20
811	VKILVAAGVAGTITVV	20
812	KILVAAGVAGTITVVV	20
815	VAAVAGTITVVVVF	20
819	AGTITVVVVFITAV	20
821	TITVVVVFITAVVR	20
822	ITVVVVFITAVVRC	20
839	APHLKAAQKNKQNSE	20
879	KNLLNFVETIETKA	20
880	NLLNFVETIETKAD	20
883	LNFVETIETKADDVD	20
900	GNRVTLDPIDLEEQ	20
904	TLDLPIDLEEQTMGK	20
906	DLPIDLEEQTMGKYN	20
947	AFQIQPETPLNSKHH	20
959	KHHIQELPLDNTFV	20
960	HHHIQELPLDNTFVA	20
975	CDSISKCSSSSSDPY	20
995	GYPVTFEVPVSVHT	20
12	VLLACVVFHSGAQEK	18
13	LLACVVFHSGAQEKN	18
19	FHSGAQEKNYTIREE	18
51	LIPNKSLTTAMQFKL	18
73	PLIRIEEDTGEFTT	18
78	EEDTGEFTTGARID	18
85	FTTGARIDREKLCAG	18
113	AILPDEIFRLVKIRF	18
137	PLFPATVINISIPEN	18
144	INISIPENSAINSKY	18
148	IPENSAINSKYTLPA	18
196	DKMPQLIVQKELDRE	18
201	LIVQKELDREKDTY	18

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
220	KVEDGGFPQRSSTAI	18
228	QRSSTAILQVSVTDT	18
258	IPENAPVGTSVTQLH	18
262	APVGTSVTQLHATDA	18
282	AKIHFSFSLVSNIA	18
293	SNIARRLFHLNATTG	18
298	RLFHLNATTGLITIK	18
309	ITIKEPLDREETPNH	18
341	VLNVNVDVNDNVPSI	18
346	TDVNDNVPSIDIRYI	18
350	DNVPSIDIRYIVNPV	18
363	PVNDTVVLSNIPLN	18
370	LSENIPLNTKIALIT	18
385	VTDKDADHNGRVTCF	18
406	FRLRPVFSNQFLLET	18
440	DAGKPPLNQSAMLEI	18
452	LFIKVKDENDNAPVF	18
460	NDNAPVFTQSFVTVS	18
464	PVFTQSFVTVSIPEN	18
487	KVSAMDADSGPNAKI	18
531	EKEDKYLFTILAKDN	18
556	VFVSIIDQNDNSPVF	18
568	PVFTHNEYNFYVPEN	18
577	FYVPENLPRHGTVGL	18
595	TDPDYGDNSAVTSLI	18
598	DYGDNSAVTSLILDE	18
609	ILDENDFTIDSQTG	18
618	IDSQTGVIRPNISFD	18
625	IRPNISFDREKQESY	18
645	AEDGGRVSRSSSAKV	18
659	VTINVDVNDNKPVF	18
689	TNPGTVVFQVIAVDN	18
740	DVTDLGLHRVLVKAN	18
750	LVKANDLGQPDLSFS	18
756	LGQPDLSFSVIVNL	18
761	SLFSVIVNLFVNES	18
770	LFVNESVTNATLINE	18

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
775	SVTNATLINELVRS	18
796	PNTEIADVSSPTS DY	18
813	ILVAAGVAGTITVVV	18
833	VVRCRQAPHLKAAQK	18
838	QAPHLKAAQKNQNS	18
854	WATPNPENRQMIMMK	18
876	HSPKNLLNFVTIEE	18
890	ETKADDVSDGNGRVT	18
907	LPIDLEEQTMGKYNW	18
929	KPDSPDLARHYKSAS	18
930	PDSPDLARHYKSASP	18
962	IIQELPLDNTFVACD	18
992	SDCGYPVTTFEVPVS	18
1001	FEVPVSVHTRPVG IQ	18
223	DGGFPQRSSTAILQV	17
5	SGTYIFAVLLACVVF	16
60	AMQFKLYYKTGDVPL	16
64	KL VYKTGDVPLIRIE	16
82	GEIFTTGARIDREKL	16
105	HCFYEVEVAILPDEI	16
136	APLPATVINISIPE	16
182	QNIFGLDVIETPEGD	16
246	HPVFKETIEVSIPE	16
283	KIHFSFSLVSNIAIR	16
356	DIRYIVNPVNDTVVL	16
409	RPVFSNQFLLETAAY	16
420	TAAYLDYESTKEYAI	16
423	YLDYESTKEYAIKLL	16
450	AMLFIKVKDENDNAP	16
463	APVFTQSFVTVSIPE	16
535	KYLFTILAKDNGVPP	16
554	VTVFVSIIDQNDNSP	16
572	HNEYNFYVPENLPRH	16
574	EYNFYVPENLPRHGT	16
575	YNFYVPENLPRHGTV	16
596	DPDYGDNSAVTSLIL	16
639	YTFYVKAEDGGRVSR	16

Table XLVIII – 109P1D4v.1- DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
693	TVVFQVIAVDNDTGM	16
710	EVRYISVGGNTRDLF	16
760	DSLFSVIVNLFVNE	16
826	VVIFITAVVRCRQAP	16
945	QPAFQIQPETPLNSK	16
151	NSAINSKYTLPAAVD	15
953	ETPLNSKHIIQELP	15
1	MDLLSGTYIFAVLLA	14
9	IFAVLLACVVFHSGA	14
10	FAVLLACVVFHSGAQ	14
11	AVLLACVVFHSGAQE	14
15	ACVVFHSGAQEKNYT	14
44	LKDLNLSLIPNKSLT	14
63	FKLVYKTGDVPLIRI	14
69	TGDVPLIRIEEDTGE	14
71	DVPLIRIEEDTGEIF	14
72	VPLIRIEEDTGEIFT	14
74	LIRIEEDTGEIFTTG	14
88	GARIDREKLCAGIPR	14
107	FYEVEVAILPDEIFR	14
109	EVEVAILPDEIFRLV	14
116	PDEIFRLVKIRFLIE	14
119	IFRLVKIRFLIEDIN	14
126	RFLIEDINDNAPLFP	14
141	ATVINISIPENSAIN	14
145	NISIPENSAINSKYT	14
161	PAAVDPDVGVINGVQN	14
170	INGVQNYELIKSQNI	14
175	NYELIKSQNIFGLDV	14
176	YELIKSQNIFGLDVI	14
186	GLDVIETPEGDKMPQ	14
187	LDVIETPEGDKMPQL	14
195	GDKMPQLIVQKELDR	14
200	QLIVQKELDREKDT	14
204	QKELDREKDTYVMK	14
213	DTYVMKVVEDGGFP	14
216	VMKVVEDGGFPQRS	14

Table XLVIII – 109P1D4v.1-DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
251	ETEIEVSIPENAPVG	14
255	EVSIPENAPVGTSVT	14
261	NAPVGTSVTQLHATD	14
288	FSNLVSNIRRLFHL	14
296	ARRLFHLNATTGLIT	14
299	LFHLNATTGLITIKE	14
305	TTGLITIKEPLDREE	14
324	KLLVLASDGGLMPAR	14
325	LLVLASDGGLMPARA	14
339	AMVLNVTDVNDNVP	14
340	MVLNVTDVNDNVPS	14
342	LVNVTDVNDNVPSID	14
367	TVVLSSENIPLNTKIA	14
371	SENIPLNTKIALITY	14
415	QFLLETAAYLDYEST	14
431	EYAIKLLAADAGKPP	14
433	AIKLLAADAGKPPLN	14
434	IKLLAADAGKPPLNQ	14
443	KPPLNQSAMLFIVK	14
448	QSAMLFIVKVDENDN	14
453	FIKVKDENDNAPVFT	14
462	NAPVFTQSFVTVSIP	14
468	QSFVTVSIPENNSPG	14
470	FVTVSIPENNSPGIQ	14
480	SPGIQLTKVSAMDAD	14
502	NYLLGPDAPPEFSLD	14
518	RTGMLTVVKKLDREK	14
519	TGMLTVVKKLDREKE	14
525	VKKLDREKEDKYLFT	14
538	FTILAKDNGVPPLTS	14
553	NVTVFVSIIDQNDNS	14
586	HGTVGLITVTPDYG	14
588	TVGLITVTPDYGDN	14
591	LITVTPDYGDNSAV	14
602	NSAVTLSILDENDDF	14
604	AVTLSILDENDDFTI	14
607	LSILDENDDFIDSQ	14

Table XLVIII – 109P1D4v.1-DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
622	TGVRPNISFDREKQ	14
626	RPNISFDREKQESYT	14
656	SAKVITINVVDVNDNK	14
660	TINVVDVNDNKPVFI	14
663	VVDVNDNKPVFIVPP	14
669	NKPVFIVPPSNCSEY	14
671	PVFIVPPSNCSEYELV	14
681	SYELVLPSTNPGTVV	14
683	ELVLPSTNPGTVVFQ	14
708	NAEVYSIVGGNTRD	14
713	YSIVGGNTRDLFAID	14
730	TGNITLMEKCDVTDL	14
733	ITLMEKCDVTDLGLH	14
741	VTDLGLHRVLVKAND	14
773	NESVTNATLINELVR	14
783	NELVRKSTEAPVTPN	14
824	VVVVIFITAVVRCRQ	14
830	ITAVVRCRQAPHLKA	14
861	NRQMIMMKKKKKKKK	14
885	FVTIETKADDVDS	14
913	EQTMGKYNWVTTPTT	14
919	YNWVTTPTTFKPDSP	14
932	SPDLARHYKSASPQP	14
970	NTFVACDSISKCSSS	14
988	PYSVSDCGYPVTTFE	14
1000	TFEVPVSVHTRPVG	14
1002	EVPVSVHTRPVGIV	14

Table XLIX – 109P1D4v.1-DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
535	KYLFTILAKDNGVPP	32
827	VIFITAVVRCRQAPH	26

Table XLIX – 109P1D4v.1-DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
116	PDEIFRLVKIRFLIE	25
285	HFSFSNLVSNIRRL	25
1000	TFEVPVSVHTRPVG	25
60	AMQFKLVYKTGDVPL	24
518	RTGMLTVVKKLDREK	23
519	TGMLTVVKKLDREKE	23
882	LLNFVTIETKADDV	23
289	SNLVSNIRRLFHLN	22
636	QESYTFYVKAEDGGR	22
730	TGNITLMEKCDVTDL	22
779	ATLINELVRKSTEAP	22
1002	EVPVSVHTRPVGIV	22
12	VLLACVVFHSGAQEK	21
37	NVLIGDLLKDLNLSL	21
342	LVNVTDVNDNVPSID	21
522	LTVVKLDREKEDKY	21
808	SDYVKILVAVAGTI	21
861	NRQMIMMKKKKKKKK	21
11	AVLLACVVFHSGAQE	20
82	GEIFTTGARIDREKL	20
105	HCFYEVEVAILPDEI	20
212	KDITYVMKVVEDGGF	20
265	GTSVTQLHATDADIG	20
293	SNIARRLFHLNATTG	20
479	NSPGIQLTKVSAMDA	20
482	GIQLTKVSAMDADSG	20
645	AEDGGRVSRSSSAKV	20
932	SPDLARHYKSASPQP	20
972	FVACDSISKCSSSSS	20
136	APLFPATVINISIP	19
184	IFGLDVIETPEGDKM	19
296	ARRLFHLNATTGLIT	19
322	NHKLLVLASDGGLMP	19
463	APVFTQSFVTVSIP	19
660	TINVVDVNDNKPVFI	19
720	TRDLFAIDQETGNIT	19
821	TITVVVIFITAVVR	19

Table XLIX – 109P1D4v.1-DRB1
1101-15-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

7	TYIFAVLLACVVFHS	18
71	DVPLIRIEEDTGEIF	18
126	RFLIEDINDNAPLFP	18
155	NSKYTLPAAVDPDVG	18
182	QNIFGLDVIETPEGD	18
213	DTYVMKVKVEDGGFP	18
379	KIALITVTDKADAHN	18
431	EYAIKLLAADAGKPP	18
485	LTKVSAMDADSGPNA	18
498	NAKINYLLGPDAPPE	18
510	PPEFSLDCRTGMLTV	18
586	HGTVGLITVTDPDYG	18
695	VFQVIAVDNDTGMNA	18
760	DSLFSVVIVNLFVNE	18
764	SVIVNLFVNESVTN	18
797	NTEIADVSSPTSDYV	18
993	DCGYPTTTFEVPVSV	18
104	EHCFYEVEVAILPDE	17
117	DEIFRLVKIRFLIED	17
210	EKDYTYVMKVKVEDG	17
246	HPVFKETEIEVSIPE	17
380	IALITVTDKADAHNG	17
449	SAMLFIKVKDENDNA	17
638	SYTFYVKAEDGGRVS	17
670	KPVFVPPSNCSYEL	17
693	TVVFQVIAVDNDTGM	17
744	LGLHRVLVKANDLGQ	17
819	AGTITVVVVIFITAV	17
925	PTTFKPDSPDLARHY	17
986	SDPYSVSDCGYPVTT	17
138	LFPATVINISIPENS	16
173	VQNYELIKSQNIFGL	16
399	FTDHEIPFRLRPVFS	16
450	AMLFIKVKDENDNAP	16
467	TQSFTVSIPENNNSP	16
500	KINYLLGPDAPPEFS	16
554	VTVFVSIIDQNDNSP	16

Table XLIX – 109P1D4v.1-DRB1
1101-15-mers

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

618	IDSQTGVIRPNISFD	16
679	NCSYELVLPSTNPGT	16
689	TNPGTVVFQVIAVDN	16
704	DTGMNAEVRYISIVGG	16
710	EVRYISIVGGNTRDLF	16
738	KCDVTDLGLHRVLVK	16
768	VNLFVNESVTNATLI	16
807	TSDYVKILVAAGVAGT	16
916	MGKYNWVTPTTFKP	16
936	ARHYKSASPQPAFQI	16

Table XXII-109P1D4
v.2 C' Terminal-A1
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

8	PTDSRTSTI	16
5	HTRPTDSRT	10
12	RTSTIEICS	10
10	DSRTSTIEI	8
14	STIEICSEI	8

Table XXIII
109P1D4v.2
C' Terminal-A0201
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

14	STIEICSEI	20
8	PTDSRTSTI	13
10	DSRTSTIEI	11
5	HTRPTDSRT	10

Table
XXIV-
109P1D4
v.2 C'
Terminal
A0203-9-
mers

No
Results
Found.

Table XXV-109P1D4
v.2 C' Terminal-A3
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	SVHTRPTDS	15
1	PVSVHTRPT	10
4	VHTRPTDSR	9
5	HTRPTDSRT	9
7	RPTDSRTST	9
8	PTDSRTSTI	9
14	STIEICSEI	8

Table XXVI-109P1D4
v.2 C' Terminal-A26
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
14	STIEICSEI	18
3	SVHTRPTDS	11
8	PTDSRTSTI	11
12	RTSTIEICS	11
1	PVSVHTRPT	10
5	HTRPTDSRT	10
10	DSRTSTIEI	9

Table XXVII 109P1D4v.2 C' Terminal-B0702 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPTDSRTST	19
1	PVSVHTRPT	10
5	HTRPTDSRT	9
10	DSRTSTIEI	9

Table XXVIII 109P1D4v.2 C' Terminal-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		

Table XXVIII 109P1D4v.2 C' Terminal-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
8	PTDSRTSTI	14
10	DSRTSTIEI	13
14	STIEICSEI	11
3	SVHTRPTDS	10
5	HTRPTDSRT	7

Table XXIX 109P1D4v.2 C' Terminal-B1510- 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
4	VHTRPTDSR	11
1	PVSVHTRPT	4
5	HTRPTDSRT	4
6	TRPTDSRTS	4

Table XXX 109P1D4v.2 C' Terminal-B2705 9-mers		
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Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
11	SRTSTIEIC	13
4	VHTRPTDSR	12
6	TRPTDSRTS	12
14	STIEICSEI	12
10	DSRTSTIEI	9
7	RPTDSRTST	8
8	PTDSRTSTI	8

Table XXXI 109P1D4v.2 C' Terminal-B2709 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
11	SRTSTIEIC	12
6	TRPTDSRTS	11
14	STIEICSEI	10
8	PTDSRTSTI	9
10	DSRTSTIEI	8

Table XXXII 109P1D4v.2 C' Terminal-B4402 9-mers		
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Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

14	STIEICSEI	13
8	PTDSRTSTI	12
10	DSRTSTIEI	11

Table XXXIII
109P1D4v.2
C'Terminal-B5101
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

10	DSRTSTIEI	17
7	RPTDSRTST	13
8	PTDSRTSTI	12
14	STIEICSEI	12

Table XXXIV
109P1D4v.2
C' Terminal-A1-10-
mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

9	PTDSRTSTIE	16
6	HTRPTDSRTS	10

Table XXXV
109P1D4v.2
C'Terminal-A0201-10-
mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

8	RPTDSRTSTI	10
10	TDSRTSTIEI	10
13	RTSTIEICSE	10
14	TSTIEICSEI	9
4	SVHTRPTDSR	8
6	HTRPTDSRTS	8
7	TRPTDSRTST	6
1	VPVSVHTRPT	5

Table
XXXVI
109P1D4v.2
C'Terminal-
A0203-10-
mers

No Results
Found.

Table XXXVII
109P1D4v.2 - C'
Terminal-A3-10-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

4	SVHTRPTDSR	17
2	PVSVHTRPTD	15
8	RPTDSRTSTI	12
6	HTRPTDSRTS	10

Table XXXVIII
109P1D4v.2 C'
terminal-A26-10-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

13	RTSTIEICSE	13
4	SVHTRPTDSR	12
11	DSRTSTIEIC	12
2	PVSVHTRPTD	11
6	HTRPTDSRTS	10
9	PTDSRTSTIE	9

Table XXXIX
109P1D4v.2
C'Terminal-B0702
10-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

1	VPVSVHTRPT	18
8	RPTDSRTSTI	18
10	TDSRTSTIEI	9

Table XL-
109P1D4
v.2
C'Terminal
B08-10-
mers

No
Results
Found.

Table XLI- 109P1D4 v.2 C' Terminal- B1510- 10-mers
No Results Found.

Table XLII- 109P1D4 v.2 C' Terminal- B2705- 10-mers
No Results Found.

Table XLIII- 109P1D4 v.2 C' Terminal- B2709- 10-mers
No Results Found.

Table XLIV 109P1D4v.2 C' terminal-B4402- 10-mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine
10 TDSRTSTIEI 12
8 RPTDSRTSTI 11
14 TSTIEICSEI 8

Table XLV- 109P1D4 v.2 C' Terminal- B5101- 10-mers
No Results Found.

Table XLVI-109P1D4v.2 C' Terminal-DRB1 0101 15-mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
3 TFEVPVSVHTRPTDS 17
9 SVHTRPTDSRTSTIE 17
1 VITFEVPVSVHTRPT 16
6 VPVSVHTRPTDSRTS 16
11 HTRPTDSRTSTIEIC 15
4 FEVPVSVHTRPTDSR 14
7 PVSVHTRPTDSRTST 14
13 RPTDSRTSTIEICSE 14
5 EVPVSVHTRPTDSRT 8

Table XLVII-109P1D4v.2 C' Terminal-DRB1 0301 15-mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
10 VHTRPTDSRTSTIEI 17
5 EVPVSVHTRPTDSRT 16
7 PVSVHTRPTDSRTST 11
3 TFEVPVSVHTRPTDS 10
1 VITFEVPVSVHTRPT 9

Table XLVIII-109P1D4v.2 C' Terminal-DRB1 0401 15-mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
1 VITFEVPVSVHTRPT 22
4 FEVPVSVHTRPTDSR 18
10 VHTRPTDSRTSTIEI 18
3 TFEVPVSVHTRPTDS 14
5 EVPVSVHTRPTDSRT 14
9 SVHTRPTDSRTSTIE 12
11 HTRPTDSRTSTIEIC 12
13 RPTDSRTSTIEICSE 12

Table XLIX-109P1D4v.2 C' Terminal-DRB1 1101 15-mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
3 TFEVPVSVHTRPTDS 25
5 EVPVSVHTRPTDSRT 15
1 VITFEVPVSVHTRPT 13

Table XXII-109P1D4 v.2-N' terminal-A1-9- mers
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight
19 LIQQTVTSV 26
11 QIFQVL_CGL 24
8 VLIQIFQVL 23

15	VLCGLIQQT	22
7	WVLIQIFQV	20
18	GLIQQTVTS	19
24	VTSPGMDL	16
16	LCGLIQQTV	14
22	QTVTSVPGM	14
25	TSVPGMDLL	14
2	RTERQWVLI	13
9	LIQIFQVLC	13

Table XXIII-109P1D4
v.2 N' terminal-
A0201
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

19	LIQQTVTSV	26
11	QIFQVLCGL	24
8	VLIQIFQVL	23
15	VLCGLIQQT	22
7	WVLIQIFQV	20
18	GLIQQTVTS	19
24	VTSPGMDL	16
16	LCGLIQQTV	14
22	QTVTSVPGM	14
25	TSVPGMDLL	14
2	RTERQWVLI	13
9	LIQIFQVLC	13

Table XXIV-
109P1D4
v.2 N' terminal-
A0203
9-mers

No
Results
Found.

Table XXV-109P1D4
v.2 N' terminal-A3-
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

18	GLIQQTVTS	21
14	QVLCGLIQQ	19
8	VLIQIFQVL	17
7	WVLIQIFQV	16
26	SVPGMDLLS	16
15	VLCGLIQQT	15
23	TVTSVPGMD	14
9	LIQIFQVLC	13
29	GMDLLSGTY	12
2	RTERQWVLI	11
11	QIFQVLCGL	11
19	LIQQTVTSV	11

Table XXVI
109P1D4v.2 N'
terminal-A26-9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

11	QIFQVLCGL	20
24	VTSPGMDL	17
4	ERQWVLIQI	16
14	QVLCGLIQQ	16
22	QTVTSVPGM	16
7	WVLIQIFQV	15
23	TVTSVPGMD	15
8	VLIQIFQVL	14
25	TSVPGMDLL	14
5	RQWVLIQIF	13

Table XXVI
109P1D4v.2 N'
terminal-A26-9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

29	GMDLLSGTY	13
26	SVPGMDLLS	12
1	MRTERQWVL	11

Table XXVII-
109P1D4
v.2 N' terminal-B0702
9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

24	VTSPGMDL	16
27	VPGMDLLSG	13
8	VLIQIFQVL	12
1	MRTERQWVL	11
25	TSVPGMDLL	11
11	QIFQVLCGL	10
2	RTERQWVLI	9
15	VLCGLIQQT	8
17	CGLIQQTVT	8
19	LIQQTVTSV	8
22	QTVTSVPGM	8

Table XXVIII
109P1D4v.2 N'
terminal-B08-9-mers

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
1	MRTERQWVL	20
8	VLIQIFQVL	17
11	QIFQVLCGL	14
24	TSVPGMDL	12
25	TSVPGMDLL	10

Table XXIX-109P1D4 v.2 N' terminal-B1510 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
25	TSVPGMDLL	15
1	MRTERQWVL	13
8	VLIQIFQVL	13
24	TSVPGMDL	13
11	QIFQVLCGL	11
5	RQWVLIQIF	8
22	QTVTSVPGM	8

Table XXX-109P1D4 v.2 N' terminal-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		

Table XXX-109P1D4 v.2 N' terminal-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
1	MRTERQWVL	25
4	ERQWVLIQI	20
5	RQWVLIQIF	18
11	QIFQVLCGL	17
8	VLIQIFQVL	16
29	GMDLLSGTY	15
25	TSVPGMDLL	14

Table XXXI-109P1D4 v.2 N' terminal-B2709 9-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
1	MRTERQWVL	21
4	ERQWVLIQI	19
2	RTERQWVLI	13
5	RQWVLIQIF	12
8	VLIQIFQVL	12
11	QIFQVLCGL	12
25	TSVPGMDLL	12
7	WVLIQIFQV	11
22	QTVTSVPGM	11

Table XXXII 109P1D4v.2 N' terminal-B4402-9-mers		
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Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
8	VLIQIFQVL	16
25	TSVPGMDLL	14
4	ERQWVLIQI	13
5	RQWVLIQIF	13
11	QIFQVLCGL	13
29	GMDLLSGTY	13
1	MRTERQWVL	12
3	TERQWVLIQ	12
2	RTERQWVLI	11
24	TSVPGMDL	11
12	IFQVLCGLI	9

Table XXXIII 109P1D4v.2 N' terminal-B5101-9mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
4	ERQWVLIQI	14
19	LIQQTTSV	14
27	VPGMDLLSG	13
1	MRTERQWVL	12
12	IFQVLCGLI	12
16	LCGLIQQTV	12
17	CGLIQQTVT	12
2	RTERQWVLI	11
7	WVLIQIFQV	11
8	VLIQIFQVL	11
11	QIFQVLCGL	10
20	IQQTTSVP	8
28	PGMDLLSGT	8

Table XXXIII 109P1D4v.2 N' terminal-B5101- 9mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
24	VTSVPGMDL	7
25	TSVPGMDLL	7

Table XXXIV 109P1D4v.2- N' terminal-A1-10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
2	RTERQWVLIQ	23
25	TSVPGMDLLS	16
28	PGMDLLSGTY	15
29	GMDLLSGTYI	11

Table XXXV-109P1D4 v.2-N' terminal-A0201- 10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
18	GLIQQTVTSV	29
15	VLGGLIQQTV	25
10	IQIFQVLCGL	18
11	QIFQVLCGLI	17
29	GMDLLSGTYI	17

Table XXXV-109P1D4 v.2-N' terminal-A0201- 10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
7	WVLIQIFQVL	16
8	VLQIFQVLC	15
9	LIQIFQVLCG	15
24	VTSVPGMDLL	15
26	SVPGMDLLSG	15

Table XXXVI- 109P1D4 v.2-N' terminal- A0203- 10-mers		
No Results Found.		

Table XXXVII 109P1D4v.2 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
26	SVPGMDLLSG	18
7	WVLIQIFQVL	17
8	VLQIFQVLC	17
14	QVLCGLIQQT	17
15	VLGGLIQQTV	16
18	GLIQQTVTSV	16
19	LIQQTVTSVP	15
23	TVTSVPGMDL	14

Table XXXVII 109P1D4v.2 N' terminal-A3-10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
9	LIQIFQVLCG	12
28	PGMDLLSGTY	12
11	QIFQVLCGLI	11
17	CGLIQQTVTS	11
2	RTERQWVLIQ	10

Table XXXVIII 109P1D4v.2 N' terminal-A26-10-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
4	ERQWVLIQIF	22
23	TVTSVPGMDL	22
7	WVLIQIFQVL	18
26	SVPGMDLLSG	17
10	IQIFQVLCGL	16
24	VTSVPGMDLL	16
14	QVLCGLIQQT	15
22	QTVTSVPGMD	14
2	RTERQWVLIQ	13
28	PGMDLLSGTY	13

Table XXXIX 109P1D4v.2 N' terminal-B0702-10mer		
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Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
27	VPGMDLLSGT	17
7	WVLIQIFQVL	12
24	VTSPVGMDDL	12
10	IQIFQVLCGL	11
23	TVTSVPGMDL	10
16	LCGLIQQTVT	9
1	MRTERQWVLI	8
3	TERQWVLIQI	8
15	VLCGLIQQTV	8
18	GLIQQTVTSV	8
21	QQTVTSPVGM	8
29	GMDLLSGTYI	8

Table XL 109P1D4v.2 N' terminal- B08-10mers		
No Results Found.		

Table XLI 109P1D4v.2 N' terminal- B1510- 10mer		
No Results Found.		

Table XLII 109P1D4v.2 N' terminal- B2705- 10mer		
No Results Found.		

Table XLIII 109P1D4v.2 N' terminal- B2709- 10mer		
No Results Found.		

Table XLIV 109P1D4v.2 N' terminalB4402-10mer		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
3	TERQWVLIQI	21
4	ERQWVLIQIF	15
10	IQIFQVLCGL	14
7	WVLIQIFQVL	13
28	PGMDLLSGTY	13
24	VTSPVGMDDL	12
11	QIFQVLCGLI	11

Table XLV 109P1D4v.2 N' terminal- B5101- 10mer		
No Results Found.		

Table XLVI-109P1D4v.2 N' terminal-DRB1 0101 15-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
27	VPGMDLLSGTYIFAV	34
21	QQTVTSPVGMDDL	31

Table XLVI-109P1D4v.2 N' terminal-DRB1 0101 15-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
4	ERQWVLIQIFQVLCG	26
10	IQIFQVLCGLIQQTV	26
5	RQWVLIQIFQVLCGL	25
13	FQVLCGLIQQTVTSV	24
15	VLCGLIQQTVTSVPG	23
16	LCGLIQQTVTSVPGM	23
9	LIQIFQVLCGLIQQT	22
17	CGLIQQTVTSVPGMD	22
8	VLIQIFQVLCGLIQQ	17

Table XLVII-109P1D4v.2 N' terminal-DRB1 0301- 15mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
5	RQWVLIQIFQVLCGL	21
21	QQTVTSPVGMDDL	21
6	QWVLIQIFQVLCGLI	19
13	FQVLCGLIQQTVTSV	17
12	IFQVLCGLIQQTVTS	14
29	GMDLLSGTYIFAVLL	13
9	LIQIFQVLCGLIQQT	12
25	TSVPGMDLLSGTYIF	12
27	VPGMDDL	12
28	PGMDLLSGTYIFAVL	12
7	WVLIQIFQVLCGLI	11
16	LCGLIQQTVTSVPGM	11
24	VTSPVGMDDL	11

Table XLVIII-109P1D4v.2 N' terminal-DRB1 0401-15-mers		
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Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
13	FQVLCGLIQQT VTSV	26
4	ERQWVLIQIFQVLCG	22
10	IQIFQVLCGLIQQT V	22
6	QWVLIQIFQVLCGLI	20
9	LIQIFQVLCGLIQQT	20
21	QQT VTSVPGMDLLSG	20
27	VPGMDLLSGTYIFAV	20
3	TERQWVLIQIFQVLC	18
14	QVLCGLIQQT VTSVP	18
5	RQWVLIQIFQVLCGL	14
7	WVLIQIFQVLCGLIQ	14
12	IFQVLCGLIQQT VTS	14
16	LCGLIQQT VTSVPGM	14
17	CGLIQQT VTSVPGMD	14
29	GMDLLSGTYIFAVLL	14

Table XLIX-109P1D4v.2 N' Terminal-DRB1 1101 15-mers		
Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
10	IQIFQVLCGLIQQT V	18
24	VTSVPGMDLLSGTYI	18
4	ERQWVLIQIFQVLCG	16
17	CGLIQQT VTSVPGMD	15
9	LIQIFQVLCGLIQQT	14
21	QQT VTSVPGMDLLSG	14
6	QWVLIQIFQVLCGLI	13
7	WVLIQIFQVLCGLIQ	12
13	FQVLCGLIQQT VTSV	12
18	GLIQQT VTSVPGMDL	12
27	VPGMDLLSGTYIFAV	12
29	GMDLLSGTYIFAVLL	12

Table XXII-109P1D4 v.3-A1-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
78	TSHGLPLGY	26
234	SAQASALCY	23
135	NCTQEC LIY	21
62	SSDGGLGDH	19
69	DHDAGSLTS	18
100	RTEGDGNSD	18
106	NSDPESTFI	18
111	STFIPGLKK	18
83	PLGYPQEEY	17
108	DPESTFIPG	17
37	KSEGKVAGK	16
61	SSSDGGLGD	15
132	ASDNCTQEC	15
288	SVDQGVQGS	15
294	QGSATSQFY	15
302	YTMSERLHP	15
310	PSDDSIKVI	15
87	PQEEYFDRA	14
145	HSDACWMPA	14
304	MSERLHPSD	14
10	MKEVVR SCT	13
154	SLDHSSSSQ	13
186	VTQTIALCH	13
198	VTQTIALCH	13
256	SPLPQVIAL	13

Table XXIII-109P1D4 v.3-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		

Table XXIII-109P1D4 v.3-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
74	SLTSTSHGL	23
215	ALHHSPLV	23
285	GLCSVDQGV	22
307	RLHPSDDSI	22
203	ALCHSPPI	21
256	SPLPQVIAL	21
281	QGADGLCSV	21
238	SALCYSPL	20
166	SALCHSPPL	19
190	IALCHSPPV	19
214	SALHHSPL	19
227	ALHHSPPSA	19
5	HTRPPMKEV	18
250	AAISHSSPL	18
253	SHSSPLPQV	18
267	SQAQSSVSL	18
121	AEITVQPTV	17
140	CLYGHSDA	17
147	DACWMPASL	17
178	STQHHSPRV	17
191	ALCHSPPV	17
53	HLPEGSQES	16
113	FIPGLKKA	16
124	TVQPTVEEA	16
239	ALCYSPLA	16
272	SVSLQQGWV	16
274	SLQQGWVQG	16
314	SIKVIPLTT	16
316	KVIPLTTFT	16
42	VAGKSQRRV	15
66	GLGDHDAGS	15
112	TFIPGLKKA	15
261	VIALHRSQA	15
303	TMSERLHPS	15
46	SQRRVTFHL	14

Table XXIII-109P1D4 v.3-A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
67	LG DHDAGSL	14
70	HDAGSLTST	14
81	GLPLGY PQE	14
109	PESTFIPGL	14
116	GLKKA EIT	14
141	LIYGHSDAC	14
154	SLDHSSSSQ	14
194	HSPPVIQTI	14
263	ALHRSQAQS	14
278	GWVQGADGL	14
312	DDSIKVIPL	14
77	STSHGLPLG	13
117	LKKA EITV	13
119	KAA EITVQP	13
120	AA EITVQPT	13
123	ITVQPIVEE	13
133	SDNCTQECL	13
160	SSQAQASAL	13
167	ALCHSPPLS	13
205	CHSPPIQV	13
217	HHSPPLVQA	13
241	CYSPPLAQA	13
257	PLPQVIALH	13
275	LQQGWVQGA	13
288	SVDQGVQGS	13
309	HPSDDSIKV	13
317	VIPLTIFTP	13

Table
XXIV-
109P1D4
v.3-
A0203-9-
mers

No
Results
Found.

Table XXV-109P1D4 v.3-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
3	SVHTRPPMK	25
13	VVRSC TPMK	24
29	WIHPQPQRK	22
222	LVQATALHH	22
263	ALHRSQAQS	22
41	KVAGKSQRR	21
274	SLQQGWVQG	20
316	KVIPLTIFT	20
37	KSEGVVAGK	19
260	QVIALHRSQ	19
307	RLHPSDDSI	19
111	STFIPGLKK	18
140	CLYGHSDA	18
173	PLSQASTQH	18
191	ALCHSPPV	18
210	PIQVSALHH	18
257	PLPQVIALH	18
292	GVQGSATSQ	18
314	SIKVIPLTT	18
7	RPPMKEVVR	17
185	RVTQTIALC	17
221	PLVQATALH	17
245	PLAQAAAIS	17
261	VIALHRSQA	17
33	QPQRKSE GK	16
81	GLPLGY PQE	16
83	PLGY PQEEY	16
154	SLDHSSSSQ	16
212	QVSALHHSP	16
227	ALHHSPPSA	16
44	GKSQRRVTF	15
141	LIYGHSDAC	15

Table XXV-109P1D4 v.3-A3-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
234	SAQASALCY	15
12	EVVRSC TPM	14
40	GKVAGKSQR	14
49	RVTFHLPEG	14
52	FHLPEGSQE	14
66	GLGDHDAGS	14
116	GLKKA EIT	14
122	EITVQPTVE	14
162	QAQASALCH	14
167	ALCHSPPLS	14
203	ALCHSPPI	14
215	ALHHSPPLV	14
239	ALCYSPPLA	14
272	SVSLQQGWV	14
45	KSQRRVTFH	13
53	HLPEGSQES	13
92	FDRATPSNR	13
124	TVQPTVEEA	13
189	TIALCHSPP	13
197	PVTQTIALC	13
201	TIALCHSPP	13
266	RSQAQSSVS	13
279	WVQGADGLC	13
288	SVDQGVQGS	13
308	LHPSDDSIK	13
317	VIPLTIFTP	13

Table XXVI-109P1D4 v.3-A26-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		

12	EVVRSCTPM	24
312	DDSIKVIPL	22
147	DACWMPASL	17
315	IKVIPLTTF	17
111	STFIPGLKK	16
124	TVQPTVEEA	16
256	SPLPQVIAL	16
260	QVIALHRSQ	16
313	DSIKVIPLT	16
316	KVIPLTFT	16
335	DSPMEEHPL	16
49	RVTFLPEG	15
90	EYFDRATPS	15
122	EITVQPTVE	15
127	PTVEEASDN	15
136	CTQECLYIG	15
185	RVTQTIALC	15
197	PVTQTIALC	15
288	SVDQGVQGS	15
23	STTMEIWIH	14
24	TTMEIWIHP	14
27	EIWIHPQPQ	14
110	ESTFIPGLK	14
184	PRVTQTIAL	14
188	QTIALCHSP	14
196	PPVTQTIAL	14
200	QTIALCHSP	14
208	PPPIQVSAL	14
250	AAISHSSPL	14
321	TTFTPRQQA	14
50	VTFHLPEGS	13
60	ESSSDGGLG	13
76	TSTSHGLPL	13
77	STSHGLPLG	13
78	TSHGLPLGY	13
128	TVEEASDNC	13
131	EASDNTQE	13
284	DGLCSVDQG	13
3	SVHTRPPMK	12
13	VVRSCTPMK	12
22	ESTTMEIWI	12
39	EGKVAGKSQ	12
56	EGSQESSSD	12
71	DAGSLTSTS	12

Table XXVI-109P1D4
v.3-A26-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

109	PESTFIPGL	12
123	ITVQPTVEE	12
130	EEASDNTQ	12
135	NCTQECLY	12
139	ECLYGHSD	12
212	QVSALHHSP	12
234	SAQASALCY	12
272	SVSLQQGWV	12
278	GWVQGADGL	12

Table XXVII-109P1D4
v.3-B0702-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

232	PPSAQASAL	24
256	SPLPQVIAL	23
196	PPVTQTIAL	22
208	PPPIQVSAL	22
220	PPLVQATAL	22
330	RPSRGDSPM	20
18	TPMKESTTM	19
183	SPRVQTIA	19
207	SPPPIQVSA	19
244	PPLAQAAA	19
243	SPPLAQAAA	18
309	HPSDDSIKV	18
171	SPPLSQAST	17
195	SPPVTQTIA	17
219	SPPLVQATA	17
231	SPPSAQASA	17

Table XXVII-109P1D4
v.3-B0702-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

8	PPMKEVVRS	15
7	RPPMKEVVR	14
76	TSTSHGLPL	14
114	IPGLKAAE	14
193	CHSPPVQT	14
217	HHSPPLVQA	14
312	DDSIKVIPL	14
318	IPLTFTTPR	14
46	SQRRVTFHL	13
96	TPSNRTEGD	13
109	PESTFIPGL	13
229	HHSPPSAQA	13
241	CYSPPLAQA	13
250	AAISHSSPL	13
267	SQAQSSVSL	13
324	TPRQQARPS	13
5	HTRPPMKEV	12
31	HPQPQRKSE	12
54	LPEGSQESS	12
59	QESSSDGGL	12
82	LPLGYPQEE	12
108	DPESTFIPG	12
160	SSQAQASAL	12
166	SALCHSPPL	12
169	CHSPPLSQA	12
184	PRVTQTIAL	12
205	CHSPPIQV	12
214	SALHHSPPL	12
238	SALCYSPPL	12
253	SHSSPLPQV	12
258	LPQVIALHR	12

Table XXVIII-109P1D4
v.3-B08-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
312	DDSIKVIPL	21
256	SPLPQVIAL	20
114	IPGLKKAEE	19
46	SQRRVTFHL	18
74	SLTSTSHGL	18
208	PPPIQVSAL	18
220	PPLVQATAL	18
7	RPPMKEVVR	17
115	PGLKKAEEI	17
116	GLKKAEEIT	17
196	PPVTQTIAL	17
232	PPSAQASAL	17
314	SIKVIPLTT	17
33	QPQRKSEK	16
44	GKSQRRVTF	16
166	SALCHSPPL	16
214	SALHHSPL	16
238	SALCYSPL	16
183	SPRVTQTIA	15
39	EGKVAGKSQ	14
96	TPSNRTEGD	14
147	DACWMPASL	14
250	AAISHSSPL	14
262	IALHRSQAQ	14
9	PMKEVVRSC	13
160	SSQAQASAL	13
244	PPLAQAAAI	13
267	SQAQSSVSL	13
19	PMKESTTME	12
133	SDNCTQECL	12
203	ALCHSPPI	12
307	RLHPSDDSI	12
324	TPRQQARPS	12
35	QRKSEGKVA	11
37	KSEKVGAGK	11
109	PESTFIPGL	11
184	PRVTQTIAL	11

Table XXVIII-109P1D4 v.3-B08-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
278	GWVQGADGL	11

Table XXIX-109P1D4 v.3-B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
30	IHPQQRKS	16
217	HHSPPLVQA	16
180	QHHSRVTQ	15
193	CHSPPTQT	15
205	CHSPPIQV	15
169	CHSPPLSQA	14
181	HHSPRVTQT	14
216	LHSPPLVQ	14
229	HHSPPSQA	14
256	SPLPQVIAL	14
267	SQAQSSVSL	14
44	GKSQRRVTF	13
109	PESTFIPGL	13
144	GHSDACWMP	13
228	LHSPPSAQ	13
253	SHSSPLPV	13
278	GWVQGADGL	13
4	VHTRPPMKE	12
52	FHLPEGSQE	12
69	DHDAGSLTS	12
156	DHSSSSQAQ	12
208	PPPIQVSAL	12
220	PPLVQATAL	12
232	PPSAQASAL	12

Table XXIX-109P1D4 v.3-B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
300	QFYTMSERL	12
312	DDSIKVIPL	12
59	QESSSDGGL	11
76	TSTSHGLPL	11
79	SHGLPLGYP	11
105	GNSDPESTF	11
147	DACWMPASL	11
160	SSQAQASAL	11
166	SALCHSPPL	11
184	PRVTQTIAL	11
196	PPVTQTIAL	11
214	SALHHSPL	11
238	SALCYSPL	11
46	SQRRVTFHL	10
67	LGDHDAGSL	10
74	SLTSTSHGL	10
133	SDNCTQECL	10
250	AAISHSSPL	10
264	LHRSQAQSS	10
308	LHPSDDSIK	10
315	IKVIPLTTF	10
335	DSPMEEHPL	10
18	TPMKESTTM	9
2	VSVHTRPPM	8
84	LGYPQEEYF	8
330	RPSRGDSPM	8

Table XXX-109P1D4 v.3-B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		

325	PRQQARPSR	24
184	PRVTQTIAL	22
40	GKVAGKSQR	19
278	GWVQGADGL	19
28	IWIHPQPQR	18
41	KVAGKSQRR	18
7	RPPMKEVVR	17
37	KSEGVVAGK	17
44	GKSQRRVTF	17
111	STFIPGLKK	17
315	IKVIPLTTF	17
48	RRVTFHLPE	16
99	NRTEGDGNS	16
105	GNSDPESTF	16
265	HRSQAQSSV	16
267	SQAQSSVSL	16
330	RPSRGDSPM	16
18	TPMKESTTM	15
93	DRATPSNRT	15
209	PPIQVSALH	15
220	PPLVQATAL	15
250	AAISHSSPL	15
256	SPLPQVIAL	15
257	PLPQVIALH	15
299	SQFYTMSERL	15
300	QFYTMSERL	15
318	IPLTFTFPR	15
72	AGSLTSTSH	14
109	PESTFIPGL	14
115	PGLKKAEEI	14
166	SALCHSPPL	14
173	PLSQASTQH	14
177	ASTQHHSPPR	14
214	SALHHSPPPL	14
238	SALCYSPPPL	14
306	ERLHPSDDS	14
307	RLHPSDDSI	14
333	RGDSPMEEH	14
6	TRPPMKEVV	13
14	VRSCPTMKE	13
23	STTMEIWIH	13
29	WIHPQPQRK	13
45	KSQRRVTFH	13
62	SSDGGLGDH	13

Table XXX-109P1D4
v.3-B2705-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

84	LGYPQEEYF	13
92	FDRATPSNR	13
137	TQECLYGH	13
258	LPQVIALHR	13
312	DDSIKVIPL	13
322	TFTPRQQAR	13
332	SRGDSPMEE	13
12	EVVRSCPTM	12
33	QPQRKSEK	12
35	QRKSEKVA	12
59	QESSSDGGL	12
67	LGDHDAGSL	12
78	TSHGLPLGY	12
83	PLGYPQEEY	12
86	YPQEEYFDR	12
133	SDNCTQECL	12
135	NCTQECLY	12
147	DACWMPASL	12
160	SSQAQASAL	12
196	PPVTQTIAL	12
208	PPPIQVSAL	12
221	PLVQATALH	12
232	PPSAQASAL	12
293	VQGSATSQF	12
308	LHPSDDSIK	12
329	ARPSRGDSP	12

Table XXXI-109P1D4
v.3-B2709-9-mers

Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

184	PRVTQTIAL	21
6	TRPPMKEVV	19
265	HRSQAQSSV	18
48	RRVTFHLPE	16
278	GWVQGADGL	15
256	SPLPQVIAL	14
76	TSTSHGLPL	13
166	SALCHSPPL	13
214	SALHHSPPPL	13
220	PPLVQATAL	13
238	SALCYSPPPL	13
250	AAISHSSPL	13
300	QFYTMSERL	13
307	RLHPSDDSI	13
44	GKSQRRVTF	12
67	LGDHDAGSL	12
74	SLTSTSHGL	12
99	NRTEGDGNS	12
190	IALCHSPPV	12
285	GLCSVDQGV	12
306	ERLHPSDDS	12
329	ARPSRGDSP	12
330	RPSRGDSPM	12
35	QRKSEKVA	11
59	QESSSDGGL	11
84	LGYPQEEYF	11
93	DRATPSNRT	11
105	GNSDPESTF	11
109	PESTFIPGL	11
115	PGLKKAEEI	11
121	AEITVQPTV	11
143	YGHSDACWM	11
160	SSQAQASAL	11
196	PPVTQTIAL	11
208	PPPIQVSAL	11
232	PPSAQASAL	11
244	PPLAQAAAI	11
253	SHSSPLPQV	11
267	SQAQSSVSL	11
296	SATSQFYTM	11
312	DDSIKVIPL	11
325	PRQQARPSR	11

Table XXXII 109P1D4v.3-B4402- 9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
109	PESTFIPGL	25
21	KESTTMEIW	23
59	QESSSDGGL	21
256	SPLPQVIAL	19
121	AEITVQPTV	18
250	AAISHSSPL	16
310	PSDDSIKVI	16
26	MEIWIHPQP	15
44	GKSQRRVTF	15
184	PRVTQTIAL	15
196	PPVTQTIAL	15
89	EEYFDRATP	14
160	SSQAQASAL	14
194	HSPPVTQTI	14
208	PPPIQVSAL	14
220	PPLVQATAL	14
232	PPSAQASAL	14
254	HSSPLPQVI	14
11	KEVVRCTP	13
38	SEKVVAGKS	13
46	SQRRVTFHL	13
78	TSGLPLGY	13
84	LGYPQEEYF	13
88	QEEYFDRAT	13
105	GNSDPESTF	13
106	NSDPESTFI	13
130	EEASDNCTQ	13
234	SAQASALCY	13
305	SERLHPSDD	13
312	DDSIKVIPL	13

Table XXXIII 109P1D4v.3-B5101 9-mers		
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Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
244	PPLAQAAAI	24
42	VAGKSQRRV	23
147	DACWMPASL	22
190	IALCHSPPV	22
309	HPSDDSIKV	22
115	PGLKKAEEI	21
256	SPLPQVIAL	21
220	PPLVQATAL	20
208	PPPIQVSAL	19
238	SALCYSPL	19
166	SALCHSPPL	18
196	PPVTQTIAL	18
214	SALHHSPL	18
232	PPSAQASAL	18
318	IPLTFTPR	18
82	LPLGYPQEE	17
108	DPESTFIG	17
310	PSDDSIKVI	17
7	RPPMKEVVR	16
71	DAGSLTSTS	16
250	AAISHSSPL	16
281	QGADGLCSV	16
8	PPMKEVVRS	15
18	TPMKESTTM	15
67	LGDHDAGSL	15
94	RATPSNRTE	15
134	DNCTQECLI	15
172	PPLSQASTQ	15
182	HSPRVQTIT	15
194	HSPPVTQTI	15
219	SPPLVQATA	15
246	LAQAAAISH	15
258	LPQVIALHR	15
284	DGLCSVDQG	15
6	TRPPMKEVV	14
54	LPEGSQESS	14
86	YPQEEYFDR	14

Table XXXIII 109P1D4v.3-B5101 9-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
117	LKAAEITV	14
162	QAQASALCH	14
202	IALCHSPPP	14
234	SAQASALCY	14
254	HSSPLPQVI	14
262	IALHRSQAQ	14
282	GADGLCSVD	14
312	DDSIKVIPL	14
22	ESTTMEIWI	13
114	IPGLKKAEE	13
119	KAAEITVQP	13
120	AAEITVQPT	13
121	AEITVQPTV	13
195	SPPVTQTIA	13
226	TALHHSPPS	13
268	QAQSSVSLQ	13
296	SATSQFYTM	13
300	QFYTMSERL	13
324	TPRQQARPS	13
20	MKESTTMEI	12
34	PQRKSEGKV	12
84	LGYPQEEYF	12
106	NSDPESTFI	12
131	EASDNCTQE	12
171	SPPLSQAST	12
183	SPRVQTIA	12
203	ALCHSPPI	12
207	SPPPIQVSA	12
209	PPIQVSALH	12

Table XXXIV 109P1D4v.3-A1 10-mers		
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Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
78	STSHGLPLGY	29
234	PSAQASALCY	25
135	DNCTQECLY	21
63	SSDGGLGDHD	18
101	RTEGDGNSDP	18
107	NSDPESTFIP	18
38	KSEGKVAGKS	17
312	SDDSIKVIPL	17
83	LPLGYPQEY	16
294	VQGSATSQFY	16
133	ASDNCTQECL	15

Table XXXV-109P1D4 v.3-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
67	GLGDHDAGSL	24
117	GLKKAIEITV	22
190	TIALCHSPPV	21
275	SLQQGWVQGA	21
42	KVAGKSQRRV	19
208	SPPPIQVSAL	19
215	SALHHSPLV	19
121	AAEITVQPTV	18
147	SDACWMPASL	18
250	AAAISSSPL	18
76	LTSTSHGLPL	17
120	KAAEITVQPT	17
203	IALCHSPPI	17
253	ISHSSPLPQV	17
256	SSPLPQVIAL	17
281	VQGADGLCSV	17

Table XXXV-109P1D4 v.3-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
6	HTRPPMKEVV	16
20	PMKESITMEI	16
112	STFIPGLKKA	16
124	ITVQPTVEEA	16
155	SLDHSSSSQA	16
192	ALCHSPPVQT	16
312	SDDSIKVIPL	16
74	GSLTSTSHGL	15
142	LIYGHSDACW	15
166	ASALCHSPPL	15
168	ALCHSPPLSQ	15
238	ASALCYSPPPL	15
315	SIKVIPLTTF	15
54	HLPEGSQESS	14
109	DPESTEIPGL	14
114	FIPGLKKAEE	14
115	IPGLKKAEEI	14
214	VSALHHSPPPL	14
264	ALHRSQAQSS	14
265	LHRSQAQSSV	14
267	RSQAQSSVSL	14
309	LHPSDDSIKV	14
335	GDSPMEEHPL	14
82	GLPLGYPQEE	13
160	SSSQAQASAL	13
184	SPRVQTQIAL	13
191	IALCHSPPV	13
196	SPPVTQTIAL	13
204	ALCHSPPIQ	13
216	ALHHSPLVQ	13
220	SPPLVQATAL	13
227	TALHHSPPSA	13
228	ALHHSPPSAQ	13
232	SPPSAQASAL	13
239	SALCYSPLA	13
240	ALCYSPLAQ	13

Table XXXV-109P1D4 v.3-A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
241	LCYSPPLAQA	13
244	SPPLAQAAAI	13
304	TMSERLHPSD	13
25	TTMEIWIHPQ	12
30	WIHPQPQRKS	12
34	QPQRKSEGV	12
59	SQESSSDGGL	12
133	ASDNCTQECL	12
137	CTQECLYIGH	12
141	CLYIGHSDAC	12
178	ASTQHHSPPRV	12
182	HHSPPRVQT	12
194	CHSPPVTQT	12
205	LCHSPPPIQV	12
217	LHHSPLVQA	12
257	SPLPQVIALH	12
262	VIALHRSQAQ	12
272	SSVSLQQGWV	12
278	QGWVQADGL	12
285	DGLCSVQDGV	12
289	SVDQGVQGSA	12
300	SQFYTMSERL	12
303	YTMSERLHPS	12
308	RLHPSDDSIK	12
310	HPSDDSIKVI	12

Table XXXVI 109P1D4v.3-A0203 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		

Table XXXVI 109P1D4v.3-A0203 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
243	YSPPLAQAAA	27
113	TFIPGLKAA	19
242	CYSPPLAQAA	19
157	DHSSSSQAQA	18
159	SSSSQAQASA	18
219	HSPPLVQATA	18
229	LHHSPPSAQA	18
231	HSPPSAQASA	18
241	LCYSPPLAQA	18
114	FIPGLKKAEE	17
244	SPPLAQAAAI	17

Table XXXVII 109P1D4v.3-A3 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
308	RLHPSDDSIK	30
13	EVVRSCTPMK	24
186	RVIQTIALCH	24
261	QVIALHRSQA	24
317	KVIPLTTFITP	23
192	ALCHSPPVQTQ	22
293	GVQGSATSQF	22
216	ALHHSPPLVQ	21
264	ALHRSQAQSS	21
198	PVIQTIALCH	20
222	PLVQATALHH	20
246	PLAQAAAIISH	20

Table XXXVII 109P1D4v.3-A3 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
258	PLPQVIALHR	20
168	ALCHSPPLSQ	19
273	SVSLQQGWVQ	19
315	SIKVIPLTTF	19
37	RKSEGKVAGK	18
228	ALHHSPPSAQ	18
240	ALCYSPPLAQ	18
280	WVQGADGLCS	18
44	AGKSQRRVTF	17
67	GLGDHDAGSL	17
142	LIYGHSDACW	17
155	SLDHSSSSQA	17
213	QVSALHHSP	17
28	EIWIHPQPQR	16
29	IWIHPQPQRK	16
42	KVAGKSQRRV	16
111	ESTFIPGLKK	16
7	TRPPMKEVVR	15
14	VVRSCTPMKE	15
50	RVTFLPEGS	15
117	GLKKAEEITV	15
252	AISHSSPLPQ	15
286	GLCSVDQGVQ	15

Table XXXVIII 109P1D4v.3-A26 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		

Table XXXVIII 109P1D4v.3-A26 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
13	EVVRSCTPMK	25
109	DPESTFIPGL	21
78	STSHGLPLGY	20
293	GVQGSATSQF	20
105	DGNSDPESTF	19
135	DNCTQECLY	19
76	LTSTSHGLPL	18
112	STFIPGLKKA	18
315	SIKVIPLTTF	18
91	EYFDRATPSN	16
124	ITVQPTVEEA	16
208	SPPPIQVSAL	16
261	QVIALHRSQA	16
317	KVIPLTTFITP	16
23	ESTTMEIWIH	15
25	TTMEIWIHPQ	15
28	EIWIHPQPQR	15
123	EITVQPTVEE	15
256	SSPLPQVIAL	15
312	SDDSIKVIPL	15
51	VTFHLPEGSQ	14
111	ESTFIPGLKK	14
128	PTVEEASDNC	14
137	CTQECLYIGH	14
223	LVQATALHHS	14
314	DSIKVIPLTT	14
322	TTFTPRQQAR	14
61	ESSDGGGLGD	13
70	DHDAGSLTST	13
125	TVQPTVEEAS	13
129	TVEEASDNCT	13
189	QTIALCHSPP	13
201	QTIALCHSPP	13
289	SVDQGVQGSA	13

Table XXXVIII 109P1D4v.3-A26 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
300	SQFYTMSERL	13
303	YTMSERLHPS	13

Table XXXIX 109P1D4v.3-B0702 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
184	SPRVTQTIAL	24
208	SPPPIQVSAL	23
196	SPPVTQTIAL	22
220	SPPLVQATAL	22
109	DPESTFIPGL	21
232	SPPSAQASAL	21
115	IPGLKKAEEI	19
310	HPSDDSIKVI	19
244	SPPLAQAAAI	18
87	YPQEEYFDRA	17
34	QPQRKSEGKV	16
76	LTSTSHGLPL	15
166	ASALCHSPPL	15
238	ASALCYSPPPL	15
8	RPPMKEVVRS	14
19	TPMKESTTME	14
233	PPSAQASALC	14
250	AAAISSSPL	14
267	RSQAQSSVSL	14
325	TPRQQARPSR	14
331	RPSRGDSPME	14

Table XXXIX 109P1D4v.3-B0702 10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
335	GDSPMEEHPL	14
9	PPMKEVVRS	13
133	ASDNCTQECL	13
160	SSSQAQASAL	13
214	VSAHHSPPPL	13
312	SDDSIKVIPL	13
319	IPLTFTPRQ	13
1	VPVSVHTRPP	12
46	KSQRRVTFHL	12
55	LPEGSQESS	12
83	LPLGYPQEEY	12
97	TPSNRTEGDG	12
147	SDACWMPASL	12
210	PPIQVSALHH	12
221	PPLVQATALH	12
245	PPLAQAAAI	12
256	SSPLPQVIAL	12
257	SPLPQVIALH	12

Table XL 109P1D4v.3-B08 10-mers		
No Results Found.		

Table XLI 109P1D4v.3-B1510 10-mers		
No Results Found.		

Table XLII 109P1D4v.3-B2705 10-mers		
No Results Found.		

Table XLIII 109P1D4v.3-B2709 10-mers		
No Results Found.		

Table XLIV-109P1D4 v.3-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
22	KESTTMEIWI	22
122	AEITVQPTVE	19
208	SPPPIQVSAL	18
256	SSPLPQVIAL	17
44	AGKSQRRVTF	16
196	SPPVTQTIAL	16
220	SPPLVQATAL	16
310	HPSDDSIKVI	16
133	ASDNCTQECL	15
160	SSSQAQASAL	15
184	SPRVTQTIAL	15
232	SPPSAQASAL	15
335	GDSPMEEHPL	15
27	MEIWIHPQPQ	14
78	STSHGLPLGY	14
110	PESTFIPGLK	14
166	ASALCHSPPL	14
182	HHSPPVTQTI	14
194	CHSPPVTQTI	14
238	ASALCYSPPPL	14
244	SPPLAQAAAI	14
312	SDDSIKVIPL	14

Table XLIV-109P1D4 v.3-B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
39	SEGVVAGKSQ	13
46	KSQRRVTFHL	13
74	GSLTSTSHGL	13
76	LTSTSHGLPL	13
90	EEYFDRATPS	13
109	DPESTFIPGL	13
131	EEASDNCTQE	13
250	AAAISHSSPL	13
293	GVQGSATSQF	13
300	SQFYTMSERL	13
315	SIKVIPLTTF	13
60	QESSSDGGLG	12
67	GLGDHDAGSL	12
83	LPLGYPQEEY	12
89	QEEYFDRATP	12
135	DNCTQECLII	12
139	QECLIIYGHSD	12
147	SDACWMPASL	12
234	PSAQASALCY	12
254	SHSSPLPQVI	12
306	SERLHPSDDS	12
12	KEVVRSCPTM	11
59	SQESSSDGGL	11
102	TEGDGNSDPE	11
105	DGNSDPESTF	11
130	VEEASDNCTQ	11
142	LIYGHSDACW	11
214	VSALHHSPL	11
267	RSQAQSSVSL	11
271	QSSVSLQQGW	11
278	QGWVQGADGL	11
307	ERLHPSDDSI	11

Table XLV- 109P1D4 v.3- B5101- 10-mers
No Results Found.

Table XLVI-109P1D4v.3- DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
320	SIKVIPLTFTPRQQ	30
53	QRRVTFHLPEGSQES	26
146	CLYGHSDACWMPAS	26
245	ALCYSPPLAQAAIS	26
281	LQQGWVQGADGLCSV	25
33	EIWIHPQQRKSEGK	24
70	DGGLGDHDAGSLTST	24
216	PIQVSALHHSPLVQ	24
223	HHSPLVQATALHHS	24
264	LPQVIALHRSQAQSS	24
267	VIALHRSQAQSSVSL	24
283	QGWVQGADGLCSVDQ	24
318	DDSIKVIPLTFTPR	24
23	CTPMKESTTMEIWIH	23
193	TQTIALCHSPPVTQT	23
205	TQTIALCHSPPPIQV	23
276	QSSVSLQQGWVQGAD	23
327	TTFTPRQQARPSRGD	23
4	FEVPVSVHTRPPMKE	22
38	PQPQRKSEGKVAGKS	22
158	PASLDHSSSSQAQAS	22
248	YSPPLAQAAAISHSS	22
261	SSPLQVIALHRSQA	22
296	DQGVQGSATSQFYTM	22
126	AAEITVQPTVEEASD	21
294	SVDQGVQGSATSQFY	21
305	SQFYTMSERLHPSDD	21
14	PPMKEVVRSCPTMKE	20

Table XLVI-109P1D4v.3- DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
55	RVTFLPEGSQESSS	20
270	LHRSQAQSSVSLQQG	20
29	STTMEIWIHPQPQRK	19
116	ESTFIPGLKKAIEIT	19
120	IPGLKKAIEITVQPT	19
326	LTTFTPRQQARPSRG	19
93	PQEEYFDRATPSNRT	18
153	DACWMPASLDHSSSS	18
278	SVSLQQGWVQGADGL	18
291	GLCSVDQGVQGSATS	18
332	RQQARPSRGDSPMEE	18
3	TFEVPVSVHTRPPMK	17
17	KEVVRSCPTPMKESTT	17
21	RSCTPMKESTTMEIW	17
41	QRKSEGKVAGKSQRR	17
42	RKSEGKVAGKSQRRV	17
45	EGKVAGKSQRRVTFH	17
67	SSSDGGLGDHDAGSL	17
78	AGSLTSTSHGLPLGY	17
114	DPESTFIPGLKKAEE	17
118	TFIPGLKKAIEITVQ	17
189	SPRVTTQIALCHSPP	17
201	SPPVTQIALCHSPP	17
225	SPPLVQATALHHSPP	17
228	LVQATALHHSPPSAQ	17
247	CYSPPLAQAAAISHS	17
253	AQAAAISHSSPLPQV	17
275	AQSSVSLQQGWVQGA	17
304	TSQFYTMSERLHPSD	17
309	TMSERLHPSDDSIKV	17
1	VTTFEVPVSVHTRPP	16
5	EVPVSVHTRPPMKEV	16
32	MEIWIHPQPQRKSEG	16
50	GKSQRRVTFHLPEGS	16
57	TFHLPEGSQESSSDG	16
77	DAGSLTSTSHGLPLG	16
79	GSLTSTSHGLPLGY	16

Table XLVI-109P1D4v.3- DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
82	TSTSHGLPLGYPQEE	16
87	GLPLGYPQEEYFDRA	16
94	QEEYFDRATPSNRTE	16
95	EEYFDRATPSNRTEG	16
109	GDGNSDPESTFIPGL	16
117	STFIPGLKKAIEITV	16
128	EITVQPTVEEASDNC	16
141	NCTQECLYGHSDAC	16
154	ACWMPASLDHSSSSQ	16
155	CWMPASLDHSSSSQA	16
161	LDHSSSSQAQASALC	16
163	HSSSSQAQASALCHS	16
168	QAQASALCHSPPLSQ	16
187	HHSprvtQTIALCHS	16
192	VTQTIALCHSPPVITQ	16
204	VTQTIALCHSPPIQ	16
214	PPPIQVSALHHSPL	16
222	LHHSPLVQATALHH	16
226	PPLVQATALHHSPPS	16
233	ALHHSPPSAQASALC	16
235	HHSPPSAQASALCYS	16
240	SAQASALCYSPLAQ	16
246	LCYSPPLAQAAAISH	16
249	SPPLAQAAAISHSP	16
258	ISHSSPLQVIALHR	16
268	IALHRSQAQSSVSLQ	16
292	LCSVDQGVQGSATSQ	16
300	QGSATSQFYTMSERL	16
323	VIPLTFTPRQQARP	16
7	PVSVHTRPPMKEVVR	15
13	RPPMKEVVRCTPMK	15
16	MKEVVRCTPMKEST	15
47	KVAGKSQRRVTFHLP	15
56	VTFHLPEGSQESSSD	15
72	GLGDHDAGSLTSTSH	15
75	DHDAGSLTSTSHGLP	15
85	SHGLPLGYPQEEYFD	15

Table XLVI-109P1D4v.3- DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
142	CTQECLYGHSDACW	15
156	WMPASLDHSSSSQAQ	15
169	AQASALCHSPPLSQA	15
181	SQASTQHHSPrvtQT	15
186	QHHSPrvtQTIALCH	15
198	LCHSPPVITQTIALCH	15
212	HSPPPIQVSALHHS	15
217	IQVSALHHSPLVQA	15
229	VQATALHHSPPSAQA	15
241	AQASALCYSPLAQ	15
265	PQVIALHRSQAQSSV	15
312	ERLHPSDDSIKVIPL	15

Table XLVII-109P1D4v.3 DRB1 0301 15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
108	EGDGNSDPESTFIPG	26
87	GLPLGYPQEEYFDRA	24
318	DDSIKVIPLTFTPR	20
33	EIWIHPQPQRKSEGK	19
117	STFIPGLKKAIEITV	19
13	RPPMKEVVRCTPMK	18
57	TFHLPEGSQESSSDG	18
70	DGGLGDHDAGSLTST	18
116	ESTFIPGLKKAIEIT	18
128	EITVQPTVEEASDNC	18
296	DQGVQGSATSQFYTM	18
31	TMEIWIHPQPQRKSE	17
45	EGKVAGKSQRRVTFH	17
47	KVAGKSQRRVTFHLP	17
86	HGLPLGYPQEEYFDR	17
104	SNRTEGDGNSDPEST	17

Table XLVII-109P1D4v.3 DRB1 0301 15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
120	IPGLKKAIEITVQPT	17
264	LPQVIALHRSQAQSS	17
289	ADGLCSVDQGVQGS	17
326	LTTFTPRQQARPSRG	17
5	EVPSVHTRPPMKEV	16
292	LCSVDQGVQGSATSQ	16
304	TSQFYTMSERLHPSD	16
78	AGSLTSTSHGLPLGY	14
136	EEASDNCQECLYIG	14
17	KEVVRCTPMKESTT	13
64	SQESSSDGGLGDHDA	13
69	SDGGLGDHDAGSLTS	13
126	AAEITVQPTVEEASD	13
132	QPTVEEASDNCQEC	13
243	ASALCYSPLAQAAA	13
265	PQVIALHRSQAQSSV	13

Table XLIX-109P1D4v.3 DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
13	RPPMKEVVRCTPMK	26
264	LPQVIALHRSQAQSS	26
289	ADGLCSVDQGVQGS	26
1	VTFEVPVSVHTRPP	22
153	DACWMPASLDHSSSS	22
5	EVPSVHTRPPMKEV	20
16	MKEVVRCTPMKEST	20
23	CTPMKESTTMEIWIH	20
33	EIWIHPQPQRKSEGK	20
57	TFHLPEGSQESSSDG	20
120	IPGLKKAIEITVQPT	20
132	QPTVEEASDNCQEC	20

Table XLIX-109P1D4v.3 DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
158	PASLDHSSSSQAQAS	20
177	SPPLSQASTQHHSR	20
193	TQTIALCHSPPVQT	20
216	PIQVSALHHSPLVQ	20
265	PQVIALHRSQAQSSV	20
283	QGWVQGADGLCSVDQ	20
292	LCSVDQGVQGSATSQ	20
320	SIKVIPLTFTPRQQ	20
323	VIPLTFTPRQQARP	20
56	VFHLPEGSQEASSD	18
72	GLGDHDAGSLTSTSH	18
155	CWMPASLDHSSSSQA	18
156	WMPASLDHSSSSQAQ	18
174	LCHSPPLSQASTQHH	18
186	QHHSRPTQTIALCH	18
198	LCHSPPVQTIALCH	18
222	LHHSPLVQATALHH	18
246	LCYSPPLAQAAAISH	18
251	PLAQAAAISHSSPLP	18
258	ISHSSPLQVIALHR	18
263	PLPQVIALHRSQAQS	18
269	ALHRSQAQSSVSLQQ	18
275	AQSSVSLQQGWVQGA	18
286	VQGADGLCSVDQGVQ	18
312	ERLHPSDDSIKVIPL	18
94	QEYFDRATPSNRTE	17
32	MEIWIHPQPQRKSEG	16
89	PLGYPQEYFDRATP	16
95	EEYFDRATPSNRTEG	16
116	ESTFIPGLKKAEEIT	16
146	CLYGHSDACWMPAS	16
245	ALCYSPLAQAAAIS	16
305	SQFYTMSERLHPSDD	16
45	EGKVAGKSQRRVTFH	15
3	TFEVPVSVHTRPPMK	14
29	STTMEIWIHPQPQRK	14
31	TMEIWIHPQPQRKSE	14

Table XLIX-109P1D4v.3 DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 7; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
53	QRRVTFHLPEGSQES	14
70	DGGLGDHDAGSLTST	14
78	AGSLTSTSHGLPLGY	14
117	STFIPGLKKAEEITV	14
126	AAEITVQPTVEEASD	14
128	EITVQPTVEEASDNC	14
144	QECLYGHSDACWMP	14
154	ACWMPASLDHSSSSQ	14
171	ASALCHSPPLSQAST	14
195	TIALCHSPPVQTIA	14
205	TQTIALCHSPPIQV	14
207	TIALCHSPPIQVSA	14
214	PPPIQVSALHHSPL	14
219	VSALHHSPLVQATA	14
225	SPPLVQATALHHSPP	14
226	PPLVQATALHHSPPS	14
231	ATALHHSPPSAQASA	14
243	ASALCYSPLAQAAA	14
249	SPPLAQAAAISHSSP	14
255	AAAIHSSPLPQVIA	14
261	SSPLPQVIALHRSQA	14
267	VIALHRSQAQSSVSL	14
276	QSSVSLQQGWVQGAD	14
278	SVSLQQGWVQGADGL	14
296	DQGVQGSATSQFYTM	14
311	SERLHPSDDSIKVIP	14
318	DDSIKVIPLTFTPR	14

Table XXII
109P1D4v.4-A1
9-mers

Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
2	WIHPQPQSQ	6
4	HPQPQSQRR	6
8	QSQRRTVFH	5
6	QPQSQRRVT	4

Table XXIII
109P1D4v.4-A0201
9-mers

Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

2	WIHPQPQSQ	12
5	PQPQSQRRV	7
1	IWIHPQPQS	6

Table XXIV
109P1D4v.4-A0203
9-mers

No Results Found.

Table XXV
109P1D4v.4-A3-9-mers

Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	PQSQRRTVF	15
2	WIHPQPQSQ	14
3	IHPQPQSQQR	12
8	QSQRRTVFH	12
1	IWIHPQPQS	8

Table XXVI 109P1D4v.4-A26 9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	PQSQRRTVF	9
2	WIHPQPQSQ	6
1	IWIHPQPQS	5

Table XXVII 109P1D4v.4-B0702 9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
6	QPQSQRRTV	18
4	HPQPQSQR	11
7	PQSQRRTVF	11

Table XXVIII 109P1D4v.4-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	PQSQRRTVF	15
8	QSQRRTVFH	9
4	HPQPQSQR	7

Table XXIX 109P1D4v.4 B1510-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
3	IHPQPQSQQR	14
7	PQSQRRTVF	12

Table XXX 109P1D4v.4-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
3	IHPQPQSQQR	18
4	HPQPQSQR	14
7	PQSQRRTVF	14
8	QSQRRTVFH	11

Table XXXI 109P1D4v.4 B2709-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
5	PQPQSQRRTV	9
7	PQSQRRTVF	9
1	IWIHPQPQS	4

Table XXXII 109P1D4v.4 B4402-9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	PQSQRRTVF	15
1	IWIHPQPQS	4

Table XXXIII 109P1D4v.4-B5101 9-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
6	QPQSQRRTV	14
5	PQPQSQRRTV	12
4	HPQPQSQR	11

Table XXXIV 109P1D4v.4-A1 10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
3	WIHPQPQSQR	4
5	HPQPQSRRV	4
9	QSRRVTFHL	4
6	PQPQSRRVT	2

Table XXXV 109P1D4v.4-A0201 10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
5	HPQPQSRRV	12
3	WIHPQPQSQR	10
9	QSRRVTFHL	10
1	EIWIHPQPQS	7
2	IWIHPQPQSQ	6

Table XXXVI 109P1D4v.4-A0203 10-mers		
No Results Found.		

Table XXXVII 109P1D4v.4-A3-10-mers		
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Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
3	WIHPQPQSQR	21
7	QPQSRRVTF	15
1	EIWIHPQPQS	12

Table XXXVIII 109P1D4v.4-A26 10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
1	EIWIHPQPQS	15
7	QPQSRRVTF	10
9	QSRRVTFHL	8
3	WIHPQPQSQR	7

Table XXXIX 109P1D4v.4-B0702 10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
7	QPQSRRVTF	19
5	HPQPQSRRV	17
9	QSRRVTFHL	11

Table XL- 109P1D4v.4-B08- 10-mers		
No Results Found.		

Table XLI 109P1D4v.4-B1510 10-mers		
No Results Found.		

Table XLII 109P1D4v.4-B2705 10-mers		
No Results Found.		

Table XLIII 109P1D4v.4-B2709 10-mers		
No Results Found.		

Table XLIV 109P1D4v.4-B4402 10-mers		
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
7	QPQSRRVTF	13
9	QSRRVTFHL	12

Table XLV 109P1D4v.4- B5101 10-mers
No Results Found.

Table XLVI-109P1D4v.4 DRB1 0101-15-mers
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
2 STTMEIWIHPQPQSQ 19
4 TMEIWIHPQPQSQR 19
5 MEIWIHPQPQSQRV 16
13 PQSQRRTFHLPEGS 16
8 WIHPQPQSQRRTVFH 15
6 EIWIHPQPQSQRRTV 14
10 HPQPQSQRRTVFHLP 14
12 QPQSQRRTVFHLP 14
3 TTMEIWIHPQPQSQR 12

Table XLVII-109P1D4v.4 DRB1 0301-15-mers
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
6 EIWIHPQPQSQRRTV 18
4 TMEIWIHPQPQSQR 17
10 HPQPQSQRRTVFHLP 16
2 STTMEIWIHPQPQSQ 10

Table XLVIII-109P1D4v.4 DRB1 0401-15-mers
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

4 TMEIWIHPQPQSQR 20
5 MEIWIHPQPQSQRV 16
2 STTMEIWIHPQPQSQ 14
6 EIWIHPQPQSQRRTV 14
1 ESTTMEIWIHPQPQS 12
3 TTMEIWIHPQPQSQR 12
8 WIHPQPQSQRRTVFH 12
9 IHPQPQSQRRTVFHL 12

Table XLIX-109P1D4v.4 DRB1 1101-15-mers
Each peptide is a portion of SEQ ID NO: 9; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen
2 STTMEIWIHPQPQSQ 20
13 PQSQRRTFHLPEGS 13
4 TMEIWIHPQPQSQR 12
5 MEIWIHPQPQSQRV 10
9 IHPQPQSQRRTVFHL 10

Table XXII 109P1D4v.5-A1 9-mers
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight
5 HTRPSQRRV 10
2 VSVHTRPSQ 6
8 PSQRRTVFH 5

Table XXIII 109P1D4v.5 A0201-9-mers

Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight
5 HTRPSQRRV 16
3 SVHTRPSQR 6

Table XXIV 109P1D4v.5 A0203-9- mers
No Results Found

Table XXV 109P1D4v.5-A3 9-mers
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight
3 SVHTRPSQR 24
7 RPSQRRTVF 19

Table XXVI 109P1D4v.5-A26 9-mers
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight
3 SVHTRPSQR 13
1 PVSVHTRPS 10

Table XXVI 109P1D4v.5-A26 9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
5	HTRPSQRRV	9
7	RPSQRRVTF	9

Table XXVII 109P1D4v.5 B0702-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	22
5	HTRPSQRRV	9

Table XXVIII 109P1D4v.5 B08-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	21
3	SVHTRPSQR	10

Table XXIX 109P1D4v.5 B1510-9-mers		
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Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
4	VHTRPSQRR	13
7	RPSQRRVTF	12
5	HTRPSQRRV	6
6	TRPSQRRVT	6

Table XXX 109P1D4v.5 B2705-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	18
4	VHTRPSQRR	14
3	SVHTRPSQR	12
6	TRPSQRRVT	11
8	PSQRRVTFH	11

Table XXXI 109P1D4v.5 B2709-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	13
6	TRPSQRRVT	11
5	HTRPSQRRV	10

Table XXXII 109P1D4v.5 B4402-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	15
3	SVHTRPSQR	5

Table XXXIII 109P1D4v.5 B5101-9-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	RPSQRRVTF	13
5	HTRPSQRRV	11
6	TRPSQRRVT	6

Table XXXIV 109P1D4v.5-A1 10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
6	HTRPSQRRVT	12
3	VSVHTRPSQR	5

Table XXXV 109P1D4v.5 A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
5	VHTRPSQRRV	10
6	HTRPSQRRVT	10
9	PSQRRVTFHL	7
4	SVHTRPSQRR	6

Table XXXVI 109P1D4v.5 A0203-10-mers		
No Results Found.		

Table XXXVII 109P1D4v.5-A3 10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
4	SVHTRPSQRR	15
2	PVSVHTRPSQ	13
7	TRPSQRRVTF	13
3	VSVHTRPSQR	11
6	HTRPSQRRVT	11

Table XXXVIII 109P1D4v.5-A26-10-mers		

Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
2	PVSVHTRPSQ	11
4	SVHTRPSQRR	11
7	TRPSQRRVTF	11
6	HTRPSQRRVT	9
9	PSQRRVTFHL	8
3	VSVHTRPSQR	6

Table XXXIX 109P1D4v.5 B0702-10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
8	RPSQRRVTFH	16
1	VPVSVHTRPS	12
6	HTRPSQRRVT	11
9	PSQRRVTFHL	11
7	TRPSQRRVTF	9

Table XL 109P1D4v.5 B08-10-mers		
No Results Found.		

Table XLI 109P1D4v.5 B1510-10-mers		
No Results Found.		

Table XLII 109P1D4v.5 B2705-10-mers		
No Results Found.		

Table XLIII 109P1D4v.5 B2709-10-mers		
No Results Found.		

Table XLIV 109P1D4v.5-B4402 10-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
7	TRPSQRRVTF	14
9	PSQRRVTFHL	12

Table XLV 109P1D4v.5 B5101-10-mers		
No Results Found.		

Table XLVI-109P1D4v.5 DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
4	FEVPVSVHTRPSQRR	22
3	TFEVPVSVHTRPSQR	17

Table XLVI-109P1D4v.5 DRB1 0101-15-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
1	VTTFEVPVSVHTRPS	16
13	RPSQRRVTFHLPEG	16
7	PVSVHTRPSQRRVTF	14
10	VHTRPSQRRVTFHLP	14
12	TRPSQRRVTFHLPEG	14

Table XLVII-109P1D4v.5 DRB1 0301-15-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
5	EVPSVHTRPSQRRV	16
10	VHTRPSQRRVTFHLP	16
7	PVSVHTRPSQRRVTF	12
3	TFEVPVSVHTRPSQR	10
1	VTTFEVPVSVHTRPS	9
8	VSVHTRPSQRRVTFH	8
9	SVHTRPSQRRVTFHL	8
12	TRPSQRRVTFHLPEG	8

Table XLVIII-109P1D4v.5 DRB1 0401-15-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
1	VTTFEVPVSVHTRPS	22
5	EVPSVHTRPSQRRV	20
4	FEVPVSVHTRPSQRR	18
3	TFEVPVSVHTRPSQR	14
8	VSVHTRPSQRRVTFH	12
9	SVHTRPSQRRVTFHL	12

Table XLIX-109P1D4v.5 DRB1 1101-15-mers		
Each peptide is a portion of SEQ ID NO: 11; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
3	TFEVPVSVHTRPSQR	25
5	EVPSVHTRPSQRRV	15
1	VTTFEVPVSVHTRPS	13
4	FEVPVSVHTRPSQRR	13
13	RPSQRRVTFHLPEG	13

Table XXII 109P1D4v.6 C' terminal-A1 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
5	HTRPDTSRT	10
2	VSVHTRPTD	6

Table XXIII 109P1D4v.6 C' terminal-A0201 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
5	HTRPDTSRT	10
1	PVSVHTRPT	7

Table XXIII 109P1D4v.6 C' terminal-A0201 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
3	SVHTRPTDS	6
4	VHTRPTDSR	5

Table XXIV 109P1D4v.6 C' terminal-A0203 9-mers		
No Results Found.		

Table XXV 109P1D4v.6 C' terminal-A3 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
3	SVHTRPTDS	15
1	PVSVHTRPT	10
4	VHTRPTDSR	9
5	HTRPDTSRT	9

Table XXVI 109P1D4v.6 C' terminal A26-9-mers		
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Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	SVHTRPTDS	11
1	PVSVHTRPT	10
5	HTRPTDSRT	10
2	VSVHTRPTD	5

Table XXVII
109P1D4v.6
C' terminal-B0702
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

1	PVSVHTRPT	10
5	HTRPTDSRT	9
4	VHTRPTDSR	4

Table XXVIII
109P1D4v.6
C' terminal-B08
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	SVHTRPTDS	10
5	HTRPTDSRT	7

Table XXIX
109P1D4v.6
C' terminal
B1510-9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

4	VHTRPTDSR	11
1	PVSVHTRPT	4
5	HTRPTDSRT	4

Table XXX
109P1D4v.6
C' terminal-B2705
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

4	VHTRPTDSR	12
5	HTRPTDSRT	5

Table XXXI
109P1D4v.6
C' terminal-B2709
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

Table XXXI
109P1D4v.6
C' terminal-B2709
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

2	VSVHTRPTD	2
5	HTRPTDSRT	2
4	VHTRPTDSR	1

Table XXXII
109P1D4v.6
C' terminal-B4402
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	SVHTRPTDS	4
1	PVSVHTRPT	3
5	HTRPTDSRT	3
2	VSVHTRPTD	2
4	VHTRPTDSR	2

Table XXXIII
109P1D4v.6
C' terminal-B5101
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

2	VSVHTRPTD	4
3	SVHTRPTDS	3
5	HTRPTDSRT	2

Table XXXIV
109P1D4v.6
C' terminal-A1
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

3	VSVHTRPTDS	5
4	SVHTRPTDSR	2

Table XXXV
109P1D4v.6
C' terminal-A0201
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

4	SVHTRPTDSR	8
1	VPVSVHTRPT	5
2	PVSVHTRPTD	4
5	VHTRPTDSRT	4

Table XXXVI
109P1D4v.6
C' terminal-A0203
10-mers

No Results Found.

Table XXXVII
109P1D4v.6
C' terminal-A3
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

4	SVHTRPTDSR	17
2	PVSVHTRPTD	15

Table XXXVIII
109P1D4v.6
C' terminal-A26
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

4	SVHTRPTDSR	12
2	PVSVHTRPTD	11

Table XXXIX
109P1D4v.6
C' terminal-B0702
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

1	VPVSVHTRPT	18
5	VHTRPTDSRT	6

Table XL-
109P1D4
v.6-C'
terminal-B08
10-mers

No Results Found.

Table XLI-
109P1D4
v.6-C'
terminal-B1510-
10-mers

No Results Found.

Table XLII-
109P1D4
v.6-C'
terminal-B2705-
10-mers

No Results Found.

Table XLIII
109P1D4v.6
C' terminal-B2709
10-mers

No Results
Found.

Table XLIV
109P1D4v.6
C' terminal-B4402
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

2	PVSVHTRPTD	3
4	SVHTRPTDSR	3
1	VPVSVHTRPT	2

Table XLV
109P1D4v.6
C' terminal-
B5101
10-mers

No Results
Found.

Table XLVI-109P1D4v.6
C' terminal-DRB1 0101
15-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

3	TFEVPVSVHTRPTDS	17
1	VTTFEVPVSVHTRPT	16
4	FEVPVSVHTRPTDSR	14
5	EVPVSVHTRPTDSRT	8

Table XLVII-109P1D4v.6
C' terminal-DRB1 0301
15-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

5	EVPVSVHTRPTDSRT	16
3	TFEVPVSVHTRPTDS	10
1	VTTFEVPVSVHTRPT	9

Table XLVIII-109P1D4v.6
C' terminal-DRB1 0401
15-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

1	VTTFEVPVSVHTRPT	22
4	FEVPVSVHTRPTDSR	18
3	TFEVPVSVHTRPTDS	14
5	EVPVSVHTRPTDSRT	14

Table XLIX-109P1D4v.6
C' terminal-DRB1 1101
15-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

3	TFEVPVSVHTRPTDS	25
5	EVPVSVHTRPTDSRT	15
1	VTTFEVPVSVHTRPT	13

Table XXII
109P1D4v.6
N' terminal-A1
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

6	NSDISSVVR	15
21	HKCLLSGTY	15
1	MTVGFNSDI	8
17	TINCHKCLL	8
18	TNCHKCLLS	8

Table XXIII
109P1D4v.6
N' terminal-A0201
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

7	SDISSVVRV	20
4	GFNSDISSV	18
23	CLLSGTYIF	17
1	MTVGFNSDI	15
17	TINCHKCLL	15
10	SSVVRVNTT	13
5	FNSDISSVV	12
16	NTTNCHKCL	12
8	DISSVVRVN	11
22	KCLLSGTYI	11

Table XXIV
109P1D4v.6
N' terminal-
A0203
9-mers

No Results
Found.

Table XXV 109P1D4v.6 N' terminal A3-9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
14	RVNTTNCHK	24
11	SVVRVNTTN	20
23	CLLSGTYIF	18
12	VVRVNTTNC	14
6	NSDISSVVR	13
8	DISSVVRVN	13
21	HKCLLSGT	12

Table XXVI 109P1D4v.6 N' terminal-A26 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
8	DISSVVRVN	17
16	NTTNCHKCL	17
17	TTNCHKCLL	17
11	SVVRVNTTN	16
1	MTVGFNSDI	13
21	HKCLLSGT	13
2	TVGFNSDIS	12
12	VVRVNTTNC	11
7	SDISSVVRV	10
10	SSVVRVNTT	10
14	RVNTTNCHK	10
23	CLLSGTYIF	9

Table XXVII 109P1D4v.6 N' terminal-B0702 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
9	ISSVVRVNT	12
16	NTTNCHKCL	10
17	TTNCHKCLL	10
5	FNSDISSVV	9
7	SDISSVVRV	9
22	KCLLSGTI	9
1	MTVGFNSDI	8
10	SSVVRVNTT	7
23	CLLSGTYIF	7
4	GFNSDISSV	6
20	CHKCLLSGT	6

Table XXVIII 109P1D4v.6 N' terminal-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
10	SSVVRVNTT	12
23	CLLSGTYIF	12
16	NTTNCHKCL	11
17	TTNCHKCLL	10
18	TNCHKCLLS	10
20	CHKCLLSGT	10
12	VVRVNTTNC	8
1	MTVGFNSDI	7
22	KCLLSGTI	7

Table XXIX 109P1D4v.6 N' terminal-B1510 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
17	TTNCHKCLL	12
16	NTTNCHKCL	10
20	CHKCLLSGT	10
9	ISSVVRVNT	7
23	CLLSGTYIF	7
8	DISSVVRVN	6

Table XXX 109P1D4v.6 N' terminal-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
13	VVRVNTTNCH	20
14	RVNTTNCHK	15
23	CLLSGTYIF	15
6	NSDISSVVR	14
22	KCLLSGTI	14
21	HKCLLSGT	12
1	MTVGFNSDI	11
17	TTNCHKCLL	11
16	NTTNCHKCL	10

Table XXXI 109P1D4v.6 N' terminal-B2709 9-mers		
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Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

4	GFNSDISSV	13
7	SDISSVVRV	13
22	KCLLSGTYI	12
23	CLLSGTYIFA	12
13	VRVNTTNCH	11
16	NTTNCHKCL	11
17	TTNCHKCLL	10
1	MTVGFNSDI	9
5	FNSDISSV	9

Table XXXII
109P1D4v.6
N' terminal
B4402-9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

16	NTTNCHKCL	14
21	HKCLLSGTY	12
23	CLLSGTYIFA	12
17	TTNCHKCLL	11
22	KCLLSGTYI	11
1	MTVGFNSDI	9

Table XXXIII
109P1D4v.6
N' terminal-B5101
9-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

22	KCLLSGTYI	14
1	MTVGFNSDI	13
5	FNSDISSV	13
7	SDISSVVRV	13
8	DISSVVRVNT	12
3	VGFNSDISS	10
4	GFNSDISSV	9
16	NTTNCHKCL	8
17	TTNCHKCLL	7

Table XXXIV
109P1D4v.6
N' terminal-A1
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

6	NSDISSVVRV	15
20	CHKCLLSGTY	15
17	TTNCHKCLLS	14
16	NTTNCHKCLL	8

Table XXXV
109P1D4v.6
N' terminal-A0201
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

3	VGFNSDISSV	18
6	NSDISSVVRV	16
23	CLLSGTYIFA	16
8	DISSVVRVNT	13
9	ISSVVRVNTT	13
16	NTTNCHKCLL	13
4	GFNSDISSV	12
15	VNTTNCHKCL	9
19	NCHKCLLSGT	9

Table XXXVI
109P1D4v.6
N' terminal-A0203
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

23	CLLSGTYIFA	10
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Table XXXVII
109P1D4v.6
N' terminal-A3
10-mers

Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

12	VRVNTTNCH	17
11	SVVRVNTTNC	15
14	RVNTTNCHKC	14
5	FNSDISSVVR	13
8	DISSVVRVNT	13
2	TVGFNSDISS	12
20	CHKCLLSGTY	12
23	CLLSGTYIFA	12
13	VRVNTTNCHK	11

Table XXXVII 109P1D4v.6 N' terminal-A3 10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
22	KCLLSGTYIF	10

Table XXXVIII 109P1D4v.6 N' terminal-A26 10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
16	NTTNCHKCLL	17
11	SVVRVNTTNC	15
2	TVGFNSDISS	13
8	DISSVVRVNT	13
1	MTVGFNSDIS	12
20	CHKCLLSGTY	12
14	RVNTTNCHKC	11
3	VGFNSDISSV	10
7	SDISSVVRVN	10
12	VVRVNTTNCH	10
17	TTNCHKCLLS	10
15	VNTTNCHKCL	9

Table XXXIX 109P1D4v.6 N' terminal-B0702 10-mers		
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Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
8	DISSVVRVNT	11
6	NSDISSVVRV	10
9	ISSVVRVNTT	10
15	VNTTNCHKCL	10
16	NTTNCHKCLL	10
22	KCLLSGTYIF	8
4	GFNSDISSV	7
19	NCHKCLLSGT	7
21	HKCLLSGTYI	7
23	CLLSGTYIFA	7
3	VGFNSDISSV	6

Table XL- 109P1D4 v.6 N' terminal- B08 10-mers		
No Results Found.		

Table XLI- 109P1D4 v.6 N' terminal B1510- 10-mers		
No Results Found.		

Table XLII- 109P1D4 v.6 N' terminal B2705- 10-mers		
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No Results Found.		
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Table XLIII- 109P1D4 v.6 N' terminal- B2709 10-mers		
No Results Found.		

Table XLIV-109P1D4 v.6 N' terminal B4402-10-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
22	KCLLSGTYIF	14
15	VNTTNCHKCL	13
16	NTTNCHKCLL	13
20	CHKCLLSGTY	11
21	HKCLLSGTYI	9
7	SDISSVVRVN	7

Table XLV- 109P1D4 v.6 N' terminal B5101- 10-mers		
No Results Found.		

Table XLVI-109P1D4v.6 N' terminal-DRB1 0101 15-mers		
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Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
19	NCHKCLSGTYIFAV	26
2	TVGFNSDISSVVRVN	25
9	ISSVVRVNTTNCHKC	22
10	SSVVRVNTTNCHKCL	16
20	CHKCLSGTYIFAVL	16
21	HKCLSGTYIFAVLL	16
22	KCLSGTYIFAVLLV	16
18	TNCHKCLSGTYIFA	15
6	NSDISSVVRVNTTNC	1

Table XLVII-109P1D4v.6 N' terminal-DRB1 0301 15-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
2	TVGFNSDISSVVRVN	19
6	NSDISSVVRVNTTNC	19
14	RVNTTNCHKCLSGT	16
21	HKCLSGTYIFAVLL	13
9	ISSVVRVNTTNCHKC	12
10	SSVVRVNTTNCHKCL	12
20	CHKCLSGTYIFAVL	12
12	VVRVNTTNCHKCLS	11
22	KCLSGTYIFAVLLV	11
18	TNCHKCLSGTYIFA	10

Table XLVIII-109P1D4v.6 N' terminal-DRB1 0401 15-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		

Table XLVIII-109P1D4v.6 N' terminal-DRB1 0401 15-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
2	TVGFNSDISSVVRVN	28
6	NSDISSVVRVNTTNC	26
9	ISSVVRVNTTNCHKC	20
10	SSVVRVNTTNCHKCL	14
21	HKCLSGTYIFAVLL	14
22	KCLSGTYIFAVLLV	14

Table XLIX-109P1D4v.6 N' terminal-DRB1 1101 15-mers		
Each peptide is a portion of SEQ ID NO: 13; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
6	NSDISSVVRVNTTNC	22
9	ISSVVRVNTTNCHKC	12
21	HKCLSGTYIFAVLL	12
2	TVGFNSDISSVVRVN	11
14	RVNTTNCHKCLSGT	11

Table XXII-109P1D4v.7 N' terminal-A1 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
13	SSLSPLLLV	15
12	SSSLPPLL	14

Table XXII-109P1D4v.7 N' terminal-A1 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
14	SLSPLLLVS	14
1	MFRVGFLII	11
9	ISSSSSLSP	10
11	SSSSLSPLL	8

Table XXIII-109P1D4v.7 N' terminal-A0201 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
18	LLVSVVRV	30
7	LISSSSSL	24
15	LSPLLVS	21
13	SSLSPLLLV	20
14	SLSPLLLVS	20
16	SPLLVS	19
10	SSSSSLSP	16
19	LLVSVVRV	16
6	FLISSSSS	15

Table XXIV-109P1D4v.7 N' terminal-A0203 9-mers		
No Results Found.		

Table XXV 109P1D4v.7 N' terminal-A3 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
17	PLLLVSVVR	26
14	SLSPLLLVS	21
6	FLIISSSSS	19
3	RVGFLIIS	16
7	LIISSSSSL	16
18	LLLVSVVRV	16
20	LVSVVRVNT	16
19	LLVSVVRVN	15
8	IISSSSSLS	13

Table XXVI 109P1D4v.7 N' terminal-A26 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	LIISSSSSL	19
3	RVGFLIIS	17
10	SSSSLSPL	15
4	VGFLIIS	12
11	SSSSLSPLL	11
12	SSSLPPLL	10
20	LVSVVRVNT	10

Table XXVII 109P1D4v.7 N' terminal-B0702 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
16	SPLLLVS	18
12	SSSLPPLL	14
10	SSSSLSPL	13
11	SSSSLSPLL	13
1	MFRVGFLI	11
13	SSSLPPLL	11
20	LVSVVRVNT	11
7	LIISSSSSL	10
18	LLLVSVVRV	9

Table XXVIII 109P1D4v.7 N' terminal-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	LIISSSSSL	14
1	MFRVGFLI	13
12	SSSLPPLL	13
10	SSSSLSPL	12
11	SSSSLSPLL	12
21	VSVVRVNTT	11
16	SPLLLVS	10
18	LLLVSVVRV	9
14	SLSPLLLVS	8
17	PLLLVSVVR	8
6	FLIISSSSS	7

Table XXVIII 109P1D4v.7 N' terminal-B08 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
19	LLVSVVRVN	7

Table XXIX 109P1D4v.7 N' terminal-B1510 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
11	SSSSLSPLL	12
12	SSSLPPLL	12
10	SSSSLSPL	11
7	LIISSSSSL	10
18	LLLVSVVRV	6

Table XXX 109P1D4v.7 N' terminal-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
17	PLLLVSVVR	17
7	LIISSSSSL	16

Table XXX 109P1D4v.7 N' terminal-B2705 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
2	FRVGFLIIS	15
10	SSSSLSPL	13
11	SSSSLSPLL	13
12	SSSLSPLLL	13
3	RVGFLIIS	10
4	VGFLIIS	10
1	MFRVGFLII	9
5	GFLIIS	9

Table XXXI 109P1D4v.7 N' terminal-B2709 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
18	LLLVSVVRV	13
7	LISSSSSL	12
11	SSSSLSPLL	12
13	SSLSPLL	12
2	FRVGFLIIS	11
10	SSSSLSPL	11
12	SSSLSPLLL	11
16	SPLLVS	11
1	MFRVGFLII	9
15	LSPLLVS	9

Table XXXII 109P1D4v.7 N' terminal-B4402 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
12	SSSLSPLLL	16
7	LISSSSSL	13
10	SSSSLSPL	13
11	SSSSLSPLL	13
1	MFRVGFLII	10
14	LSPLLVS	8

Table XXXIII 109P1D4v.7 N' terminal-B5101 9-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
16	SPLLVS	25
18	LLLVSVVRV	17
1	MFRVGFLII	13
15	LSPLLVS	13

Table XXXIV 109P1D4v.7 N' terminal-A1 10-mers		
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Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
11	SSSSLSPLL	14
12	SSSLSPLLV	14
13	SSSLPLLVS	13
10	SSSSLSPLL	8
14	LSPLLVS	7

Table XXXV 109P1D4v.7 N' terminal A0201-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
14	LSPLLVS	32
6	FLIIS	25
17	PLLVS	25
18	LLLVSVVRV	18
19	LLVS	18
12	SSSLSPLLV	17
20	LVSVVRVNTT	17
9	ISSSSLSPL	16
15	LSPLLVS	16

Table XXXVI 109P1D4v.7 N' terminal A0203-10-mers		
No Results Found.		

Table XXXVII 109P1D4v.7 N' terminal-A3 10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
14	SLSPLLVSV	20
3	RVGFLIIS	19
6	FLIISSSSL	19
17	PLLVSVRV	17
16	SPLLVSVR	16
18	LLVSVRVN	16
8	IISSSSLSP	15
19	LLVSVRVNT	15
7	LIISSSSLS	14
20	LVSVRVNTT	14
13	SSLPLLVSV	10

Table XXXVIII 109P1D4v.7 N' terminal A26-10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
3	RVGFLIIS	16
20	LVSVRVNTT	15
6	FLIISSSSL	14
9	ISSSSLSPL	14
11	SSSSLSPLL	11
2	FRVGFLIIS	10
7	LIISSSSLS	10
10	SSSSLSPLL	10

Table XXXIX 109P1D4v.7 N' terminal-B0702 10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
9	ISSSSLSPL	14
11	SSSSLSPLL	14
10	SSSSLSPLL	13
16	SPLLVSVR	13
14	SLSPLLVSV	11
6	FLIISSSSL	10
12	SSSSLSPLL	10
17	PLLVSVRV	9
19	LLVSVRVNT	9
20	LVSVRVNTT	9
15	LSPLLVSVV	8

Table XL 109P1D4v.7 N' terminal-B08 10-mers		
No Results Found.		

Table XLI 109P1D4v.7 N' terminal-B1510 10-mers		
No Results Found.		

Table XLII 109P1D4v.7 N' terminal-B2705 10-mers		

No Results Found.

Table XLIII 109P1D4v.7 N' terminal-B2709 10-mers		
No Results Found.		

Table XLIV 109P1D4v.7 N' terminal-B4402 10-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine		
11	SSSSLSPLL	15
6	FLIISSSSL	13
10	SSSSLSPLL	13
9	ISSSSLSPL	12

Table XLV 109P1D4v.7 N' terminal-B5101 10-mers		
No Results Found.		

Table XLVI-109P1D4v.7 N' terminal-DRB1 0101 15-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
3	RVGFLIISSSSLSP	33

Table XLVI-109P1D4v.7 N' terminal-DRB1 0101 15-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
1	MFRVGFLIISSSSSL	25
4	VGFLIISSSSSLSPL	25
12	SSSLSPLLLVS VVRV	24
15	LSPLLLSVVRVNTT	23
5	GFLIISSSSSLSPLL	22
6	FLIISSSSSLSPLLL	22
9	ISSSSSLSPLLLVS	22
20	LVS VVRVNTTNCHKC	22
2	FRVGFLIISSSSSL	21
13	SSLSPLLLVS VVRV	17

Table XLVII-109P1D4v.7 N' terminal-DRB1 0301 15-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
4	VGFLIISSSSSLSPL	20
17	PLLLSVVRVNTTNC	20
15	LSPLLLSVVRVNTT	15
5	GFLIISSSSSLSPLL	14
6	FLIISSSSSLSPLLL	13
12	SSSLSPLLLVS VVRV	13
9	ISSSSSLSPLLLVS	12
16	SPLLLVS VVRVNTTN	12
20	LVS VVRVNTTNCHKC	12
21	VS VVRVNTTNCHKCL	12
3	RVGFLIISSSSSLSP	11
8	IISSSSSLSPLLLVS	11
18	LLLS VVRVNTTNCH	11
1	MFRVGFLIISSSSSL	10
7	LISSSSSLSPLLLVS	10

Table XLVIII-109P1D4v.7 N' terminal-DRB1 0401 15-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
3	RVGFLIISSSSSLSP	28
17	PLLLSVVRVNTTNC	26
1	MFRVGFLIISSSSSL	20
4	VGFLIISSSSSLSPL	20
5	GFLIISSSSSLSPLL	20
12	SSSLSPLLLVS VVRV	20
15	LSPLLLSVVRVNTT	20
18	LLLS VVRVNTTNCH	20
20	LVS VVRVNTTNCHKC	20
2	FRVGFLIISSSSSL	18
6	FLIISSSSSLSPLLL	14
16	SPLLLVS VVRVNTTN	14
21	VS VVRVNTTNCHKCL	14

Table XLIX-109P1D4v.7 N' terminal-DRB1 1101 15-mers		
Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen		
3	RVGFLIISSSSSLSP	22
17	PLLLSVVRVNTTNC	22
1	MFRVGFLIISSSSSL	18
15	LSPLLLSVVRVNTT	14
2	FRVGFLIISSSSSL	13
5	GFLIISSSSSLSPLL	13
18	LLLS VVRVNTTNCH	13
6	FLIISSSSSLSPLLL	12
12	SSSLSPLLLVS VVRV	12
20	LVS VVRVNTTNCHKC	12
16	SPLLLVS VVRVNTTN	11

Table XXII 109P1D4v.8-A1 9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
7	KKEITVQPT	11
1	TFIPGLKKE	8

Table XXIII 109P1D4v.8 A0201-9-mers		
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight		
2	FIPGLKKEI	21
8	KEITVQPTV	16
5	GLKKEITVQ	14
4	PGLKKEITV	12

Table XXIV 109P1D4v.8 A0203-9-mers		
No Results Found		

Table XXV 109P1D4v.8 A3-9-mers		

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

5	GLKKEITVQ	16
8	KEITVQPTV	11
2	FIPGLKKEI	10
6	LKKEITVQP	9
1	TFIPGLKKE	8

Table XXVI
109P1D4v.8
A26-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

1	TFIPGLKKE	11
2	FIPGLKKEI	5
6	LKKEITVQP	5
8	KEITVQPTV	5

Table XXVII
109P1D4v.8
B0702-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	IPGLKKEIT	18
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Table XXVII
109P1D4v.8
B0702-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

7	KKEITVQPT	9
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Table XXVIII
109P1D4v.8
B08-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

3	IPGLKKEIT	18
5	GLKKEITVQ	18
2	FIPGLKKEI	13
6	LKKEITVQP	13
4	PGLKKEITV	10

Table XXIX
109P1D4v.8
B1510-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

5	GLKKEITVQ	5
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Table XXIX
109P1D4v.8
B1510-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

1	TFIPGLKKE	4
2	FIPGLKKEI	3
3	IPGLKKEIT	3
6	LKKEITVQP	3

Table XXX
109P1D4v.8
B2705-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

5	GLKKEITVQ	12
2	FIPGLKKEI	11
8	KEITVQPTV	9
1	TFIPGLKKE	8
4	PGLKKEITV	7

Table XXXI
109P1D4v.8
B2709-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

8	KEITVQPTV	12
4	PGLKKEITV	10
2	FIPGLKKEI	8

Table XXXII
109P1D4v.8
B4402-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

8	KEITVQPTV	16
2	FIPGLKKEI	12
1	TFIPGLKKE	10

Table XXXIII
109P1D4v.8
B5101-9-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight

4	PGLKKEITV	21
2	FIPGLKKEI	14
3	IPGLKKEIT	13
8	KEITVQPTV	13

Table XXXIV
109P1D4v.8
A1-10-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

1	STFIPGLKKE	10
8	KKEITVQPTV	10

Table XXXV
109P1D4v.8
A0201-10-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

3	FIPGLKKEIT	15
4	IPGLKKEITV	14
2	TFIPGLKKEI	13
8	KKEITVQPTV	13
1	STFIPGLKKE	12
6	GLKKEITVQP	12
7	LKKEITVQPT	11

Table XXXVI
109P1D4v.8
A0203-10-mers

No Results Found.

Table XXXVII
109P1D4v.8
A3-10-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

6	GLKKEITVQP	18
9	KEITVQPTVE	12
3	FIPGLKKEIT	10

Table XXXVIII
109P1D4v.8
A26-10-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

1	STFIPGLKKE	18
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Table XXXIX
109P1D4v.8
B0702-10-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine

4	IPGLKKEITV	18
3	FIPGLKKEIT	8
7	LKKEITVQPT	8
8	KKEITVQPTV	8

Table XL
109P1D4v.8
B08-10-mers

No Results Found.

Table XLI 109P1D4v.8 B1510-10-mers

No Results Found.

Table XLII 109P1D4v.8 B2705-10-mers

No Results Found.

Table XLIII 109P1D4v.8 B2709-10-mers

No Results Found.

Table XLIV 109P1D4v.8 B4402-10-mers
Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine
9 KEITVQPTVE 17
2 TFIPGLKKEI 16

Table XLV 109P1D4v.8 B5101-10-mers

No Results Found.

Table XLVI-109P1D4v.8 DRB1 0101-15-mers
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Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

9	IPGLKKEITVQPTVE	25
13	KKEITVQPTVEEASD	21
5	ESTFIPGLKKEITVQ	19
3	DPESTFIPGLKKEIT	17
6	STFIPGLKKEITVQP	16
12	LKKEITVQPTVEEAS	13

Table XLVII-109P1D4v.8 DRB1 0301-15-mers

Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

5	ESTFIPGLKKEITVQ	17
6	STFIPGLKKEITVQP	17
13	KKEITVQPTVEEASD	13
9	IPGLKKEITVQPTVE	12
1	NSDPESTFIPGLKKE	9

Table XLVIII-109P1D4v.8 DRB1 0401-15-mers
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Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

6	STFIPGLKKEITVQP	20
9	IPGLKKEITVQPTVE	20
5	ESTFIPGLKKEITVQ	16
13	KKEITVQPTVEEASD	14
2	SDPESTFIPGLKKEI	12
3	DPESTFIPGLKKEIT	12
10	PGLKKEITVQPTVEE	12
11	GLKKEITVQPTVEEA	12

Table XLIX-109P1D4v.8 DRB1 1101-15-mers
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Each peptide is a portion of SEQ ID NO: 17; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen

6	STFIPGLKKEITVQP	21
5	ESTFIPGLKKEITVQ	18
9	IPGLKKEITVQPTVE	12

Table L: Protein Characteristics of 109P1D4

109P1D4 var.1	Bioinformatic Program	URL on World Wide Web	Outcome
ORF	ORF finder		846-3911 bp (includes stop codon) 1021aa
Protein length			
Transmembrane region	TM Pred	.ch.embnet.org/	3 TM helices (aa3-aa23, aa756-aa776, aa816-aa834), N terminus intracellular
	HMMTop	.enzim.hu/hmmtop/	no TM, N terminus extracellular
	Sosui	.genome.ad.jp/SOSui/	3 TM helices (2-24aa, 756-778aa, 810-832aa), N terminus extracellular
	TMHMM	.cbs.dtu.dk/services/TMHMM	1 TM helix (813-835aa), N terminus extracellular
Signal Peptide	Signal P	.cbs.dtu.dk/services/SignalP/	yes
pI	pI/MW tool	.expasy.ch/tools/	pI 4.81
Molecular weight	pI/MW tool	.expasy.ch/tools/	112.7 kDa
Localization	PSORT	psort.nibb.ac.jp/	Plasma membrane
	PSORT II	psort.nibb.ac.jp/	67% endoplasmic reticulum
Motifs	Pfam	.sanger.ac.uk/Pfam/	Cadherin domain
	Prints	.biochem.ucl.ac.uk/	Cadherin domain, DNA topoisomerase 4B, sonic hedgehog
	Blocks	.blocks.fhcrc.org/	Cadherin domain, ribosomal protein L10E, ribulose biphosphate carboxylase (large chain), ornithine decarboxylase antizyme protein phosphatase 2C subfamily

Table LI. Exon boundaries of transcript 109P1D4 v.1

Exon	Start	End	Length
1	1	1385	1385
2	1386	4603	3218

Table LII(a). Nucleotide sequence of transcript variant 109P1D4 v.2 (SEQ ID NO: 237)

cccccttctc	ccccctcggt	aagtcctcc	ccctcgccat	tcaaaagggc	tggctcggca	60
ctggtcctt	gcagtcggcg	aactgtcggg	gcgggaggag	ccgtgagcag	tagctgcact	120
cagctgcccg	cgcggaag	aggaaggcaa	gccaaacaga	gtgcgcagag	tggcagtgcc	180
agcggcgaca	caggcagcac	aggcagcccg	ggctgcctga	atagcctcag	aaacaacctc	240
agcgactccg	gctgctctgc	ggactgcgag	ctgtggcggt	agagcccgc	acagcagtcg	300
cagtctccgt	ggagcggg	gaagcctttt	ttctcccttt	cgtttacctc	ttcattctac	360
tctaaaggca	tcgttattag	gaaaatcctg	ttgcgaataa	gaaggattcc	acagatcaca	420
taccggagag	gttttgctc	agctgctctc	aactttgtaa	tcttgtgaag	aagctgacaa	480
gcttggctga	ttgcagagca	ctatgaggac	tgaacgacag	tgggttttaa	ttcagatatt	540
tcaagtgttg	tgcggttaa	tacaacaaac	tgtacaagt	gtacctggta	tggacttggt	600
gtccgggacg	tacattttcg	cggtcctgct	agcatgcgtg	gtgttcact	ctggcgccca	660
ggagaaaaac	tacaccatcc	gagaagaaat	gccagaaaac	gtcctgatag	gcgacttggt	720
gaaagacctt	aacttgtcgc	tgattccaaa	caagtccttg	acaactgcta	tgcaattcaa	780
gctagtgtac	aagaccggag	atgtgccact	gattcgaatt	gaagaggata	ctgggtgagat	840
cttcactact	ggcgctcgca	ttgatcgtga	gaaattatgt	gctgggtatcc	caagggatga	900
gcattgcttt	tatgaagtgg	aggttgccat	tttgccggat	gaaatattta	gactgggttaa	960
gatacgtttt	ctgatagaag	atataaatga	taatgcacca	ttgttcccag	caacagttat	1020
caacatatca	attccagaga	actcggetat	aaactctaaa	tatactctcc	cagcggctgt	1080
tgatcctgac	gtaggaataa	acggagtcca	aaactacgaa	ctaattaaga	gtcaaacat	1140
ttttggcctc	gatgtcattg	aaacaccaga	aggagacaag	atgccacaac	tgattgttca	1200
aaaggagtta	gatagggaag	agaaggatac	ctacgtgatg	aaagtaaagg	ttgaagatgg	1260

tggttttct	caaagatcca	gtactgctat	tttgcaagt	agtgttactg	atacaaatga	1320
caaccacca	gtctttaagg	agacagagat	tgaagtcagt	ataccagaaa	atgtctctgt	1380
aggcacttca	gtgacacagc	tccatgccac	agatgctgac	ataggtgaaa	atgccaatga	1440
ccacttctct	ttcagcaatc	tagtctccaa	cattgccagg	agattatttc	acctcaatgc	1500
caccactgga	cttatcacaa	tcaaagaacc	actggatagg	gaagaaacac	caaaccacaa	1560
gttactgggt	ttggcaagt	atgggtggatt	gatgccagca	agagcaatgg	tgctggtaaa	1620
tgttacagat	gtcaatgata	atgtcccatc	cattgacata	agatacatcg	tcaatcctgt	1680
caatgacaca	gtgtttcttt	cagaaaaat	tccactcaac	acaaaaattg	ctctcataac	1740
tgtgacggat	aaggatgcgg	accataatgg	acgggtgaca	tgcttcacag	atcatgaaat	1800
ccctttcaga	ttaaggccag	tattcagtaa	tcagttcctc	ctggagactg	cagcataatc	1860
tgactatgag	tcacacaaa	aatatgccat	taaattactg	gctgcagatg	ctggcaaac	1920
tcctttgaa	cagtcagcaa	tgctcttcat	caaagtga	gatgaaaatg	acaatgctcc	1980
agttttcacc	cagtctttcg	taactgtttc	tattcctgag	aataactctc	ctggcatcca	2040
gttgacgaaa	gtaagtgcaa	tggtatgcaga	cagtgggctc	aatgctaaga	tcaattacct	2100
gctaggccct	gatgtccac	ctgaattcag	cctggattgt	cgtacaggca	tgctgactgt	2160
agtgaagaaa	ctagatagag	aaaaagagga	taaatattta	ttcacaattc	tggaacaaaga	2220
taacggggta	ccacccttaa	ccagcaatgt	cacagtcttt	gtaagcatta	ttgatcagaa	2280
tgacaatagc	ccagttttca	ctcacaatga	atacaacttc	tatgtcccag	aaaaccttcc	2340
aaggcatggt	acagtaggac	taatcactgt	aactgatcct	gattatggag	acaattctgc	2400
agttacgctc	tccatttttag	atgagaatga	tgacttcacc	attgattcac	aaactgggtg	2460
catccgacca	aatatttcat	ttgatagaga	aaaacaagaa	tcttacactt	tctatgtaaa	2520
ggctgaggat	gggtgtagag	tatcacgttc	ttcaagtgcc	aaagtaacca	taaatgtggt	2580
tgatgtcaat	gagaacaaa	cagttttcat	tgctcctcct	tccaactgtt	cttatgaatt	2640
ggttctaccg	tccactaatc	caggcacagt	ggtctttcag	gtaattgctg	ttgacaatga	2700
cactggcatg	aatgcagagg	ttcgttacag	cattgtagga	ggaaacacaa	gagatctgtt	2760
tgcaatcgac	caagaaacag	gcaacataac	attgatggag	aaatgtgatg	ttacagacct	2820
tggtttacac	agagtgttgg	tcaaagctaa	tgacttagga	cagcctgatt	ctctcttcag	2880
tgttgtaatt	gtcaatctgt	tcgtgaatga	gtcggtgacc	aatgctacac	tgattaatga	2940
actggtgcgc	aaaagcactg	aagcaccagt	gaccccaat	actgagatag	ctgatgtatc	3000
ctcaccaact	agtgactatg	tcaagatcct	ggttgacagt	gttgctggca	ccataactgt	3060
cgttgtagtt	attttcatca	ctgctgtagt	aagatgtcgc	caggcaccac	accttaaggc	3120
tgctcagaaa	aacaagcaga	attctgaatg	ggctacccca	aaccagaaaa	acaggcagat	3180
gataatgatg	aagaaaaaga	aaaagaagaa	gaagcattcc	cctaagaact	tgctgcttaa	3240
ttttgtcact	attgaagaaa	ctaaggcaga	tgatgttgac	agtgatggaa	acagagtcac	3300
actagacctt	cctattgatc	tagaagagca	aacaatggga	aagtacaatt	gggtaactac	3360
acctactact	ttcaagccc	acagcctga	tttgcccga	cactacaaat	ctgcctctcc	3420
acagcctgcc	ttccaaattc	agcctgaaac	tccctgaaat	tcgaagcacc	acatcatcca	3480
agaactgcct	ctcgataaca	cctttgtggc	ctgtgactct	atctccaagt	gttcctcaag	3540
cagttcagat	ccctacagcg	tttctgactg	tggtatccca	gtgacgacct	tcgaggtacc	3600
tgtgtccgta	cacaccagac	cgactgattc	caggacatca	actattgaaa	tctgcagtga	3660
gatataactt	tctaggaaca	acaaaattcc	attccccttc	caaaaaattt	caatgattgt	3720
gattttcaaaa	ttaggctaag	atcattaatt	ttgtaatcta	gatttcccat	tataaaagca	3780
agcaaaaatc	atcttaaaaa	tgatgtccta	gtgaaccttg	tgctttcttt	agctgtaatc	3840
tggaatgga	aatttaaaat	ttatggaaga	gacagtgcag	cacaataaca	gagtactctc	3900
atgctgtttc	tctgtttgct	ctgaatcaac	agccatgatg	taatataagg	ctgtcttggt	3960
gtatacactt	atggttaata	tatcagtcac	gaaacatgca	attacttgcc	ctgtctgatt	4020
gttgaataat	taaaacatta	tctccaggag	tttggaagt	agctgaacta	gccaaactac	4080
tctctgaaag	gtatccaggg	caagagacat	ttttaagacc	ccaaacaaa	aaaaaacaaa	4140
acaaaaacac	tctggttcag	tgttttgaaa	atattcacta	acataatatt	gctgagaaaa	4200
tcatttttat	taccaccac	tctgcttaaa	agttgagtgg	gccgggcgcg	gtggctcacg	4260
cctgtaatcc	cagcactttg	ggaggccgag	gcggttgat	cacgagggtc	ggagattgag	4320
accatcctgg	ctaacacggg	gaaaccccat	ctccactaaa	aatacaaaaa	attagcctgg	4380
cgtggtggcg	ggcgctgta	gtcccagcta	ctcgaggagg	tgaggcagga	gaatagcgtg	4440
aaccggggag	gcggagcttg	cagtgcgcg	agatggcgcc	actgcactcc	agcctgggtg	4500
acagagcaag	actctgtctc	aaaaagaaaa	aaatgttcaa	tgatagaaaa	taattttact	4560
aggtttttat	gttgattgta	ctcatgctgt	tccactcctt	ttaattatta	aaaagttatt	4620
tttggtggg	tggttggtg	cacacctgta	atccacgac	tttgaggagg	cgaggtgggt	4680
ggatcacctg	aggtcaggag	ttcaagacca	gtctggccaa	cat		4720

Table LIII(a). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 238) and 109P1D4 v.2 (SEQ ID NO: 239)
 Score = 5920 bits (3079), Expect = 0.0Identities = 3079/3079 (100%) Strand = Plus / Plus

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V.1 : 800 agtgtgtgtcggggtaatacaacaaactgtaacaagtgtacctgggtatggacttgttgtc 859
      |||
V.2 : 544 agtgtgtgtcggggtaatacaacaaactgtaacaagtgtacctgggtatggacttgttgtc 603

V.1 : 860 cgggacgtacattttcgcggtcctgctagcatgcgtggtgttccactctggcgcccagga 919
      |||
V.2 : 604 cgggacgtacattttcgcggtcctgctagcatgcgtggtgttccactctggcgcccagga 663

V.1 : 920 gaaaaactacaccatccgagaagaaatgccagaaaacgtcctgataggcgacttgttgaa 979
      |||
V.2 : 664 gaaaaactacaccatccgagaagaaatgccagaaaacgtcctgataggcgacttgttgaa 723

V.1 : 980 agaccttaacttgtcgtgattccaacaagtcttgacaactgctatgcagttcaagct 1039
      |||
V.2 : 724 agaccttaacttgtcgtgattccaacaagtcttgacaactgctatgcagttcaagct 783

V.1 : 1040 agtgtacaagaccggagatgtgccactgattcgaattgaaggatactggtgagatctt 1099
      |||
V.2 : 784 agtgtacaagaccggagatgtgccactgattcgaattgaaggatactggtgagatctt 843

V.1 : 1100 cactactggcgctcgcatgtatcgatgagaaattatgtgctggtatcccaagggatgagca 1159
      |||
V.2 : 844 cactactggcgctcgcatgtatcgatgagaaattatgtgctggtatcccaagggatgagca 903

V.1 : 1160 ttgcttttatgaagtggaggttgccattttgccggatgaaatatttagactggttaagat 1219
      |||
V.2 : 904 ttgcttttatgaagtggaggttgccattttgccggatgaaatatttagactggttaagat 963

V.1 : 1220 acgttttctgatagaagatataaatgataatgcaccattgttcccagcaacagttatcaa 1279
      |||
V.2 : 964 acgttttctgatagaagatataaatgataatgcaccattgttcccagcaacagttatcaa 1023

V.1 : 1280 catatcaattccagagaactcggctataaactctaaatatactctcccagcggtgttga 1339
      |||
V.2 : 1024 catatcaattccagagaactcggctataaactctaaatatactctcccagcggtgttga 1083

V.1 : 1340 tcctgacgtaggaataaacggagttcaaaactacgaactaattaagagtcaaaacatttt 1399
      |||
V.2 : 1084 tcctgacgtaggaataaacggagttcaaaactacgaactaattaagagtcaaaacatttt 1143

V.1 : 1400 tggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgattgttcaaaa 1459
      |||
V.2 : 1144 tggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgattgttcaaaa 1203

V.1 : 1460 ggagttagataggaagagaaggatacctacgtgatgaaagtaaagggtgaagatggtgg 1519
      |||
V.2 : 1204 ggagttagataggaagagaaggatacctacgtgatgaaagtaaagggtgaagatggtgg 1263

V.1 : 1520 ctttcctcaaagatccagtactgctattttgcaagtgagtgttactgatacaaatgacaa 1579
      |||
V.2 : 1264 ctttcctcaaagatccagtactgctattttgcaagtgagtgttactgatacaaatgacaa 1323

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V.1 : 1580 ccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgctcctgtagg 1639
|||||
V.2 : 1324 ccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgctcctgtagg 1383
|||||

V.1 : 1640 cacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgccaagatcca 1699
|||||
V.2 : 1384 cacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgccaagatcca 1443
|||||

V.1 : 1700 cttctctttcagcaatctagctccaacattgccaggagattatttcacctcaatgccac 1759
|||||
V.2 : 1444 cttctctttcagcaatctagctccaacattgccaggagattatttcacctcaatgccac 1503
|||||

V.1 : 1760 cactggacttatcacaatcaaagaaccactggatagggagaacacaccaaaccacaagtt 1819
|||||
V.2 : 1504 cactggacttatcacaatcaaagaaccactggatagggagaacacaccaaaccacaagtt 1563
|||||

V.1 : 1820 actggttttggcaagtgatggtggattgatgccagcaagagcaatggtgctggtaaagt 1879
|||||
V.2 : 1564 actggttttggcaagtgatggtggattgatgccagcaagagcaatggtgctggtaaagt 1623
|||||

V.1 : 1880 tacagatgtcaatgataatgtcccatccattgacataagatacatcgtcaatcctgtcaa 1939
|||||
V.2 : 1624 tacagatgtcaatgataatgtcccatccattgacataagatacatcgtcaatcctgtcaa 1683
|||||

V.1 : 1940 tgacacagttgttctttcagaaaatattccactcaacaccaaattgctctcataactgt 1999
|||||
V.2 : 1684 tgacacagttgttctttcagaaaatattccactcaacaccaaattgctctcataactgt 1743
|||||

V.1 : 2000 gacggataaggatgcggaccataatggcagggtgacatgcttcacagatcatgaaatccc 2059
|||||
V.2 : 1744 gacggataaggatgcggaccataatggcagggtgacatgcttcacagatcatgaaatccc 1803
|||||

V.1 : 2060 tttcagattaaggccagttattcagtaatcagttcctcctggagactgcagcatatcttga 2119
|||||
V.2 : 1804 tttcagattaaggccagttattcagtaatcagttcctcctggagactgcagcatatcttga 1863
|||||

V.1 : 2120 ctatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggcaaacctcc 2179
|||||
V.2 : 1864 ctatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggcaaacctcc 1923
|||||

V.1 : 2180 tttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaatgctccagt 2239
|||||
V.2 : 1924 tttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaatgctccagt 1983
|||||

V.1 : 2240 tttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggcatccagtt 2299
|||||
V.2 : 1984 tttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggcatccagtt 2043
|||||

V.1 : 2300 gacgaaagtaagtgcattggatgcagacagtgaggcctaagtctaagatcaattacctgct 2359
|||||
V.2 : 2044 gacgaaagtaagtgcattggatgcagacagtgaggcctaagtctaagatcaattacctgct 2103
|||||

V.1 : 2360 aggccctgatgctccacctgaattcagcctggattgtcgtagcaggcatgctgactgtagt 2419
|||||
V.2 : 2104 aggccctgatgctccacctgaattcagcctggattgtcgtagcaggcatgctgactgtagt 2163
|||||

V.1 : 2420 gaagaaactagatagagaaaaagaggataaatattttattcacaattctggcaaaagataa 2479
|||||
V.2 : 2164 gaagaaactagatagagaaaaagaggataaatattttattcacaattctggcaaaagataa 2223

V.1 : 2480 cggggtaccacccttaaccagcaatgtcacagtcctttgtaagcattattgatcagaatga 2539
|||||
V.2 : 2224 cggggtaccacccttaaccagcaatgtcacagtcctttgtaagcattattgatcagaatga 2283

V.1 : 2540 caatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaaccttccaag 2599
|||||
V.2 : 2284 caatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaaccttccaag 2343

V.1 : 2600 gcatggtacagtaggactaatcactgtaactgatcctgattatggagacaattctgcagt 2659
|||||
V.2 : 2344 gcatggtacagtaggactaatcactgtaactgatcctgattatggagacaattctgcagt 2403

V.1 : 2660 tacgctctccatttttagatgagaatgatgacttcaccattgattcacaaactggtgtcat 2719
|||||
V.2 : 2404 tacgctctccatttttagatgagaatgatgacttcaccattgattcacaaactggtgtcat 2463

V.1 : 2720 ccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctatgtaaaggc 2779
|||||
V.2 : 2464 ccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctatgtaaaggc 2523

V.1 : 2780 tgaggatggtggttagagtatcacgttcttcaagtgccaaagtaaccataaatgtggttga 2839
|||||
V.2 : 2524 tgaggatggtggttagagtatcacgttcttcaagtgccaaagtaaccataaatgtggttga 2583

V.1 : 2840 tgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttatgaattggt 2899
|||||
V.2 : 2584 tgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttatgaattggt 2643

V.1 : 2900 tctaccgtccactaatccaggcacagtggtctttcaggtaattgctgttgacaatgacac 2959
|||||
V.2 : 2644 tctaccgtccactaatccaggcacagtggtctttcaggtaattgctgttgacaatgacac 2703

V.1 : 2960 tggcatgaatgcagaggttcggttacagcattgtaggaggaacacacagagatctgtttgc 3019
|||||
V.2 : 2704 tggcatgaatgcagaggttcggttacagcattgtaggaggaacacacagagatctgtttgc 2763

V.1 : 3020 aatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttacagaccttg 3079
|||||
V.2 : 2764 aatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttacagaccttg 2823

V.1 : 3080 ttacacagagtgttggtcaaagctaatacttaggacagcctgattctctcttcagtgt 3139
|||||
V.2 : 2824 ttacacagagtgttggtcaaagctaatacttaggacagcctgattctctcttcagtgt 2883

V.1 : 3140 tgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgattaatgaact 3199
|||||
V.2 : 2884 tgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgattaatgaact 2943

V.1 : 3200 ggtgcgcaaaagcactgaagcaccagtgaccccaaatactgagatagctgatgtatcctc 3259
|||||
V.2 : 2944 ggtgcgcaaaagcactgaagcaccagtgaccccaaatactgagatagctgatgtatcctc 3003

V.1 : 3260 accaactagtgtactatgtcaagatcctggttgagctgttgcctggcaccataactgtcgt 3319
 |||
 V.2 : 3004 accaactagtgtactatgtcaagatcctggttgagctgttgcctggcaccataactgtcgt 3063

V.1 : 3320 tgtagttatattcatcactgctgttagtaagatgtcgccaggcaccacacctaaggctgc 3379
 |||
 V.2 : 3064 tgtagttatattcatcactgctgttagtaagatgtcgccaggcaccacacctaaggctgc 3123

V.1 : 3380 tcagaaaaacaagcagaattctgaatgggctaccccaaaccagaaaaacaggcagatgat 3439
 |||
 V.2 : 3124 tcagaaaaacaagcagaattctgaatgggctaccccaaaccagaaaaacaggcagatgat 3183

V.1 : 3440 aatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacttgctgcttaattt 3499
 |||
 V.2 : 3184 aatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacttgctgcttaattt 3243

V.1 : 3500 tgtcactattgaagaaactaaggcagatgatgttgacagtgtggaacagagtcacact 3559
 |||
 V.2 : 3244 tgtcactattgaagaaactaaggcagatgatgttgacagtgtggaacagagtcacact 3303

V.1 : 3560 agaccttcctattgatctagaagagcaacaatgggaaagtacaattgggtaactacacc 3619
 |||
 V.2 : 3304 agaccttcctattgatctagaagagcaacaatgggaaagtacaattgggtaactacacc 3363

V.1 : 3620 tactactttcaagcccgacagccctgatttggcccgacactacaaatctgcctctccaca 3679
 |||
 V.2 : 3364 tactactttcaagcccgacagccctgatttggcccgacactacaaatctgcctctccaca 3423

V.1 : 3680 gcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatcatccaaga 3739
 |||
 V.2 : 3424 gcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatcatccaaga 3483

V.1 : 3740 actgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcctcaagcag 3799
 |||
 V.2 : 3484 actgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcctcaagcag 3543

V.1 : 3800 ttcagatccctacagcggtttctgactgtggctatccagtgacgaccttcgaggtacctgt 3859
 |||
 V.2 : 3544 ttcagatccctacagcggtttctgactgtggctatccagtgacgaccttcgaggtacctgt 3603

V.1 : 3860 gtccgtacacaccagaccg 3878
 |||
 V.2 : 3604 gtccgtacacaccagaccg 3622

Table LIV(a). Peptide sequences of protein coded by 109P1D4 v.2 (SEQ ID NO: 240)

MRTERQWVLI	QIFQVLCGLI	QQTVTSVPGM	DLLSGTYIFA	VLLACVVFHS	GAQEKNYTIR	60
EEMPENVLIG	DLLKDLNLSL	IPNKSLTTAM	QFKLVYKTGD	VPLIRIEEDT	GEIFTTGARI	120
DREKLCAGIP	RDEHCFYEVE	VAILPDEIFR	LVKIRFLIED	INDNAPLFPA	TVINISIPEN	180
SAINSKYTLF	AAVDPDVGIN	GVQNYELIKS	QNIFGLDVIE	TPEGDKMPQL	IVQKELDREE	240
KDITYVMKV	EDGGFPQRSS	TAILQVSVTD	TNDNHPVFKE	TEIEVSIPEN	APVGTSVTQL	300
HATDADIGEN	AKIHFSFSNL	VSNIRRLFH	LNATTGLITI	KEPLDREETP	NHKLVLVLS	360
GGLMPARAMV	LVNVTVDNDN	VPSIDIRYIV	NPVNDTVVLS	ENIPLNTKIA	LITVTDKAD	420
HNGRVTCTFD	HEIPFRLRPV	FSNQFLLETA	AYLDYESTKE	YAIKLLAADA	GKPLNQSAM	480
LFIKVKDEND	NAPVFTQSFV	TVSIPENNSP	GIQLTKVSAM	DADSGPNAKI	NYLLGPDAPP	540
EFSLDCRTGM	LTVVKKLDRE	KEDKYLFTIL	AKDNGVPPLT	SNVTVFVSII	DQNDNSPVFT	600

HNEYNFYVPE	NLPRHGTVGL	ITVTDPDYGD	NSAVTLSILD	ENDDFTIDSQ	TGVIRPNISF	660
DREKQESYTF	YVKAEDGGRV	SRSSSAKVTI	NVVDVNDNKP	VFIVPPSNCS	YELVLPSTNP	720
GTVVVFQVIAV	DNDTGMNAEV	RYSIVGGNTR	DLFAIDQETG	NITLMEKCDV	TDLGLHRVLV	780
KANDLGQPD	LFSVVIVNLF	VNESVTNATL	INELVRKSTE	APVTPNTEIA	DVSSPTS DYV	840
KILVAAGT	ITVVVIFIT	AVVRCRQAPH	LKAAQKNKQN	SEWATPNPEN	RQMIMMKKKK	900
KKKKHSPKNL	LLNFVTIET	KADDVDSGN	RVTLDLPIDL	EEQTMGKYNW	VTTPTTFKPD	960
SPDLARHYKS	ASPQPAFQIQ	PETPLNSKHH	IIQELPLDNT	FVACDSISKC	SSSSSDPYSV	1020
SDCGYPVTTF	EVPVSVHTRP	TDSRTSTIEI	CSEI			1054

Table LV(a). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 241) and 109P1D4 v.2 (SEQ ID NO: 242)
 Score = 2006 bits (5197), Expect = 0.0, Identities = 1012/1017 (99%), Positives = 1013/1017 (99%)

V.1	: 1	MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSITTA	60
V.2	: 30	MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSITTA	89
V.1	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	120
V.2	: 90	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	149
V.1	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.2	: 150	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	209
V.1	: 181	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	240
V.2	: 210	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	269
V.1	: 241	DTNDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFNLVSNIAARRLF	300
V.2	: 270	DTNDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFNLVSNIAARRLF	329
V.1	: 301	HLNATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYI	360
V.2	: 330	HLNATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYI	389
V.1	: 361	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCTDHEIPFRLRPVFSNQFLET	420
V.2	: 390	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCTDHEIPFRLRPVFSNQFLET	449
V.1	: 421	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	480
V.2	: 450	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	509
V.1	: 481	PGIQLTKVSAMDADSGPNAKINYLGPDPAPPEFSLDCRTGMLTVVKKLREKEDKYLFTI	540
V.2	: 510	PGIQLTKVSAMDADSGPNAKINYLGPDPAPPEFSLDCRTGMLTVVKKLREKEDKYLFTI	569
V.1	: 541	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTTHNEYNFYVPENLPRHGTVGLITVTDPDYG	600
V.2	: 570	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTTHNEYNFYVPENLPRHGTVGLITVTDPDYG	629
V.1	: 601	DNSAVTLSILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
V.2	: 630	DNSAVTLSILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	689
V.1	: 661	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNODTGMNAEVRYISIVGGNT	720
V.2	: 690	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNODTGMNAEVRYISIVGGNT	749
V.1	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNAT	780
V.2	: 750	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNAT	809
V.1	: 781	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAGTITVVVIFITAVVRCRQAP	840
V.2	: 810	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAGTITVVVIFITAVVRCRQAP	869

V.1 : 841 HLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNFVTIEETKADDVDSG 900
 HLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNFVTIEETKADDVDSG
 V.2 : 870 HLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNFVTIEETKADDVDSG 929
 HLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNFVTIEETKADDVDSG
 V.1 : 901 NRVTLDLPLDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH 960
 NRVTLDLPLDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH
 V.2 : 930 NRVTLDLPLDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH 989
 NRVTLDLPLDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH
 V.1 : 961 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVFPVSVHTRPVGIQVS 1017
 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVFPVSVHTRP + S
 V.2 : 990 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVFPVSVHTRPTDSRTS 1046
 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVFPVSVHTRPTDSRTS

Table LII(b). Nucleotide sequence of transcript variant 109P1D4 v.3 (SEQ ID NO: 243)

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Table LIII(b). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 244) and 109P1D4 v.3 (SEQ ID NO: 245)
Score = 7456 bits (3878), Expect = 0.0 Identities = 3878/3878 (100%) Strand = Plus / Plus

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V.1 : 1 ctggtgggtccagttacctccaagatatggaatacactcctgaaatatcctgaaaactttt 60
V.3 : 1 ctggtgggtccagttacctccaagatatggaatacactcctgaaatatcctgaaaactttt 60

V.1 : 61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgacttt 120
V.3 : 61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgacttt 120

V.1 : 121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcac 180
V.3 : 121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcac 180

V.1 : 181 atgatagttgttaccatgttttaggcatttagtcacatcaaccctctcctctcccaaactt 240
V.3 : 181 atgatagttgttaccatgttttaggcatttagtcacatcaaccctctcctctcccaaactt 240

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V.3 : 181 atgatatgttgttaccatgttttaggcattagtcacatcaacccctctcctctcccaaactt 240

V.1 : 241 ctcttcttcaaatacaacttttattagtcctctctttataatgattccttgccctcgttta 300
|||||
V.3 : 241 ctcttcttcaaatacaacttttattagtcctctctttataatgattccttgccctcgttta 300

V.1 : 301 tccagatcaatttttttctactttgatgccagagctgaagaaatggactactgtataaa 360
|||||
V.3 : 301 tccagatcaatttttttctactttgatgccagagctgaagaaatggactactgtataaa 360

V.1 : 361 ttattcattgccaaagagaataattgcattttaaacccatattataacaaagaataatgat 420
|||||
V.3 : 361 ttattcattgccaaagagaataattgcattttaaacccatattataacaaagaataatgat 420

V.1 : 421 tataatttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatt 480
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V.3 : 421 tataatttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatt 480

V.1 : 481 ttaattatttgtattctctttaactatcttggtatattaaagtattatcttttatatt 540
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V.3 : 481 ttaattatttgtattctctttaactatcttggtatattaaagtattatcttttatatt 540

V.1 : 541 tatcaatggtggacacttttataggtactctgtgtcattttggatactgtaggtatctta 600
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V.3 : 541 tatcaatggtggacacttttataggtactctgtgtcattttggatactgtaggtatctta 600

V.1 : 601 tttcatttatctttattcttaagtacgaattcataatatttgattcagaacaaatttat 660
|||||
V.3 : 601 tttcatttatctttattcttaagtacgaattcataatatttgattcagaacaaatttat 660

V.1 : 661 cactaattaacagagtgatcaattatgctaacatctcatttactgattttaatttaaaaca 720
|||||
V.3 : 661 cactaattaacagagtgatcaattatgctaacatctcatttactgattttaatttaaaaca 720

V.1 : 721 gtttttgttaacatgcatgtttaggggttggtcttctaataatttcttcttcttctct 780
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V.3 : 721 gtttttgttaacatgcatgtttaggggttggtcttctaataatttcttcttcttctct 780

V.1 : 781 ctctcctcttcttttggtcagtggtgtgcgggttaatacaacaaactgtaacaagtgtac 840
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V.3 : 781 ctctcctcttcttttggtcagtggtgtgcgggttaatacaacaaactgtaacaagtgtac 840

V.1 : 841 ctggtatggacttggtgtccgggacgtacattttcgcggtcctgctagcatgctggtgt 900
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V.3 : 841 ctggtatggacttggtgtccgggacgtacattttcgcggtcctgctagcatgctggtgt 900

V.1 : 901 tccactctggcgccaggagaaaaactacaccatccgagaagaaatgccagaaaacgtcc 960
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V.3 : 901 tccactctggcgccaggagaaaaactacaccatccgagaagaaatgccagaaaacgtcc 960

V.1 : 961 tgataggcgacttggtgaaagaccttaacttgctgctgattccaaacaagtccttgacaa 1020
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V.3 : 961 tgataggcgacttggtgaaagaccttaacttgctgctgattccaaacaagtccttgacaa 1020

V.1 : 1021 ctgctatgcagttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaag 1080

V.3 : 1021 ||| ctgctatgcagttcaagctagtgtagaagaccggagatgtgccactgattcgaattgaag 1080

V.1 : 1081 aggatactggtgagatcttcactactggcgctcgcatcgatcgtagaaaattatgtgctg 1140
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V.3 : 1081 aggatactggtgagatcttcactactggcgctcgcatcgatcgtagaaaattatgtgctg 1140

V.1 : 1141 gtatcccaagggatgagcattgcttttatgaagtggaggttgccattttgccggatgaaa 1200
|||

V.3 : 1141 gtatcccaagggatgagcattgcttttatgaagtggaggttgccattttgccggatgaaa 1200

V.1 : 1201 tatttagactggttaagatacgttttctgatagaagataaaatgataatgcaccattgt 1260
|||

V.3 : 1201 tatttagactggttaagatacgttttctgatagaagataaaatgataatgcaccattgt 1260

V.1 : 1261 tcccagcaacagttatcaacatatcaattccagagaactcggtataaaactctaaatata 1320
|||

V.3 : 1261 tcccagcaacagttatcaacatatcaattccagagaactcggtataaaactctaaatata 1320

V.1 : 1321 ctctcccagcggctgttgatcctgacgttaggaataaacggagttcaaaactacgaactaa 1380
|||

V.3 : 1321 ctctcccagcggctgttgatcctgacgttaggaataaacggagttcaaaactacgaactaa 1380

V.1 : 1381 ttaagagtcaaaacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgc 1440
|||

V.3 : 1381 ttaagagtcaaaacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgc 1440

V.1 : 1441 cacaactgattgttcaaaaggagtttagatagggagaaggatacctacgtgatgaaag 1500
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V.3 : 1441 cacaactgattgttcaaaaggagtttagatagggagaaggatacctacgtgatgaaag 1500

V.1 : 1501 taaaggttgaagatggtggctttcctcaaagatccagtactgctattttgcaagtgaagt 1560
|||

V.3 : 1501 taaaggttgaagatggtggctttcctcaaagatccagtactgctattttgcaagtgaagt 1560

V.1 : 1561 ttactgatacaaatgacaaccaccagtcctttaaggagacagagattgaagtcagtatac 1620
|||

V.3 : 1561 ttactgatacaaatgacaaccaccagtcctttaaggagacagagattgaagtcagtatac 1620

V.1 : 1621 cagaaaatgctcctgtaggcacttcagtgaacagctccatgccacagatgctgacatag 1680
|||

V.3 : 1621 cagaaaatgctcctgtaggcacttcagtgaacagctccatgccacagatgctgacatag 1680

V.1 : 1681 gtgaaaatgccaagatccacttctctttcagcaatctagtctccaacattgccaggagat 1740
|||

V.3 : 1681 gtgaaaatgccaagatccacttctctttcagcaatctagtctccaacattgccaggagat 1740

V.1 : 1741 tatttcacctcaatgccaccactggacttatcacaatcaaagaaccactggatagggaaag 1800
|||

V.3 : 1741 tatttcacctcaatgccaccactggacttatcacaatcaaagaaccactggatagggaaag 1800

V.1 : 1801 aaacaccaaaccacaagttactggttttggcaagtgatggtggattgatgccagcaagag 1860
|||

V.3 : 1801 aaacaccaaaccacaagttactggttttggcaagtgatggtggattgatgccagcaagag 1860

V.1 : 1861 caatggctgctggtaaatgttacagatgtcaatgataatgtcccatccattgacataagat 1920
|||||
V.3 : 1861 caatggctgctggtaaatgttacagatgtcaatgataatgtcccatccattgacataagat 1920

V.1 : 1921 acatcgtcaatcctgtcaatgacacagttgttctttcagaaaaattccactcaacacca 1980
|||||
V.3 : 1921 acatcgtcaatcctgtcaatgacacagttgttctttcagaaaaattccactcaacacca 1980

V.1 : 1981 aaattgctctcataactgtgacggataaggatgcgaccataatggcaggggtgacatgct 2040
|||||
V.3 : 1981 aaattgctctcataactgtgacggataaggatgcgaccataatggcaggggtgacatgct 2040

V.1 : 2041 tcacagatcatgaaatccctttcagattaaggccagttattcagtaatcagttcctcctg 2100
|||||
V.3 : 2041 tcacagatcatgaaatccctttcagattaaggccagttattcagtaatcagttcctcctg 2100

V.1 : 2101 agactgcagcatatcttgactatgagtcacaaaaagaatatgccattaaattactggctg 2160
|||||
V.3 : 2101 agactgcagcatatcttgactatgagtcacaaaaagaatatgccattaaattactggctg 2160

V.1 : 2161 cagatgctggcaaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatg 2220
|||||
V.3 : 2161 cagatgctggcaaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatg 2220

V.1 : 2221 aaaatgacaatgctccagttttcaccagtccttcgtaactgtttctattcctgagaata 2280
|||||
V.3 : 2221 aaaatgacaatgctccagttttcaccagtccttcgtaactgtttctattcctgagaata 2280

V.1 : 2281 actctcctggcatccagttgacgaaagtaagtgaatggatgcagacagtgggcctaag 2340
|||||
V.3 : 2281 actctcctggcatccagttgacgaaagtaagtgaatggatgcagacagtgggcctaag 2340

V.1 : 2341 ctaagatcaattacctgctagggcctgatgctccacctgaattcagcctggattgtcgta 2400
|||||
V.3 : 2341 ctaagatcaattacctgctagggcctgatgctccacctgaattcagcctggattgtcgta 2400

V.1 : 2401 caggcatgctgactgtagtgaagaaactagatagagaaaaaggagataaatatttattca 2460
|||||
V.3 : 2401 caggcatgctgactgtagtgaagaaactagatagagaaaaaggagataaatatttattca 2460

V.1 : 2461 caattctggcaaaagataacggggtaccacccttaaccagcaatgtcacagtctttgtaa 2520
|||||
V.3 : 2461 caattctggcaaaagataacggggtaccacccttaaccagcaatgtcacagtctttgtaa 2520

V.1 : 2521 gcattattgatcagaatgacaatagcccagttttcactcacaatgaatacaacttctatg 2580
|||||
V.3 : 2521 gcattattgatcagaatgacaatagcccagttttcactcacaatgaatacaacttctatg 2580

V.1 : 2581 tcccagaaaaccttccaaggcatggtacagtaggactaatcactgtaactgatcctgatt 2640
|||||
V.3 : 2581 tcccagaaaaccttccaaggcatggtacagtaggactaatcactgtaactgatcctgatt 2640

V.1 : 2641 atggagacaattctgcagttacgctctccatttttagatgagaatgatgacttcaccattg 2700
|||||
V.3 : 2641 atggagacaattctgcagttacgctctccatttttagatgagaatgatgacttcaccattg 2700

V.1 : 2701 attcacaactggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatctt 2760
|||||
V.3 : 2701 attcacaactggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatctt 2760
|||||

V.1 : 2761 acacttttctatgtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaag 2820
|||||
V.3 : 2761 acacttttctatgtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaag 2820
|||||

V.1 : 2821 taaccataaatgtggttgatgtcaatgacaacaaccagttttcattgtccctccttcca 2880
|||||
V.3 : 2821 taaccataaatgtggttgatgtcaatgacaacaaccagttttcattgtccctccttcca 2880
|||||

V.1 : 2881 actgttcttatgaattggttctaccgtccactaatccaggcacagtggctcttccaggtaa 2940
|||||
V.3 : 2881 actgttcttatgaattggttctaccgtccactaatccaggcacagtggctcttccaggtaa 2940
|||||

V.1 : 2941 ttgctgttgacaatgacactggcatgaatgcagagggttcgttacagcattgtagaggaa 3000
|||||
V.3 : 2941 ttgctgttgacaatgacactggcatgaatgcagagggttcgttacagcattgtagaggaa 3000
|||||

V.1 : 3001 acacaagagatctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaat 3060
|||||
V.3 : 3001 acacaagagatctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaat 3060
|||||

V.1 : 3061 gtgatgttacagaccttggtttacacagagtgttggtcaaagctaatacttaggacagc 3120
|||||
V.3 : 3061 gtgatgttacagaccttggtttacacagagtgttggtcaaagctaatacttaggacagc 3120
|||||

V.1 : 3121 ctgattctctcttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatg 3180
|||||
V.3 : 3121 ctgattctctcttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatg 3180
|||||

V.1 : 3181 ctacactgattaatgaactggtgcgcaaaagcactgaagcaccagtgaccccaaatactg 3240
|||||
V.3 : 3181 ctacactgattaatgaactggtgcgcaaaagcactgaagcaccagtgaccccaaatactg 3240
|||||

V.1 : 3241 agatagctgatgtatcctcaccaactagtactatgtcaagatcctggttcagctgttg 3300
|||||
V.3 : 3241 agatagctgatgtatcctcaccaactagtactatgtcaagatcctggttcagctgttg 3300
|||||

V.1 : 3301 ctggcaccataactgtcgtttagttattttcatcactgctgtagtaagatgtcgccagg 3360
|||||
V.3 : 3301 ctggcaccataactgtcgtttagttattttcatcactgctgtagtaagatgtcgccagg 3360
|||||

V.1 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420
|||||
V.3 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420
|||||

V.1 : 3421 cagaaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480
|||||
V.3 : 3421 cagaaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480
|||||

V.1 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagtg 3540
|||||
V.3 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagtg 3540
|||||

v.1 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaaacatgggaaagt 3600
 ||||||||||||||||||
 v.3 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaaacatgggaaagt 3600

 v.1 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttgcccgacact 3660
 ||||||||||||||||||
 v.3 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttgcccgacact 3660

 v.1 : 3661 acaaatctgcctctccacagcctgccttccaaattcagcctgaaactcccctgaattcga 3720
 ||||||||||||||||||
 v.3 : 3661 acaaatctgcctctccacagcctgccttccaaattcagcctgaaactcccctgaattcga 3720

 v.1 : 3721 agcaccacatcatccaagaactgcctctcgataacaccttctgtggcctgtgactctatct 3780
 ||||||||||||||||||
 v.3 : 3721 agcaccacatcatccaagaactgcctctcgataacaccttctgtggcctgtgactctatct 3780

 v.1 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840
 ||||||||||||||||||
 v.3 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840

 v.1 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878
 ||||||||||||||||||
 v.3 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878

Table LIV(b). Peptide sequences of protein coded by 109P1D4 v.3 (SEQ ID NO: 246)

MDLLSGTYIF	AVLLACVVFH	SGAQEKNYTI	REEMPENVLI	GDLLKDLNLS	LIPNKSLLTA	60
MQFKLVYKTG	DVPLIRIEED	TGEIFTTGAR	IDREKLCAGI	PRDEHCFYEV	EVAILPDEIF	120
RLVKIRFLIE	DINDNAPLFP	ATVINISIPE	NSAINSKYTL	PAAVDPDVGI	NGVQNYELIK	180
SQNI FGLDVI	ETPEGDKMPQ	LIVQKELDRE	EKDTYVMKVK	VEDGGFPQRS	STAILQVSVT	240
DTNDNHPVFK	ETEIEVSIPE	NAPVGTSVTQ	LHATDADIGE	NAKIHFSFSN	LVSNIARRLF	300
HLNATTGLIT	IKEPLDREET	PNHKLLVLAS	DGGLMPARAM	VLNVNVDVND	NVPSIDIRYI	360
VNPVNDTVVL	SENIPLNTKI	ALITVTDKDA	DHNGRVTCT	DHEIPFRLRP	VFSNQFLLET	420
AAYLDYESTK	EYAIKLLAAD	AGKPPLNQSA	MLFIKVKDEN	DNAPVFTQSF	VTVSIPENNS	480
PGIQLTKVSA	MDADSGPNAK	INYLLGPDAP	PEFSLDCRTG	MLTVVKKLDR	EKEDKYLFTI	540
LAKDNGVPPL	TSNVTVFVSI	IDQNDNSPVF	THNEYNFYVP	ENLPRHGTVG	LITVTPDPYG	600
DNSAVTSLIL	DENDFTIDS	QTGVIRPNIS	FDREKQESYT	FYVKAEDGGR	VSRSSSAKVT	660
INVVDVNDNK	PVFIVPPSNC	SYELVLPSTN	PGTVVFQVIA	VDNDTGMNAE	VRYISVGGNT	720
RDLFAIDQET	GNITLMEKCD	VTDLGLHRLV	VKANDLGQPD	SLFSVIVNL	FVNESVTNAT	780
LINELVRKST	EAPVTPNTEI	ADVSSPTS DY	KKILVA AVAG	TITVVVVFIF	TAVVRCRQAP	840
HLKAAQKNKQ	NSEWATPNPE	NRQMIMMKKK	KKKKKHSPKN	LLLNFTVIEE	TKADDVDS DG	900
NRVTLDLPID	LEEQTMGKYN	WVTTPTFKFP	DSPDLARHYK	SASPQAFQI	QPETPLNSKH	960
HIIQELPLDN	TFVACDSISK	CSSSSSDPYS	VSDCGYPVTT	FEVPVSVHTR	PPMKEVVRSC	1020
TPMKESTTME	IWIHPQPQRK	SEKVVAGKSQ	RRVTFHLPEG	SQESSSDGGL	GDHDAGSLTS	1080
TSHGLPLGYP	QEEYFDRATP	SNRTEGDGNS	DPESTFIPGL	KKAAEITVQP	TVEEASDNCT	1140
QECLIYGHSD	ACWMPASLDH	SSSSQAQASA	LCHSPPLSQA	STQHHSERV	QTIALCHSPP	1200
VTQTIALCHS	PPPIQVSALH	HSPPLVQATA	LHHSPPSAQA	SALCYSPPLA	QAAAISHSSP	1260
LPQVIALHRS	QAQSSVSLQQ	GWVQGADGLC	SVDQGVQGSA	TSQFYTM SER	LHPSDDSIKV	1320
IPLTTFTPRQ	QARPSRGDSP	IMEEHPL				1347

Table LV(b). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 247) and 109P1D4 v.3 (SEQ ID NO: 248)
 Score = 2005 bits (5195), Expect = 0.0Identities = 1011/1011 (100%), Positives = 1011/1011 (100%)

v.1 : 1 MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA 60
 MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA
 v.3 : 1 MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA 60

 v.1 : 61 MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVAILPDEIF 120

V.3	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	120
V.1	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.3	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.1	: 181	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	240
V.3	: 181	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	240
V.1	: 241	DTNDNHPVFKETEIEVSI PENAPVGT SVTQLHATDADIGENAKIHFSFSLVSNIAARRLF	300
V.3	: 241	DTNDNHPVFKETEIEVSI PENAPVGT SVTQLHATDADIGENAKIHFSFSLVSNIAARRLF	300
V.1	: 301	HLNATTGLITIKEPLDREETPNHKLLVLASDGGLMPARAMVLNVTDVNDNVPSIDIRYI	360
V.3	: 301	HLNATTGLITIKEPLDREETPNHKLLVLASDGGLMPARAMVLNVTDVNDNVPSIDIRYI	360
V.1	: 361	VNPNVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLEET	420
V.3	: 361	VNPNVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLEET	420
V.1	: 421	AAYLDYESTKEYAIKLLAADAGKPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	480
V.3	: 421	AAYLDYESTKEYAIKLLAADAGKPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	480
V.1	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540
V.3	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540
V.1	: 541	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPPDYG	600
V.3	: 541	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPPDYG	600
V.1	: 601	DNSAVTLSILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
V.3	: 601	DNSAVTLSILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
V.1	: 661	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT	720
V.3	: 661	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT	720
V.1	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFSVVIIVNLFVNESVTNAT	780
V.3	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFSVVIIVNLFVNESVTNAT	780
V.1	: 781	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVVFITAVVRCRQAP	840
V.3	: 781	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVVFITAVVRCRQAP	840
V.1	: 841	HLKAAQKNKQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIEETKADDVDSG	900

Table LII(c). Nucleotide sequence of transcript variant 109P1D4 v.4 (SEQ ID NO: 249)

ctgggtggtcc	agtacctcca	aagatatgga	atacactcct	gaaatatacct	gaaaaactttt	60
ttttttcaga	atcctttaat	aagcagttat	gtcaatctga	aagttgctta	cttgactttt	120
atattaatag	ctattcttgt	ttttcttatc	caaagaaaaa	tcctctaata	cccttttcac	180
atgatagttg	ttaccatgtt	taggcattag	tcacatcaac	ccctctcctc	tcccaaactt	240
ctcttcttca	aatcaaactt	tattagttccc	tcctttataa	tgattccttg	cctcgtttta	300
tccagatcaa	ttttttttca	ctttgatgcc	cagagctgaa	gaaatggact	actgtataaa	360
ttattcattg	ccaagagaat	aattgcattt	taaaccata	ttataacaaa	gaataatgat	420
tatatattgt	gatttgaac	aaataccctt	tattttccct	taactattga	attaaatatt	480
ttaattattt	gtattctctt	taactatctt	ggatatatta	agtattatct	tttatatatt	540
tatcaatggt	ggacactttt	ataggtactc	tgtgtcattt	ttgatactgt	aggtatctta	600
tttcatttat	ctttattctt	aatgtacgaa	ttcataatat	ttgattcaga	acaaatttat	660
cactaattaa	cagagtgtca	attatgctaa	catctcattt	actgatttta	atttaaaaca	720
gtttttgtta	acatgcatgt	ttagggttgg	cttcttaata	atttcttctt	cctcttctct	780

ctctcctctt	cttttggtca	gtgttggtcg	ggtaataaca	acaaactgta	acaagtgtac	840
ctgggtatgga	cttgttggtcc	gggacgtaca	ttttcgcggt	cctgctagca	tgcgtgggtgt	900
tccactctgg	cgcccaggag	aaaaactaca	ccatccgaga	agaaatgcc	gaaaacgtcc	960
tgataggcga	cttgttgaaa	gaccttaact	tgtcgctgat	tccaaacaag	tccttgacaa	1020
ctgctatgca	gttcaagcta	gtgtacaaga	ccggagatgt	gccactgatt	cgaattgaag	1080
aggatactgg	tgagatcttc	actactggcg	ctcgcatgga	tcgtgagaaa	ttatgtgctg	1140
gtatcccaag	ggatgagcat	tgcttttatg	aagtggaggt	tgccattttg	ccggatgaaa	1200
tatttagact	ggtaagata	cgttttctga	tagaagatat	aaatgataat	gcaccattgt	1260
tcccagcaac	agttatcaac	atatcaattc	cagagaactc	ggctataaac	tctaaatata	1320
ctctcccagc	ggctgttgat	cctgacgtag	gaataaacgg	agttcaaaac	tacgaactaa	1380
ttaagagtca	aaacattttt	ggcctcgatg	tcattgaaac	accagaagga	gacaagatgc	1440
cacaactgat	tgttcaaaa	gagttagata	gggaagagaa	ggatacctac	gtgatgaaag	1500
taaaggttga	agtggtggc	tttctcaaaa	gattccagtag	tgctattttg	caagtgaagt	1560
ttactgatac	aaatgacaac	caccagtcct	ttaaggagac	agagattgaa	gtcagtatac	1620
cagaaaatgc	tcctgtaggc	acttcagtg	cacagctcca	tgccacagat	gctgacatag	1680
gtgaaaatgc	caagatccac	ttctctttca	gcaatctagt	ctccaacatt	gccaggagat	1740
tatttcacct	caatgccacc	actggactta	tcacaatcaa	agaaccactg	gatagggaag	1800
aaacacccaaa	ccacaagtta	ctgggttttg	caagtgtagg	tggtattgatg	ccagcaagag	1860
caatgggtgt	ggttaaatgtt	acagatgtca	atgataatgt	cccatccatt	gacataagat	1920
acatcggtcaa	tcctgtcaat	gacacagttg	ttctttcaga	aaatattcca	ctcaacacca	1980
aaattgctct	cataactgtg	acggataagg	atgctggacca	taatggcagg	gtgacatgct	2040
tcacagatca	tgaatccct	ttcagattaa	ggccagtagt	cagtaatcag	ttctcctgg	2100
agactgcagc	atatcttgac	tatgagttca	caaaagaata	tgccattaaa	ttactggctg	2160
cagatgctgg	caaacctcct	ttgaatcagt	cagcaatgct	cttcatcaaa	gtgaaagatg	2220
aaaaagacaa	tgctccagtt	ttcaccaggt	ttctcgtaac	tgtttctatt	cctgagaata	2280
actctcctgg	catccagttg	acgaaagtta	gtgcaatgga	tgacagacgt	gggcctaattg	2340
ctaaagatcaa	ttacctgcta	ggcctgatg	ctccacctga	attcagcctg	gattgtcgtta	2400
caggcatgct	gactgtagtg	aagaaactag	atagagaaaa	agaggataaa	tatttattca	2460
caattctggc	aaaagataac	gggtaccac	ccttaaccag	caatgtcaca	gtctttgtaa	2520
gcattattga	tcagaatgac	aatagcccag	ttttcactca	caatgaatac	aacttctatg	2580
tcccagaaaa	ccttccaagg	catggtagac	taggactaat	cactgtaact	gatcctgatt	2640
atggagacaa	ttctgcagtt	acgctctcca	ttttagatga	gaatgatgac	ttcaccattg	2700
attcacaaaac	tggtgtcatc	cgaccaaata	tttcatttga	tagagaaaaa	caagaatctt	2760
acactttcta	tgtaaaggct	gaggatgggt	gtagagtatc	acgttcttca	agtgccaaaag	2820
taaccataaa	tgtggttgat	gtcaatgaca	acaaaccagt	tttcattgtc	cctccttcca	2880
actgttctta	tgaattggtt	ctaccgtcca	ctaatccagg	cacagtggtc	tttcaggtaa	2940
ttgctgttga	caatgacact	ggcatgaatg	cagaggttcg	ttacagcatt	gtaggaggaa	3000
acacaagaga	tctgtttgca	atcgaccaag	aaacaggcaa	cataacattg	atggagaaat	3060
gtgatgttac	agaccttggt	ttacacagag	tggttggtcaa	agctaattgac	ttaggacagc	3120
ctgattctct	cttcagtgtt	gtaattgtca	atctgttcgt	gaatgagtcg	gtgaccaatg	3180
ctacactgat	taatgaactg	gtgcgcaaaa	gcactgaagc	accagtgacc	ccaaatactg	3240
agatagctga	tgtatcctca	ccaactagtg	actatgtcaa	gatcctgggt	gcagctgttg	3300
ctggcaccat	aactgtcgtt	gtagttattt	tcactactgc	tgtagtaaga	tgctgccagg	3360
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Table LIII(c). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 250) and 109P1D4 v.4 (SEQ ID NO: 251)
Score = 7456 bits (3878), Expect = 0.0Identities = 3878/3878 (100%) Strand = Plus / Plus

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V.4 : 1 ctgggtggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttt 60

V.1 : 61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtacttt 120
||||| 120
V.4 : 61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtacttt 120

V.1 : 121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcac 180
||||| 180
V.4 : 121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcac 180

V.1 : 181 atgatagttgttaccatgttttaggcattagtcacatcaacccctctcctctccaaactt 240
||||| 240
V.4 : 181 atgatagttgttaccatgttttaggcattagtcacatcaacccctctcctctccaaactt 240

V.1 : 241 ctcttcttcaaatcaaaactttattagtcctcctttataatgattccttgccctcgtttta 300
||||| 300
V.4 : 241 ctcttcttcaaatcaaaactttattagtcctcctttataatgattccttgccctcgtttta 300

V.1 : 301 tccagatcaatttttttctactttgatgccagagctgaagaaatggactactgtataaa 360
||||| 360
V.4 : 301 tccagatcaatttttttctactttgatgccagagctgaagaaatggactactgtataaa 360

V.1 : 361 ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat 420
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V.4 : 361 ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat 420

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V.4 : 421 tatattttgtgatttgtaacaaataccctttattttcccttaactattgaattaaatatt 480

V.1 : 481 ttaattatttgtattctctttaactatcttgggtatattaagattatcttttatatt 540
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V.4 : 481 ttaattatttgtattctctttaactatcttgggtatattaagattatcttttatatt 540

V.1 : 541 tatcaatgggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta 600
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V.4 : 541 tatcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta 600

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V.4 : 601 tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat 660

V.1 : 661 cactaattaacagagtgtcaattatgctaactctcatttactgattttaatttaaaca 720
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V.4 : 661 cactaattaacagagtgtcaattatgctaactctcatttactgattttaatttaaaca 720

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V.4 : 721 gtttttgtaacatgcatgtttaggggtggcttcttaataatttcttctcctcttctct 780

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V.4 : 781 ctctcctcttcttttggtcagtggtgtgctgggttaatacaacaaactgtaacaagtgtac 840

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V.4 : 961 tgataggcgacttgttgaaagaccttaacttgcgctgattccaacaagtccttgacaa 1020

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V.4 : 1021 ctgctatgcagttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaag 1080

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V.4 : 1081 aggatactggtgagatcttactactggcgctcgcatgtatcgtagagaaattatgtgctg 1140

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V.4 : 1141 gtatcccaagggatgagcattgcttttatgaagtggaggttgccattttgccggatgaaa 1200

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V.4 : 1201 tatttagactgggttaagatacgttttctgatagaagatataaatgataatgcaccattgt 1260

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V.4 : 1261 tcccgacaacagttatcaacatatcaattccagagaactcggtataaaactctaataata 1320

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V.4 : 1321 ctctcccagcggtgttgatcctgacgttaggaataaacggagttcaaaactacgaactaa 1380

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V.4 : 1381 ttaagagtcaaaacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgc 1440
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V.4 : 1441 cacaactgattgttcaaaaggagttagataggggaagagaaggatacctacgtgatgaaag 1500
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V.4 : 1801 aaacaccaaaccacaaagttactggttttggcaagtgatgggtgattgatgccagcaagag 1860
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V.1 : 3001 acacaagagatctgtttgcaatcgaccaagaaacaggcaacataacattgatggagaaat 3060
|||||
V.4 : 3001 acacaagagatctgtttgcaatcgaccaagaaacaggcaacataacattgatggagaaat 3060
|||||

V.1 : 3061 gtgatgttacagaccttggtttacacagagtgttggtcaaagctaattgacttaggacagc 3120
|||||
V.4 : 3061 gtgatgttacagaccttggtttacacagagtgttggtcaaagctaattgacttaggacagc 3120

V.1 : 3121 ctgattctctcttcagtggttgaattgtcaatctgttcgtgaatgagtcggtgaccaatg 3180
|||||
V.4 : 3121 ctgattctctcttcagtggttgaattgtcaatctgttcgtgaatgagtcggtgaccaatg 3180

V.1 : 3181 ctacactgattaatgaactggcgcaaaagcactgaagcaccagtgaccccaaatactg 3240
|||||
V.4 : 3181 ctacactgattaatgaactggcgcaaaagcactgaagcaccagtgaccccaaatactg 3240

V.1 : 3241 agatagctgatgtatcctcaccaactagtgactatgtcaagatcctggttgacagctgttg 3300
|||||
V.4 : 3241 agatagctgatgtatcctcaccaactagtgactatgtcaagatcctggttgacagctgttg 3300

V.1 : 3301 ctggcaccataactgtcgtttagttattttcatcactgctgtagtaagatgtcgccagg 3360
|||||
V.4 : 3301 ctggcaccataactgtcgtttagttattttcatcactgctgtagtaagatgtcgccagg 3360

V.1 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420
|||||
V.4 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420

V.1 : 3421 cagaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480
|||||
V.4 : 3421 cagaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480

V.1 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagtg 3540
|||||
V.4 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagtg 3540

V.1 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaaacaatgggaaagt 3600
|||||
V.4 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaaacaatgggaaagt 3600

V.1 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttggcccgacact 3660
|||||
V.4 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttggcccgacact 3660

V.1 : 3661 acaaactctgcctctccacagcctgccttcctcaaatcagcctgaaactcccctgaattcga 3720
|||||
V.4 : 3661 acaaactctgcctctccacagcctgccttcctcaaatcagcctgaaactcccctgaattcga 3720

V.1 : 3721 agcaccacatcatccaagaactgcctctcgataaacacctttgtggcctgtgactctatct 3780
|||||
V.4 : 3721 agcaccacatcatccaagaactgcctctcgataaacacctttgtggcctgtgactctatct 3780

V.1 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840
|||||
V.4 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840

V.1 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878
|||||
V.4 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878

Table LIV(c). Peptide sequences of protein coded by 109P1D4 v.4 (SEQ ID NO: 252)

MDLLSGTYIF	AVLLACVVFH	SGAQEKNTYI	REEMPENVLI	GDLLKDLNLS	LIPNKSLTTA	60
MQFKLVYKTG	DVPLIRIEED	TGEIFTTGAR	IDREKLCAGI	PRDEHCFYEV	EVAILPDEIF	120
RLVKIRFLIE	DINDNAPLFP	ATVINISIPE	NSAINSKYTL	PAAVDPDVGI	NGVQNYELIK	180
SQNIFGLDVI	ETPEGDKMPQ	LIVQKELDRE	EKDTYVMKVK	VEDGGFPQRS	STAILQVSVT	240
DTNDNHPVFK	ETEIEVSIPE	NAPVGTSVTQ	LHATDADIGE	NAKIHFSFSN	LVSNIARRLF	300
HLNATTGLIT	IKEPLDREET	PNHKLLVLAS	DGGLMPARAM	VLNVNVDVND	NVPSIDIRYI	360
VNPVNDTVVL	SENIPLNTKI	ALITVTDKDA	DHNGRVTCFT	DHEIPFRLRP	VFSNQFLEET	420
AAYLDYESTK	EYAIKLLAAD	AGKPPLNQSA	MLFIKVKDEN	DNAPVFTQSF	VTVSIPENNS	480
PGIQLTKVSA	MDADSGPNAK	INYLLGPDAP	PEFSLDCRTG	MLTVVKKLDL	EKEDKYLFTI	540
LAKDNGVPP	TSNVTVFVSI	IDQNDNSPVF	THNEYNFYVP	ENLPRHGTVG	LITVTDPDYG	600
DNSAVTLSIL	DENDDFTIDS	QTGVIRPNIS	FDREKQESYT	FYVKAEDGGR	VSRSSSAKVT	660
INVVDVNDNK	PVFIVPPSNC	SYELVLPSTN	PGTVVFQVIA	VDNDTGMNAE	VRYSIVGGNT	720
RDLFAIDQET	GNITLMEKCD	VTDLGLHRVL	VKANDLGQPD	SLFSVVIVNL	FVNESVTNAT	780
LINELVRKST	EAPVTPNTEI	ADVSSPTSDY	VKILVAAVAG	TITVVVVIFI	TAVVRCRQAP	840
HLKAAQKNKQ	NSEWATPNPE	NRQMIMMKKK	KKKKKHSPKN	LLLNFVTIEE	TKADDVDSOG	900
NRVTLDLPID	LEEQTMGKYN	WVTPTTFEKP	DSPDLARHYK	SASPQPAFQI	QPETPLNSKH	960
HIIQELPLDN	TFVACDSISK	CSSSSSDPYS	VSDCGYPVTT	FEVPVSVHTR	PPMKEVVRSK	1020
TPMKESTTME	IWIHPQPQSQ	RRVTFHLPEG	SQESSSDGGL	GDHDAGSLTS	TSHGLPLGYP	1080
QEEYFDRATP	SNRTEGDGNS	DPESTFIPGL	KKAAEITVQP	TVEEASDNCT	QECLIIYGHSD	1140
ACWMPASLDH	SSSSQAQASA	LCHSPPLSQA	STQHHSRVRT	QTIALCHSPP	VTQTIALCHS	1200
PPPIQVSALH	HSPPLVQATA	LHHSPPSAQA	SALCYSPLPA	QAAAISHSSP	LPQVIALHRS	1260
QAQSSVSLQQ	GWVQGADGLC	SVDQGVQGSA	TSQFYTMSEK	LHPSDDSIKV	IPLTFTTPRQ	1320
QARPSRGDSP	IMEEHPL					1337

Table LV(c). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 253) and 109P1D4 v.4 (SEQ ID NO: 254)
Score = 2005 bits (5195), Expect = 0.0Identities = 1011/1011 (100%), Positives = 1011/1011 (100%)

V.1	: 1	MDLLSGTYIFAVLLACVVFHSGAQEKNTYIREEMPENVLIGDLLKDLNLSLIPNKSLTTA	60
V.4	: 1	MDLLSGTYIFAVLLACVVFHSGAQEKNTYIREEMPENVLIGDLLKDLNLSLIPNKSLTTA	60
V.1	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVVEVAILPDEIF	120
V.4	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVVEVAILPDEIF	120
V.1	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.4	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.1	: 181	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVKVEDGGFPQRSSTAILQVSVT	240
V.4	: 181	SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVKVEDGGFPQRSSTAILQVSVT	240
V.1	: 241	DTNDNHPVFKETEIEVSIPEAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIARRLF	300
V.4	: 241	DTNDNHPVFKETEIEVSIPEAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIARRLF	300
V.1	: 301	HLNATTGLITIKEPLDREETPNHKLLVLASDGGLMPARAMVLNVNVDVNDNVPSIDIRYI	360
V.4	: 301	HLNATTGLITIKEPLDREETPNHKLLVLASDGGLMPARAMVLNVNVDVNDNVPSIDIRYI	360
V.1	: 361	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLEET	420
V.4	: 361	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLEET	420
V.1	: 421	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFVTVSIPENNS	480
V.4	: 421	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFVTVSIPENNS	480
V.1	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540
V.4	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540

V.4	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLEFTI	540
V.1	: 541	LAKDNGVPPLTSNVTVEFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	600
		LAKDNGVPPLTSNVTVEFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	
V.4	: 541	LAKDNGVPPLTSNVTVEFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	600
V.1	: 601	DNSAVTLSILDENDDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
		DNSAVTLSILDENDDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	
V.4	: 601	DNSAVTLSILDENDDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
V.1	: 661	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNT	720
		INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNT	
V.4	: 661	INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNT	720
V.1	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNAT	780
		RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNAT	
V.4	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNAT	780
V.1	: 781	LINELVRKSTEAPVTPNTEIADVSSPTSVDYVKILVAAGTITVTVVIFITAVVRCRQAP	840
		LINELVRKSTEAPVTPNTEIADVSSPTSVDYVKILVAAGTITVTVVIFITAVVRCRQAP	
V.4	: 781	LINELVRKSTEAPVTPNTEIADVSSPTSVDYVKILVAAGTITVTVVIFITAVVRCRQAP	840
V.1	: 841	HLKAAQKNKQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIETKADDVDSGD	900
		HLKAAQKNKQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIETKADDVDSGD	
V.4	: 841	HLKAAQKNKQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIETKADDVDSGD	900
V.1	: 901	NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH	960
		NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH	
V.4	: 901	NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH	960
V.1	: 961	HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP	1011
		HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP	
V.4	: 961	HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP	1011

Table LII(d). Nucleotide sequence of transcript variant 109P1D4 v.5 (SEQ ID NO: 255)

ctggtggtcc	agtaacctcca	aagatatgga	atacactcct	gaaatatacct	gaaaactttt	60
ttttttcaga	atcctttaat	aagcagttat	gtcaatctga	aagttgctta	cttgtaacttt	120
atattaatag	ctattcttgt	ttttcttatac	caaagaaaaa	tcctctaatac	cccttttcac	180
atgatagttg	ttacatggt	taggcattag	tcacatcaac	ccctctcctc	tcccaaaact	240
ctcttcttca	aatcaaaact	tattagtcct	tcctttataa	tgattccttg	cctcggttta	300
tccagatcaa	ttttttttca	ctttgatgcc	cagagctgaa	gaaatggact	actgtataaa	360
ttattcattg	ccaagagaat	aattgcattt	taaaccata	ttataacaaa	gaataatgat	420
tatatattgt	gatttgtaac	aaataccctt	tattttccct	taactattga	attaaatatt	480
ttaattattt	gtattctctt	taactatctt	ggtatattaa	agtattatct	tttatatatt	540
tatcaatggt	ggacactttt	ataggtactc	tgtgtcattt	ttgatactgt	aggatctta	600
tttcattttat	ctttattctt	aatgtacgaa	ttcataatat	ttgattcaga	acaaatttat	660
cactaattaa	acagtggtca	attatgctaa	catctcattt	actgatttta	atttaaaaca	720
gtttttgtta	acatgcatgt	ttaggggttg	cttcttaata	atttcttctt	cctcttctct	780
ctctcctctt	cttttggtca	gtgttggtcg	ggtaataaca	acaaactgta	acaagtgtac	840
ctggtatgga	cttggtgtcc	gggacgtaca	tttctcggtt	cctgctagca	tgctgtggtg	900
tccactctgg	cgcccaggag	aaaaactaca	ccatccgaga	agaaatgcca	gaaaacgtcc	960
tgataggcga	cttggtgaaa	gaccttaact	tgctcgctgat	tccaaacaag	tccttgacaa	1020
ctgctatgca	gttcaagcta	gtgtacaaga	ccggagatgt	gccactgatt	cgaattgaag	1080
aggatactgg	tgagatcttc	actactggcg	ctcgcatgta	tcgtgagaaa	ttatgtgctg	1140
gtatcccaag	ggatgagcat	tgcttttatg	aagtggaggt	tgccattttg	ccggatgaaa	1200
tatttagact	ggttaagata	cgttttctga	tagaagatat	aaatgataat	gcaccattgt	1260
tcccagcaac	agttatcaac	atatcaattc	cagagaactc	ggctataaac	tctaaatata	1320
ctctcccagc	ggctgttgat	cctgacgtag	gaataaacgg	agttcaaaaac	tacgaactaa	1380
ttaagagtca	aaacattttt	ggcctcgatg	tcattgaaac	accagaagga	gacaagatgc	1440
cacaactgat	gtttcaaaaag	gagttagata	gggaagagaa	ggatacctac	gtgatgaaag	1500
taaagggtga	agatggtggc	tttctcaaaa	gatccagtac	tgctattttg	caagtgagtg	1560
ttactgatac	aaatgacaac	cacccagtct	ttaaggagac	agagattgaa	gtcagtatac	1620
cagaaaatgc	tcctgtaggc	acttcagtga	cacagctcca	tgccacagat	gctgacatag	1680
gtgaaaatgc	caagatccac	ttctctttca	gcaatctagt	ctccaacatt	gccaggagat	1740
tatttcacct	caatgccacc	actggactta	tcacaatcaa	agaaccactg	gatagggaag	1800

aaacacccaaa	ccacaagtta	ctgggttttgg	caagtgatgg	tggattgatg	ccagcaagag	1860
caatgggtgct	ggtaaagtgt	acagatgtca	atgataatgt	cccatccatt	gacataagat	1920
acatcgtaaa	tcctgtcaat	gacacagttg	ttctttcaga	aaatattcca	ctcaacacca	1980
aaattgctct	cataactgtg	acggataagg	atgcggacca	taatggcagg	gtgacatgct	2040
tcacagatca	tgaatccct	ttcagattaa	ggccagtatt	cagtaatcag	ttcctcctgg	2100
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cagatgtgg	caaacctcct	ttgaatcagt	cagcaatgct	cttcatcaaa	gtgaaagatg	2220
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gcattattga	tcagaatgac	aatagcccag	ttttcactca	caatgaatac	aacttctatg	2580
tcccagaaaa	ccttccaagg	catggtacag	taggactaat	cactgtaact	gatcctgatt	2640
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acactttcta	tgtaaaggct	gaggatgggtg	gtagagtatc	acgttcttca	agtgccaaag	2820
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ctggcaccat	aactgtcgtt	gtagtatttt	tcatactctg	tgtagttaaga	tgtcgccagg	3360
caccacacct	taaggctgct	cagaaaaaca	agcagaattc	tgaatgggct	accccaaac	3420
cagaaaacag	gcagatgata	atgatgaaga	aaaagaaaaa	gaagaagaag	cattccccta	3480
agaacttgct	gcttaatttt	gtcactattg	aagaaactaa	ggcagatgat	gttgacagtg	3540
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acaattgggt	aactacacct	actactttca	agcccgacag	ccctgatttg	gcccgcact	3660
acaaatctgc	ctctccacag	cctgccttcc	aaattcagcc	tgaactccc	ctgaattcga	3720
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gccacagctc	tccctgtcca	caggttattg	ccctccatcg	tagtcaggcc	caatcatcag	4560
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ccttagtcaa	tagttaacca	aaaaattgca	attgttttaa	ttcagaatgt	gtattttaaa	4980
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attttctaag	tttaccttta	gtttacctaa	acttttgttc	agataacgtt	aaaaggata	5220
cgtactctag	cccttttttg	ggctttcttt	ttgatttttg	tttgttgttt	tcagtttttt	5280
tgttgttgtt	agtgagtctc	ccttcaaaat	acgcagtagg	tagtgtaaat	actgcttgtt	5340
tgtgtctctc	tgtgtctatg	ttttctacct	tattccaata	ctatatgtgt	gataaaattt	5400
gtatatacat	tttcaataaa	gaatatgtat	aaactgtaca	gatctagatc	tacaacctat	5460
ttctctactc	tttagtagag	ttcgagacac	agaagtgcaa	taactgccct	aattaagcaa	5520

ctatttgtta	aaaagggcct	ctttttactt	taatagttta	gtgtaaagta	catcagaaat	5580
aaagctgtat	ctgccatttt	aagcctgtag	tccattatta	cttgggtctt	tacttctggg	5640
aatttgtatg	taacagccta	gaaaattaaa	aggaggtgga	tgcattccaa	gcacgagtca	5700
cttaaaatat	cgacggtaaa	ctactatttt	gtagagaaac	tcaggaagat	ttaaatgttg	5760
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actgtagata	aaaccatata	ctaaatctat	aagactaagg	gatttttggt	attctagctc	5880
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cacatgactg	cttcttgtag	tcaacaagaa	ataccaataa	cacacacaga	acaaaaacca	6060
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atgatctaca	cacacacaca	cacacacacg	tgcacacaca	cacacattta	aatgataata	7020
aaagaagagg	ttgaaagatt	attaaataac	ttatcaggca	tctcaatggg	tactatctat	7080
gttagtga	atcaaatagg	actcaaagtt	ggatatttgg	gatttttctt	ctgacagtat	7140
aatttattga	gttactaggg	aggttcttaa	atcctcatat	ctggaaactt	gtgacgtttt	7200
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ttctatttca	ggttctgtat	tgcattgttt	cttattaata	tatattaata	aaagttatga	9060
gaaat						9065

Table LIII(d). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 256) and 109P1D4 v.5 (SEQ ID NO: 257)
 Score = 7456 bits (3878), Expect = 0.0 Identities = 3878/3878 (100%) Strand = Plus / Plus

```

V.1 : 1   ctggtggtccagttacctccaaagatatggaatacactcctgaaatatcctgaaaactttt 60
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V.5 : 1   ctggtggtccagttacctccaaagatatggaatacactcctgaaatatcctgaaaactttt 60

V.1 : 61   ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgacttt 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 61   ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgacttt 120

V.1 : 121  atattaatagctattcttggtttttcttatccaaagaaaaatcctctaatacccccttttcac 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 121  atattaatagctattcttggtttttcttatccaaagaaaaatcctctaatacccccttttcac 180

V.1 : 181  atgatagttgttaccatgttttaggcattagtcacatcaaccctctcctctcccaaactt 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 181  atgatagttgttaccatgttttaggcattagtcacatcaaccctctcctctcccaaactt 240

V.1 : 241  ctcttcttcaaatcaaacctttattagtcctcctttataatgattccttgccctcgtttta 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 241  ctcttcttcaaatcaaacctttattagtcctcctttataatgattccttgccctcgtttta 300

V.1 : 301  tccagatcaattttttttcactttgatgccagagctgaagaaatggactactgtataaa 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 301  tccagatcaattttttttcactttgatgccagagctgaagaaatggactactgtataaa 360

V.1 : 361  ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 361  ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat 420

V.1 : 421  tatattttgtagtttgtaacaaataaccctttattttcccttaactattgaattaaatatt 480
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V.5 : 421  tatattttgtagtttgtaacaaataaccctttattttcccttaactattgaattaaatatt 480

V.1 : 481  ttaattatttgtagtttctctttaactatcttggtatattaaagtattatcttttatatatt 540
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V.5 : 481  ttaattatttgtagtttctctttaactatcttggtatattaaagtattatcttttatatatt 540

V.1 : 541  tatcaatggtggacacttttatagggtactctgtgtcatttttgatactgtaggtatctta 600
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V.5 : 541  tatcaatggtggacacttttatagggtactctgtgtcatttttgatactgtaggtatctta 600

V.1 : 601  tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat 660
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V.5 : 601  tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat 660

V.1 : 661  cactaattaacagagtgtaattatgctaactctcatttactgattttaatttaaaaca 720
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V.5 : 661  cactaattaacagagtgtaattatgctaactctcatttactgattttaatttaaaaca 720

V.1 : 721  gtttttgtaacatgcatgttttaggggttggtcttctaataatttcttcttctctctct 780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
V.5 : 721  gtttttgtaacatgcatgttttaggggttggtcttctaataatttcttcttctctctct 780

V.1 : 781  ctctcctcttctttttggtcagtggtgtgcgggtaatacaacaaactgtaacaagtgtac 840

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V.5 : 781 |||||
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V.1 : 841 ctgggatggacttggtgtccgggacgtacattttcgcggtcctgctagcatgcgtgggtg 900
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V.5 : 841 ctgggatggacttggtgtccgggacgtacattttcgcggtcctgctagcatgcgtgggtg 900
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V.1 : 901 tccactctggcgccaggagaaaaactacaccatccgagaagaaatgccagaaaaactgcc 960
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V.5 : 901 tccactctggcgccaggagaaaaactacaccatccgagaagaaatgccagaaaaactgcc 960
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V.1 : 961 tgataggcgacttggtgaaagaccttaacttgctgctgattccaaacaagtccttgacaa 1020
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V.5 : 961 tgataggcgacttggtgaaagaccttaacttgctgctgattccaaacaagtccttgacaa 1020
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V.1 : 1021 ctgctatgcagttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaag 1080
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V.5 : 1021 ctgctatgcagttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaag 1080
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V.1 : 1081 aggatactggtgagatcttcactactggcgctcgcatgtgagaaattatgtgctg 1140
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V.5 : 1081 aggatactggtgagatcttcactactggcgctcgcatgtgagaaattatgtgctg 1140
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V.1 : 1141 gtatcccaagggatgagcattgcttttatgaagtggaggttgccattttgccggatgaaa 1200
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V.5 : 1141 gtatcccaagggatgagcattgcttttatgaagtggaggttgccattttgccggatgaaa 1200
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V.5 : 1201 tatttagactgggttaagatacgttttctgatagaagatataaatgataatgcaccattgt 1260
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V.1 : 1261 tcccagcaacagttatcaacatatcaattccagagaactcggtataaactctaaatata 1320
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V.5 : 1261 tcccagcaacagttatcaacatatcaattccagagaactcggtataaactctaaatata 1320
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V.5 : 1321 ctctcccagcggtgttgatcctgacgtaggaataaacggaggttcaaaactacgaactaa 1380
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V.1 : 1381 ttaagagtcaaaacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgc 1440
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V.5 : 1381 ttaagagtcaaaacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgc 1440
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V.1 : 1441 cacaactgattgttcaaaaggagttagatagggagagaaggatacctacgtgatgaaag 1500
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V.5 : 1441 cacaactgattgttcaaaaggagttagatagggagagaaggatacctacgtgatgaaag 1500
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V.1 : 1501 taaagggttgagatgggtggctttcctcaaagatccagtactgctattttgcaagtgagtg 1560
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V.5 : 1501 taaagggttgagatgggtggctttcctcaaagatccagtactgctattttgcaagtgagtg 1560
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V.1 : 1561 ttactgatacaaatgacaaccacccagtctttaaggagacagagattgaagtcagtatac 1620
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V.5 : 1561 ttactgatacaaatgacaaccacccagtctttaaggagacagagattgaagtcagtatac 1620
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V.1 : 1621 cagaaaatgctcctgtaggcacttcagtgacacagctccatgccacagatgctgacatag 1680
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V.5 : 1621 cagaaaatgctcctgtaggcacttcagtgacacagctccatgccacagatgctgacatag 1680
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V.5 : 1681 gtgaaaatgccaaagatccacttctctttcagcaatctagtctccaacattgccaggagat 1740
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V.1 : 1741 tatttcacctcaatgccaccactggacttatcacaatcaaagaaccactggataggggaag 1800
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V.5 : 1741 tatttcacctcaatgccaccactggacttatcacaatcaaagaaccactggataggggaag 1800
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V.5 : 1801 aaacaccaaaccacaagttactggttttggcaagtgatggtggattgatgccagcaagag 1860
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V.5 : 1861 caatgggtgctggtaaatgttacagatgtcaatgataatgtcccatccattgacataagat 1920
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V.1 : 1921 acatcgtcaatcctgtcaatgacacagttgttctttcagaaaatattccactcaacacca 1980
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V.5 : 1921 acatcgtcaatcctgtcaatgacacagttgttctttcagaaaatattccactcaacacca 1980
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V.1 : 1981 aaattgctctcataactgtgacggataaggatgcggaaccataatggcaggggtgacatgct 2040
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V.5 : 1981 aaattgctctcataactgtgacggataaggatgcggaaccataatggcaggggtgacatgct 2040
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V.5 : 2041 tcacagatcatgaaatccctttcagattaaggccagtattcagtaatcagttcctcctgg 2100
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V.1 : 2101 agactgcagcatatcttgactatgagtccacaaaagaatatgccattaaattactggctg 2160
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V.5 : 2101 agactgcagcatatcttgactatgagtccacaaaagaatatgccattaaattactggctg 2160
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V.5 : 2161 cagatgctggcaaacctcctttgaatcagtcagcaatgctcttcacaaagtgaagatg 2220
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V.1 : 2221 aaaatgacaatgctccagttttcaccagtccttcgtaactgtttctattcctgagaata 2280
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V.5 : 2221 aaaatgacaatgctccagttttcaccagtccttcgtaactgtttctattcctgagaata 2280
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V.1 : 2281 actctcctggcatccagttgacgaaagtaagtgaatggatgcagacagtgggcctaag 2340
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V.5 : 2281 actctcctggcatccagttgacgaaagtaagtgaatggatgcagacagtgggcctaag 2340
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V.5 : 2341 ctaagatcaattacctgctagggcctgatgctccacctgaattcagcctggattgtcgta 2400
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V.1 : 2401 caggcatgctgactgtagtgaagaaactagatagagaaaaaggataaatattttattca 2460
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V.5 : 2401 caggcatgctgactgtagtgaagaaactagatagagaaaaaggataaatattttattca 2460
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V.1 : 2461 caattctggcaaaagataaacggggtaccacccttaaccagcaatgtcacagtctttgtaa 2520
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V.5 : 2461 caattctggcaaaagataaacggggtaccacccttaaccagcaatgtcacagtctttgtaa 2520
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V.5 : 2641 atggagacaattctgcagttacgctctccatttttagatgagaatgatgacttcaccattg 2700
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V.5 : 2701 attcacaactggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatctt 2760
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V.1 : 2761 acactttctatgtaaaggctgaggatggtggttagagtatcacgttcttcaagtgccaaag 2820
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V.5 : 2761 acactttctatgtaaaggctgaggatggtggttagagtatcacgttcttcaagtgccaaag 2820
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V.5 : 2821 taaccataaatgtggttgatgtcaatgacaacaaaccagttttcattgtccctccttcca 2880
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V.5 : 2881 actgttcttatgaattggttctaccgtccactaatccaggcacagtggtctttcaggtaa 2940
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V.1 : 2941 ttgctgttgacaatgacactggcatgaatgcagaggttcggttacagcattgtaggaggaa 3000
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V.5 : 2941 ttgctgttgacaatgacactggcatgaatgcagaggttcggttacagcattgtaggaggaa 3000
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V.5 : 3001 acacaagagatctgtttgcaatcgaccaagaaacagggaacataacattgatggagaaat 3060
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V.5 : 3061 gtgatgttacagaccttggtttacacagagtggttggtcaaagctaatacttaggacagc 3120
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V.5 : 3121 ctgattctctcttcagtggttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatg 3180
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V.1 : 3181 ctacactgattaatgaactggtgcgcaaaagcactgaagcaccagtgaccccaaatactg 3240
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V.5 : 3181 ctacactgattaatgaactggtgcgcaaaagcactgaagcaccagtgaccccaaatactg 3240
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V.5 : 3241 agatagctgatgtatcctcaccaactagtgactatgtcaagatcctggttcagctgttg 3300
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V.1 : 3301 ctggcaccataactgtcggttagttattttcatcactgctgtagtaagatgtcgccagg 3360
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 V.5 : 3301 ctggcaccataactgtcggttagttattttcatcactgctgtagtaagatgtcgccagg 3360

V.1 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420
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 V.5 : 3361 caccacaccttaaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacc 3420

V.1 : 3421 cagaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480
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 V.5 : 3421 cagaaaacaggcagatgataatgatgaagaaaaagaaaaagaagaagcattccccta 3480

V.1 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagt 3540
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 V.5 : 3481 agaacttgctgcttaattttgtcactattgaagaaactaaggcagatgatgttgacagt 3540

V.1 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaacaatgggaaagt 3600
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 V.5 : 3541 atggaacagagtcacactagaccttcctattgatctagaagagcaacaatgggaaagt 3600

V.1 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttggcccgacact 3660
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 V.5 : 3601 acaattgggtaactacacctactactttcaagcccgacagccctgatttggcccgacact 3660

V.1 : 3661 acaaatctgcctctccacagcctgccttccaaattcagcctgaaactcccctgaattcga 3720
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 V.5 : 3661 acaaatctgcctctccacagcctgccttccaaattcagcctgaaactcccctgaattcga 3720

V.1 : 3721 agcaccacatcatccaagaactgcctctcgataaacacctttgtggcctgtgactctatct 3780
 |||||
 V.5 : 3721 agcaccacatcatccaagaactgcctctcgataaacacctttgtggcctgtgactctatct 3780

V.1 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840
 |||||
 V.5 : 3781 ccaagtgttcctcaagcagttcagatccctacagcgtttctgactgtggctatccagtga 3840

V.1 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878
 |||||
 V.5 : 3841 cgaccttcgaggtacctgtgtccgtacacaccagaccg 3878

Table LIV(d). Peptide sequences of protein coded by 109P1D4 v.5 (SEQ ID NO: 258)

MDLLSGTYIF	AVLLACVVFH	SGAQEKNYTI	REEMPENVLI	GDLLKDLNLS	LIPNKSLLTTA	60
MQFKLVYKTG	DVPLIRIEED	TGEIFTTGAR	IDREKLCAGI	PRDEHCFYEV	EVAILPDEIF	120
RLVKIRFLIE	DINDNAPLFP	ATVINISIPE	NSAINSKYTL	PAAVDPDVGI	NGVQNYELIK	180
SQNI FGLDVI	ETPEGDKMPQ	LIVQKELDRE	EKDTYVMKVK	VEDGGFPQRS	STAILQVSVT	240
DTNDNHPVFK	ETEIEVSIPE	NAPVGTSVTQ	LHATDADIGE	NAKIHFSFSN	LVSNIARRLF	300
HLNATTGLIT	IKEPLDREET	PNHKLLVLAS	DGGLMPARAM	VLVNVTDVND	NVPSIDIRYI	360
VNPVNDTVVL	SENIPLNTKI	ALITVTDKDA	DHNGRVTCFT	DHEIPFRLRP	VFSNQFLLT	420
AAYLDYESTK	EYAIKLLAAD	AGKPPLNQSA	MLFIKVKDEN	DNAPVFTQSF	VTVSIPENNS	480
PGIQLTKVSA	MDADSGPNAK	INYLLGPDAP	PEFSLDCRTG	MLTVVKKLDL	EKEDKYLFTI	540
LAKDNGVPPL	TSNVTVFVSI	IDQNDNSPVF	THNEYNFYVP	ENLPRHGTVG	LITVTDPDYG	600
DNSAVTSLIL	DENDDFIDS	QTGVIRPNIS	FDREKQESYT	FYVKAEDGGR	VSRSSSAKVT	660
INVVDVNDNK	PVFIVPPSNC	SYELVLPSTN	PGTVVVFQVIA	VNDNTGMNAE	VRYSIIVGNT	720
RDLFAIDQET	GNITLMEKCD	VTDLGLHRVL	VKANDLGQPD	SLFSVVIVNL	FVNESVTNAT	780
LINELVRKST	EAPVTPNTEI	ADVSSPTS DY	VKILVA AVAG	TITVVVVIFI	TAVVRCRQAP	840

HLKAAQKNKQ	NSEWATPNPE	NRQMIMMKKK	KKKKKHSPKN	LLLNFTVIEE	TKADDVDSGD	900
NRVTLDLPID	LEEQTGMKYN	WVTPTTFKP	DSPDLARHYK	SASPQPAFQI	QPETPLNSKH	960
HIIQELPLDN	TFVACDSISK	CSSSSSDPYS	VSDCGYPVTT	FEVPVSVHTR	PSQRRVTFHL	1020
PEGSQESSSD	GGLGDHDAGS	LTSTSHGLPL	GYPQEEYFDR	ATPSNRTEGD	GNSDPESTFI	1080
PGLKKAEEIT	VQPTVEEASD	NCTQECLYIG	HSDACWMPAS	LDHSSSSQAQ	ASALCHSPPL	1140
SQASTQHHSP	RVTQTIALCH	SPVVTQTIAL	CHSPPIQVS	ALHHSPPPLVQ	ATALHHSPPS	1200
AQASALCYSP	PLAQAAAIHS	SSPLPQVIAL	HRSQAQSSVS	LQQGWVQCAD	GLCSVDQGVQ	1260
GSATSQFYTM	SERLHPSDDS	IKVIPLTTFT	PRQQARPSRG	DSPIMEEHPL		1310

Table LV(d). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 259) and 109P1D4 v.5 (SEQ ID NO: 260)
 Score = 2005 bits (5195), Expect = 0.0Identities = 1011/1011 (100%), Positives = 1011/1011 (100%)

V.1	: 1	MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA	60
		MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA	
V.5	: 1	MDLLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTA	60
V.1	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	120
		MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	
V.5	: 61	MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF	120
V.1	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
		RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	
V.5	: 121	RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK	180
V.1	: 181	SQNIIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	240
		SQNIIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	
V.5	: 181	SQNIIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT	240
V.1	: 241	DTNDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIAARRLF	300
		DTNDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIAARRLF	
V.5	: 241	DTNDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIAARRLF	300
V.1	: 301	HLNATTGLITIKEPLDREETPNHKLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYI	360
		HLNATTGLITIKEPLDREETPNHKLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYI	
V.5	: 301	HLNATTGLITIKEPLDREETPNHKLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYI	360
V.1	: 361	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLET	420
		VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLET	
V.5	: 361	VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLET	420
V.1	: 421	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	480
		AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	
V.5	: 421	AAYLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNS	480
V.1	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540
		PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	
V.5	: 481	PGIQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI	540
V.1	: 541	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	600
		LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	
V.5	: 541	LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYG	600
V.1	: 601	DNSAVTLSILDENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
		DNSAVTLSILDENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	
V.5	: 601	DNSAVTLSILDENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT	660
V.1	: 661	INVVDVNDNKPVFIVPPSNCSEYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT	720
		INVVDVNDNKPVFIVPPSNCSEYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT	
V.5	: 661	INVVDVNDNKPVFIVPPSNCSEYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT	720
V.1	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRLVLVKANDLGQPDLSFVIVNLFVNESVTNAT	780
		RDLFAIDQETGNITLMEKCDVTDGLHRLVLVKANDLGQPDLSFVIVNLFVNESVTNAT	
V.5	: 721	RDLFAIDQETGNITLMEKCDVTDGLHRLVLVKANDLGQPDLSFVIVNLFVNESVTNAT	780
V.1	: 781	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVTVVIFITAVVRCRQAP	840
		LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVTVVIFITAVVRCRQAP	
V.5	: 781	LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVTVVIFITAVVRCRQAP	840

V.1 : 841 HLKAAQKNKQNSEWATPNPENRQIMMMKKKKKKHSPKNLLLNFTIEETKADDVDSGD 900
 HLKAAQKNKQNSEWATPNPENRQIMMMKKKKKKHSPKNLLLNFTIEETKADDVDSGD
 V.5 : 841 HLKAAQKNKQNSEWATPNPENRQIMMMKKKKKKHSPKNLLLNFTIEETKADDVDSGD 900
 V.1 : 901 NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH 960
 NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH
 V.5 : 901 NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH 960
 V.1 : 961 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP 1011
 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP
 V.5 : 961 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP 1011

Table LI(e). Nucleotide sequence of transcript variant 109P1D4 v.6 (SEQ ID NO: 261)

ggcagctcgcc	gaactgtctg	ggcgggagga	gccgtgagca	gtagctgcac	tcagctgccc	60
gcgcggcaaa	gaggaaggca	agccaaacag	agtgcgcaga	gtggcagtcg	cagcggcgac	120
acaggcagca	caggcagccc	gggctgcctg	aatagcctca	gaaacaacct	cagcgactcc	180
ggctgctctg	cggactgcga	gctgtggcgg	tagagcccg	tacagcagtc	gcagctcccg	240
tggagcgggc	ggaagccttt	tttctccctt	tcgtttacct	cttcattcta	ctctaaaggc	300
atcgattatta	gaggtgtctt	aaaaagtaca	gatcaactgg	atggatgaat	ggatggaaga	360
ggatggaata	tcttaacaaa	acacattttc	cttaagttaa	ttcatgcata	ctccaaataa	420
aatacagaat	gtgaagtatc	tctgaactgt	gctgttgaa	atggtagcta	ctagctacat	480
gaaaatcctg	ttgtgaataa	gaaggattcc	acagatcaca	taccagagcg	gttttgccctc	540
agctgctctc	aactttgtaa	tcttgtgaag	aagctgacaa	gcttggctga	ttgcagtgca	600
ctatgaggac	tgaatgacag	tgggttttaa	ttcagatatt	tcaagtgttg	tgccgggttaa	660
tacaacaaac	tgtcacaaat	gtttgttgct	cgggacgtac	atcttcgcgg	tcctgctagt	720
atgcgtggtg	ttccactctg	gcgcccagga	gaaaaactac	accatccgag	aagaaattcc	780
agaaaacgtc	ctgataggca	acttggttaa	agaccttaac	ttgtcgtgta	ttccaaacaa	840
gtccttgaca	actactatgc	agttcaagct	agtgtacaag	accggagatg	tgccactgat	900
tcgaattgaa	gaggatactg	gtgagatctt	cactaccggc	gctcgcattg	atcgtgagaa	960
attatgtgct	ggtattccaa	gggatgagca	tgtcttttat	gaagtggagg	ttgccatttt	1020
gccggtgaa	atatttagac	tgggttaagat	acgttttctg	atagaagata	taaataataa	1080
tgcaccattg	ttcccagcaa	cagttatcaa	catatcaatt	ccagagaact	cggctataaa	1140
ctctaaatat	actctcccag	cggctgttga	tcctgacgta	ggcataaacg	gagttcaaaa	1200
ctacgaacta	attaagagtc	aaaacatttt	tggcctcgat	gtcattgaaa	caccagaagg	1260
agacaagatg	ccacaactga	ttgttcaaaa	ggagtttagat	agggaagaga	aggataccta	1320
tgtgatgaaa	gtaaagggtg	aagatggtgg	ctttctcaa	agatccagta	ctgctatttt	1380
gcaagttaagt	gttatcgata	caaatagaca	ccaccagtc	tttaaggaga	cagagattga	1440
agtcagtata	ccagaaaatg	ctcctgtagg	cacttcagtg	acacagctcc	atgccacaga	1500
tgctgacata	ggtgaaaatg	ccaagatcca	cttctcttcc	agcaatctag	tctccaacat	1560
tgccaggaga	ttatttcacc	tcaatgccac	cactggactt	atcacaatca	aagaaccact	1620
ggatagggaa	gaaacaccaa	accacaagtt	actggttttg	gcaagtgtat	gtggattgat	1680
gccagcaaga	gcaatggtgc	tggtaaagt	tacagatgtc	aatgataatg	tcccatccat	1740
tgacataaga	tacatcgta	atcctgtcaa	tgacacagtt	gttctttcag	aaaatatccc	1800
actcaacacc	aaaattgtct	tcataactgt	gacggataag	gatgcggacc	ataatggcag	1860
ggtgacatgc	ttcacagatc	atgaaattcc	tttcagatta	aggccagtat	tcagtaataa	1920
gttctctctg	gagaatgcag	catatcttga	ctatgagtcc	acaaaagaat	atgccattaa	1980
attactggct	gcagatgctg	gcaaacctcc	tttgaatcag	tcagcaatgc	tcttcatcaa	2040
agtgaagat	gaaaatgaca	atgctccagt	tttcaccag	tctttcgtaa	ctgtttctat	2100
tcctgagaat	aactctcctg	gcattccagt	gatgaaagta	agtgcacagg	atgcagacag	2160
tgggcctaata	gctgagatca	attacctgct	aggccctgat	gctccacctg	aattcagcct	2220
ggatcgctcg	acaggcatgc	tgactgtagt	gaagaaacta	gatagagaaa	aagaggataa	2280
atatttatct	acaattctgg	caaaagataa	tggggtacca	cccttaacca	gcaatgtcac	2340
agtctttgta	agcattattg	atcagaatga	caatagccca	gttttctact	acaatgaata	2400
caaattctat	gtcccagaaa	accttccaag	gcattggtaca	gtaggactaa	tactgtaac	2460
tgatcctgat	tatggagaca	attctgcagt	tacgctctcc	atcttagatg	agaatgatga	2520
cttcaccatt	gattcacaaa	ctggtgtcat	ccgaccaa	atctcatttg	atagagaaaa	2580
acaagaatct	tacactttct	atgtaaaggc	tgaggatggt	ggtagagtat	cacgttcttc	2640
aagtgcacaa	gtaaccataa	atgtggttga	tgtcaatgac	aacaaaccag	ttttcattgt	2700
ccctccttac	aactattctt	atgaattggt	tctaccgtcc	actaatccag	gcacagtggg	2760
ctttcaggta	attgctgttg	acaatgacac	tggcatgaat	gcagagggtc	gttacagcat	2820
tgtaggagga	aacacaagag	atctgtttgc	aatcgaccaa	gaaacaggca	acataacatt	2880
gatggagaaa	tgtgatgtta	cagaccttgg	tttacacaga	gtgttggtca	aagctaataa	2940

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cttaggacag cctgattctc tcttcagtgt tgtaattgtc aatctgttcg tgaatgagtc 3000
agtgaccaat gctacactga ttaatgaact ggtgcgcaaa agcattgaag caccagtgc 3060
cccaaatact gagatagctg atgtatcctc accaactagt gactatgtca agatcctggt 3120
tgcagctgtt gctggcacca taactgtcgt tgtagtattt ttcactactg ctgtagtaag 3180
atgtcgccag gcaccacacc ttaaggctgc tcagaaaaac atgcagaatt ctgaatgggc 3240
taccctaaac ccagaaaaca ggcagatgat aatgatgaag aaaaagaaaa agaagaagaa 3300
gcattcccct aagaacctgc tgccttaattt tgtcactatt gaagaaacta aggcagatga 3360
tgttgacagt gatggaaaca gagtcacact agaccttcct attgatctag aagagcaaac 3420
aatgggaaag tacaattggg taactacacc tactacttct aagcctgaca gccctgattt 3480
ggcccgacac tacaatctg cctctccaca gcctgccttc caaattcagc ctgaaactcc 3540
cctgaatttg aagcaccaca tcatccaaga actgcctctc gataaacctt ttgtggcctg 3600
tgactctatc tccaagtgtt cctcaagcag atcagctccc tacagcgttt ctgactgtgg 3660
ctatcgatg agaaccttcg aggtacctgt gtccgtacac accagaccga ctgattccag 3720
gacatgaact attgaaatct gcagtgagat gtaactttct aggaacaaca aaattccatt 3780
ccccctccaa aaaatttcaa tggattgtga tttcaaaatt aggctaagat cattaatttt 3840
gtaatctaga tttccatta taaaagcaag caaaaatcat cttaaaaatg atgtcctagt 3900
gaaccttgtg ctttcttttag ctgtaatctg gcaatggaaa tttaaaattt atggaagaga 3960
cagtgcagca caataacaga gtactctcat gctgtttctc tgtttgctct gaatcaacag 4020
ccatgatgta atataaggct gtcttggtgt atcaccttat gggttaataa tcagtcatga 4080
aacatgcaat tacttgccct gtctgattgt tgaataatta aaacattatc ttccaggagt 4140
ttggaagtga gctgaactag ccaaactact ctctgaaagg tatccagggc aagagacatt 4200
tttaagaccc caaacaacaa aaaaacaaaa ccaaaacact ctgggttcagt gttttgaaaa 4260
tattcactaa cataatattg ctgagaaaat catttttatt acccaccact ctgcttaaaa 4320
gttgagtggg ccgggcgcgg tggctcacgc ctgtaatccc agcactttgg gaggccgagg 4380
cgggtggatc acgaggtcag gagattgaga ccactctggc taacacggtg aaacccatc 4440
tccactaaaa atacaaaaaa ttagcctggc gtggtggcgg gcgcctgtag tcccagctac 4500
tcgggaggct gaggcaggag aatagcgtga acccgggagg cggagcttgc agtgagccga 4560
gatggcgcca ctctgcactc cagcctgggt gacagagcaa gactctgtct caaaaagaaa 4620
aaaatgttca atgatagaaa ataattttac taggttttta tgttgattgt actcatggtg 4680
ttccactcct ttttaattatt aaaaagttat ttttgggtg ggtgtggtg ctcacaccgt 4740
aatcccagca ctttgggagg ccgaggtggg tggatcacct gaggtcagga gttcaagacc 4800
agntnggcca acatggcgaa acccgtttt 4830

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Table LIII(e). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 262) and 109P1D4 v.6 (SEQ ID NO: 263)
Score = 5676 bits (2952), Expect = 0.0, Identities = 3002/3027 (99%) Strand = Plus / Plus

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V.1 : 852 ttgttggtccgggacgtacattttcgcggtcctgctagcatgcgtggtgttccactctggc 911
      |||
V.6 : 683 ttgttggtccgggacgtacattttcgcggtcctgctagtagatgcgtggtgttccactctggc 742

V.1 : 912 gccaggagaaaaactacaccatccgagaagaaatgccagaaaacgtcctgataggcgac 971
      |||
V.6 : 743 gccaggagaaaaactacaccatccgagaagaaattccagaaaacgtcctgataggcaac 802

V.1 : 972 ttgttgaaagaccttaacttgtcgtgattccaaacaagtccttgacaactgctatgcag 1031
      |||
V.6 : 803 ttgttgaaagaccttaacttgtcgtgattccaaacaagtccttgacaactactatgcag 862

V.1 : 1032 ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggt 1091
      |||
V.6 : 863 ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggt 922

V.1 : 1092 gagatcttcactactggcgctcgcatctgctgagaaattatgtgctggtatcccaagg 1151
      |||
V.6 : 923 gagatcttcactaccggcgctcgcatctgctgagaaattatgtgctggtatcccaagg 982

V.1 : 1152 gatgagcattgcttttatgaagtggagggtgccattttgccggatgaaatatttagactg 1211
      |||
V.6 : 983 gatgagcattgcttttatgaagtggagggtgccattttgccggatgaaatatttagactg 1042

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V.1 : 1212 gtttaagatacgttttctgatagaagatataaatgataatgcaccattgttcccagcaaca 1271
|||||
V.6 : 1043 gtttaagatacgttttctgatagaagatataaatgataatgcaccattgttcccagcaaca 1102
|||||

V.1 : 1272 gttatcaacatatcaattccagagaactcggctataaactctaaatatactctcccagcg 1331
|||||
V.6 : 1103 gttatcaacatatcaattccagagaactcggctataaactctaaatatactctcccagcg 1162
|||||

V.1 : 1332 gctgttgatcctgcagtaggaataaacggagttcaaaactacgaactaattaagagtcaa 1391
|||||
V.6 : 1163 gctgttgatcctgcagtaggcataaacggagttcaaaactacgaactaattaagagtcaa 1222
|||||

V.1 : 1392 aacatTTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAAGTGATT 1451
|||||
V.6 : 1223 aacatTTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAAGTGATT 1282
|||||

V.1 : 1452 gttcaaaaggagttagatagggagaagagatacctacgtgatgaaagtaaagggtgaa 1511
|||||
V.6 : 1283 gttcaaaaggagttagatagggagaagagatacctatgtgatgaaagtaaagggtgaa 1342
|||||

V.1 : 1512 gatggtggctttcctcaaagatccagtactgctatTTTGCAAGTGAGTGTTACTGATACA 1571
|||||
V.6 : 1343 gatggtggctttcctcaaagatccagtactgctatTTTGCAAGTAAGTGTTACTGATACA 1402
|||||

V.1 : 1572 aatgacaaccacccagtcctttaaggagacagagattgaagtcagtataaccagaaaaatgct 1631
|||||
V.6 : 1403 aatgacaaccacccagtcctttaaggagacagagattgaagtcagtataaccagaaaaatgct 1462
|||||

V.1 : 1632 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1691
|||||
V.6 : 1463 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1522
|||||

V.1 : 1692 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1751
|||||
V.6 : 1523 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1582
|||||

V.1 : 1752 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaagaaacaccaaac 1811
|||||
V.6 : 1583 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaagaaacaccaaac 1642
|||||

V.1 : 1812 cacaagttactggTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAGCAATGGTGCTG 1871
|||||
V.6 : 1643 cacaagttactggTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAGCAATGGTGCTG 1702
|||||

V.1 : 1872 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1931
|||||
V.6 : 1703 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1762
|||||

V.1 : 1932 cctgtcaatgacacagttgttctttcagaaaatattccactcaacaccaaattgtctc 1991
|||||
V.6 : 1763 cctgtcaatgacacagttgttctttcagaaaatattccactcaacaccaaattgtctc 1822
|||||

V.1 : 1992 ataactgtgacggataaggatgcgaccataatggcagggtgacatgcttcacagatcat 2051
|||||

V.6 : 1823 ataactgtgacggataaggatgcggaaccataatggcagggatgacatgcttcacagatcat 1882

V.1 : 2052 gaaatccctttcagattaaggccagtattcagtaatcagttcctcctggagactgcagca 2111
||||| |||||||

V.6 : 1883 gaaatccctttcagattaaggccagtattcagtaatcagttcctcctggagaatgcagca 1942

V.1 : 2112 tatcttgactatgagtcacacaaaagaatatgccattaaattactggctgcagatgctggc 2171
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V.6 : 1943 tatcttgactatgagtcacacaaaagaatatgccattaaattactggctgcagatgctggc 2002

V.1 : 2172 aaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaat 2231
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V.6 : 2003 aaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaat 2062

V.1 : 2232 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2291
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V.6 : 2063 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2122

V.1 : 2292 atccagttgacgaaagtaagtgaatggatgcagacagtgggcctaatactgagatcaat 2351
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V.6 : 2123 atccagttgatgaaagtaagtgaacggatgcagacagtgggcctaatactgagatcaat 2182

V.1 : 2352 tacctgctaggccctgatgctccacctgaattcagcctggattgtcgtacaggcatgctg 2411
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V.6 : 2183 tacctgctaggccctgatgctccacctgaattcagcctggatcgtcgtacaggcatgctg 2242

V.1 : 2412 actgtagtgaagaaactagatagagaaaaaggagataaatatttattcacaaattctggca 2471
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V.6 : 2243 actgtagtgaagaaactagatagagaaaaaggagataaatatttattcacaaattctggca 2302

V.1 : 2472 aaagataacggggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2531
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V.6 : 2303 aaagataatggggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2362

V.1 : 2532 cagaatgacaatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaac 2591
||||| |||||||

V.6 : 2363 cagaatgacaatagcccagttttcactcacaatgaatacaaatctatgtcccagaaaac 2422

V.1 : 2592 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2651
||||| |||||||

V.6 : 2423 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2482

V.1 : 2652 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaact 2711
||||| |||||||

V.6 : 2483 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaact 2542

V.1 : 2712 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2771
||||| |||||||

V.6 : 2543 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2602

V.1 : 2772 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2831
||||| |||||||

V.6 : 2603 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2662

V.1 : 2832 gtgggtgatgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttat 2891

V.6 : 2663 |||gtggtgatgtcaatgacaacaaccagttttcattgtccctccttacaactattcttat 2722

V.1 : 2892 gaattgggttctaccgtccactaatccaggcacagtggctttcaggtaattgctgttgac 2951
|||||

V.6 : 2723 gaattgggttctaccgtccactaatccaggcacagtggctttcaggtaattgctgttgac 2782

V.1 : 2952 aatgacactggcatgaatgcagagggttcgttacagcattgtaggaggaaacacaagagat 3011
|||||

V.6 : 2783 aatgacactggcatgaatgcagagggttcgttacagcattgtaggaggaaacacaagagat 2842

V.1 : 3012 ctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttaca 3071
|||||

V.6 : 2843 ctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttaca 2902

V.1 : 3072 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 3131
|||||

V.6 : 2903 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 2962

V.1 : 3132 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgatt 3191
|||||

V.6 : 2963 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcagtgaccaatgctacactgatt 3022

V.1 : 3192 aatgaactggtgcgcaaaagcactgaagcaccagtgaccccaatactgagatagctgat 3251
|||||

V.6 : 3023 aatgaactggtgcgcaaaagcattgaagcaccagtgaccccaatactgagatagctgat 3082

V.1 : 3252 gtatcctcaccaactagtgactatgtcaagatcctggttgagctgttgctggcaccata 3311
|||||

V.6 : 3083 gtatcctcaccaactagtgactatgtcaagatcctggttgagctgttgctggcaccata 3142

V.1 : 3312 actgtcgttgtagttattttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3371
|||||

V.6 : 3143 actgtcgttgtagttattttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3202

V.1 : 3372 aaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaaccagaaaaacagg 3431
|||||

V.6 : 3203 aaggctgctcagaaaaacatgcagaattctgaatgggctaccccaaaccagaaaaacagg 3262

V.1 : 3432 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacttgctg 3491
|||||

V.6 : 3263 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacctgctg 3322

V.1 : 3492 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgatggaacaga 3551
|||||

V.6 : 3323 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgatggaacaga 3382

V.1 : 3552 gtcacactagaccttcctattgatctagaagagcaaacaatgggaaagtacaattgggta 3611
|||||

V.6 : 3383 gtcacactagaccttcctattgatctagaagagcaaacaatgggaaagtacaattgggta 3442

V.1 : 3612 actacacctactactttcaagcccgacagccctgatttggcccgacactacaaatctgcc 3671
|||||

V.6 : 3443 actacacctactactttcaagcctgacagccctgatttggcccgacactacaaatctgcc 3502

v.1 : 3672 tctccacagcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatc 3731
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.6 : 3503 tctccacagcctgccttccaaattcagcctgaaactcccctgaatttgaagcaccacatc 3562
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.1 : 3732 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcc 3791
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.6 : 3563 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcc 3622
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.1 : 3792 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgacgaccttcgag 3851
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.6 : 3623 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgacaaccttcgag 3682
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.1 : 3852 gtacctgtgtccgtacacaccagaccg 3878
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.6 : 3683 gtacctgtgtccgtacacaccagaccg 3709
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Table LIV(e). Peptide sequences of protein coded by 109P1D4 v.6 (SEQ ID NO: 264)

MTVGFNSDIS	SVVRVNTTNC	HKCLLSGTYY	FAVLLVCVVF	HSGAQEKNYT	IREEIPENVL	60
IGNLLKDLNL	SLIPNKSLTT	TMQFKLVYKT	GDVPLIRIEE	DTGEIFTTGA	RIDREKLCAG	120
IPRDEHCFYE	VEVAILPDEI	FRLVKIRFLI	EDINDNAPLF	PATVINISIP	ENSAINSKYT	180
LPAAVDPDVG	INGVQNYELI	KSQNIFGLDV	IETPEGDKMP	QLIVQKELDR	EEKDTYVMKV	240
KVEDGGFPQR	SSTAILQVSV	TDTNDNHPVF	KETEIEVSIP	ENAPVGTSTV	QLHATDADIG	300
ENAKIHFSFS	NLVSNIARRL	FHLNATTGLI	TIKEPLDREE	TPNHKLLVLA	SDGGLMPARA	360
MVLVNVTDVN	DNVPSIDIRY	IVNPVNDTVV	LENIPLNTK	IALITVTDKD	ADHNGRVTCF	420
TDHEIPFRLR	PVFSNQFLLE	NAAYLDYEST	KEYAIKLLAA	DAGKPPLNQS	AMLFIKVKDE	480
NDNAPVFTQS	FVTVSIPENN	SPGIQLMKVS	ATDADSGPNA	EINYLLGPDA	PPEFSLDRRT	540
GMLTVVKKLD	REKEDKYLFT	ILAKDNGVPP	LTSNVTVFVS	IIDQNDNSPV	FTHNEYKFYV	600
PENLPRHGTV	GLITVTDPDY	GDNSAVTLSI	LDENDDFTID	SQTGVIRPNI	SFDREKQESY	660
TFYVKAEDGG	RVSRSSSAKV	TINVVDVNDN	KPVFIVPPYN	YSYELVLPST	NPGTVVFQVI	720
AVDNDTGMNA	EVRSIVGGN	TRDLFAIDQE	TGNITLMEKC	DVTDLGLHRV	LVKANDLGQP	780
DSLFSVVIVN	LFVNESVTNA	TLINELVRKS	IEAPVTPNTE	IADVSSPTSD	YVKILVAAVA	840
GTITVVVVIF	ITAVVRCRQA	PHLKAAQKNM	QNSEWATPNP	ENRQMIMMKK	KKKKKKHSPK	900
NLLLNEVTIE	ETKADDVDS	GNRVTLDLPI	DLEEQTMGKY	NWVTTPTTFK	PDSPDLARHY	960
KSASPQPAFQ	IQPETPLNLK	HHIIQELPLD	NTFVACDSIS	KCSSSSSDPY	SVSDCGYPVT	1020
TFEVPVSVHT	RPTDSRT					1037

Table LV(e). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 265) and 109P1D4 v.6 (SEQ ID NO: 266)
 Score = 1966 bits (5093), Expect = 0.0, Identities = 994/1009 (98%), Positives = 997/1009 (98%)

v.1 : 3	LLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLTTAMQ	62
	LLSGTYIFAVLL CVVFHSGAQEKNYTIREE+PENVLIG+LLKDLNLSLIPNKSLTT MQ	
v.6 : 24	LLSGTYIFAVLLVCVVFHSGAQEKNYTIREEIPENVLIGNLLKDLNLSLIPNKSLTTTMMQ	83
v.1 : 63	FKLIVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	122
	FKLIVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	
v.6 : 84	FKLIVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	143
v.1 : 123	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	182
	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	
v.6 : 144	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	203
v.1 : 183	NIFGLDVJETPEGDKMPQLIVQKELDREEDTYVMKVVEDGGFPQRSSTAILQVSVTDT	242
	NIFGLDVJETPEGDKMPQLIVQKELDREEDTYVMKVVEDGGFPQRSSTAILQVSVTDT	
v.6 : 204	NIFGLDVJETPEGDKMPQLIVQKELDREEDTYVMKVVEDGGFPQRSSTAILQVSVTDT	263
v.1 : 243	NDNHPVFKETEIEVSIPENAPVGTSTVQLHATDADIGENAKIHFSFNLVSNIARRLFHL	302
	NDNHPVFKETEIEVSIPENAPVGTSTVQLHATDADIGENAKIHFSFNLVSNIARRLFHL	
v.6 : 264	NDNHPVFKETEIEVSIPENAPVGTSTVQLHATDADIGENAKIHFSFNLVSNIARRLFHL	323
v.1 : 303	NATTGLITIKEPLDREETPNHKLLVLASDGGILMPARAMVLNVNVDVNDNVPSIDIRYIVN	362
	NATTGLITIKEPLDREETPNHKLLVLASDGGILMPARAMVLNVNVDVNDNVPSIDIRYIVN	
v.6 : 324	NATTGLITIKEPLDREETPNHKLLVLASDGGILMPARAMVLNVNVDVNDNVPSIDIRYIVN	383

V.1	: 363	PVNDTVVLSENIPLNTKIALITVTDKDADHNGRVTCFTDHEIPFRLRPVFSNQFLETA	422
V.6	: 384	PVNDTVVLSENIPLNTKIALITVTDKDADHNGRVTCFTDHEIPFRLRPVFSNQFLE AA	443
V.1	: 423	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFKVKDENDNAPVFTQSFVTVSIPENNSPG	482
V.6	: 444	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFKVKDENDNAPVFTQSFVTVSIPENNSPG	503
V.1	: 483	IQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTILA	542
V.6	: 504	IQLKVSADADSGPNAEINYLLGPDAPPEFSLDRRTGMLTVVKKLDREKEDKYLFTILA	563
V.1	: 543	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYFYVPENLPRHGTVGLITVTDPDYGDN	602
V.6	: 564	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEY FYVPENLPRHGTVGLITVTDPDYGDN	623
V.1	: 603	SAVTLISILDENDDFIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	662
V.6	: 624	SAVTLISILDENDDFIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	683
V.1	: 663	VVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	722
V.6	: 684	VVDVNDNKPVFIVPP N SYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	743
V.1	: 723	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVIVNLFVNESVTNATLI	782
V.6	: 744	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVIVNLFVNESVTNATLI	803
V.1	: 783	NELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAGVAGTITVVVIFITAVVRCRQAPHL	842
V.6	: 804	NELVRKS EAPVTPNTEIADVSSPTS DYVKILVAAGVAGTITVVVIFITAVVRCRQAPHL	863
V.1	: 843	KAAQKNQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIEETKADDVSDGNGR	902
V.6	: 864	KAAQKN QNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIEETKADDVSDGNGR	923
V.1	: 903	VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLNSKHHI	962
V.6	: 924	VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLN KHHI	983
V.1	: 963	IQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPSVHTRP	1011
V.6	: 984	IQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPSVHTRP	1032

Table LII(f). Nucleotide sequence of transcript variant 109P1D4 v.7 (SEQ ID NO: 267)

ggtggtccag	tacctccaaa	gatattggaat	acactcctga	aatatcctga	aacctttttt	60
ttttcagaat	cctttaataa	gcagttatgt	caatctgaaa	gttgcttact	tgtactttat	120
attaatagct	attcttggtt	ttcttatcca	aagaaaaatc	ctctaattccc	cttttcacat	180
gatagttggt	accatgttta	ggcgtagtc	acatcaaccc	ctctcctctc	ccaaacttct	240
cttcttcaaa	tcaaacttta	ttagtccctc	ctttataatg	attccttgcc	tccttttatc	300
cagatcaatt	ttttttcact	ttgatgccca	gagctgaaga	aatggactat	tgtataaatt	360
attcattgcc	aagagaataa	ttgcatttta	aacctatggt	ataacaaaga	ataatgatta	420
tattttgtga	tttgtaacaa	atacccttta	ttttccctta	actattgaat	taaatatttt	480
aattatttgt	attctcttta	actatcttgg	tatatataag	tattatcttt	tatatattta	540
tcaatggtgg	acacttttat	aggtactctg	tgctattttt	gatactgtag	gtatcttatt	600
tcatttatct	ttattcttaa	tgtacgaatt	cataatattt	gattcagaac	agatttatca	660
ctaattaaca	gagtgatcaat	tatgctaaca	tctcattttac	tgattttta	ttaaaacagt	720
ttttgttaac	atgcatgttt	aggggtggct	tcttaataat	ttcttcttcc	tcttctctct	780
ctcctcttct	tttggtcagt	gttggtcggt	ttaatacaac	aaactgtcac	aagtgtttgt	840
tgtccgggac	gtacattttc	gcggtcctgc	ttagtatcgt	gggtgtccac	tctggcgccc	900
aggagaaaaa	ctacaccatc	cgagaagaaa	ttccagaaaa	cgtcctgata	ggcaacttgt	960
tgaaagacct	taacttgtcg	ctgattccaa	acaagtcctt	gacaactact	atgcagttca	1020
agctagtgtg	caagaccgga	gatgtgccac	tgattcgaat	tgaagaggat	actgggtgaga	1080
tcttcactac	cggcgctcgc	attgatcgtg	agaaattatg	tgctgggtatc	ccaagggatg	1140
agcattgctt	ttatgaagtg	gaggttgcca	ttttgccgga	tgaaatattt	agactgggtta	1200
agatacgttt	tctgatagaa	gatataaatg	ataatgcacc	attgttccca	gcaacagtta	1260

tcaacatata	aattccagag	aactcggcta	taaactctaa	atatactctc	ccagcggctg	1320
ttgatcctga	cgtaggcata	aacggagttc	aaaactacga	actaattaag	agtcaaaaaca	1380
tttttggcct	cgatgtcatt	gaaacaccag	aaggagacaa	gatgccacaa	ctgattgttc	1440
aaaaggagtt	agatagggaa	gagaaggata	cctatgtgat	gaaagtaaag	gttgaagatg	1500
gtggctttcc	tcaaatgatcc	agtactgcta	ttttgcaagt	aagtgttact	gatacaaatg	1560
acaaccaccc	agtctttaag	gagacagaga	ttgaagtcag	tataccagaa	aatgctcctg	1620
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tcaatgacac	agttgttctt	tcagaaaata	ttccactcaa	caccaaattt	gctctcataa	1980
ctgtgacgga	taaggatgcg	gaccataatg	gcagggtgac	atgcttcaca	gatcatgaaa	2040
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ctcctttgaa	tcagtcagca	atgctcttca	tcaaagtga	agatgaaaat	gacaatgctc	2220
cagttttcac	ccagtctttc	gtaactgttt	ctattcctga	gaataactct	cctggcatcc	2280
agttgatgaa	agtaagtgca	acggatgcag	acagtgggcc	taatgctgag	atcaattacc	2340
tgctaggccc	tgatgctcca	cctgaattca	gcctggatcg	tcgtacaggc	atgctgactg	2400
tagtgaagaa	actagataga	gaaaaagagg	ataaatattt	attcacaatt	ctggcaaaaag	2460
ataatggggg	accaccctta	accagcaatg	tcacagtctt	tgtaagcatt	attgatcaga	2520
atgacaatag	cccagttttc	actcacaatg	aatacaaat	ctatgtccca	gaaaaccttc	2580
caaggcatgg	tacagtagga	ctaactactg	taactgatcc	tgattatgga	gacaattctg	2640
cagttacgct	ctccattttta	gatgagaatg	atgacttcac	cattgattca	caaactgggtg	2700
tcacccgacc	aaatattttca	tttgatagag	aaaaacaaga	atcttacact	ttctatgtaa	2760
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acactggcat	gaatgcagag	gttcgttaca	gcattgtagg	aggaaacaca	agagatctgt	3000
ttgcaatcga	ccaagaaaca	ggcaacataa	cattgatgga	gaaatgtgat	gttacagacc	3060
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gtgttgtaat	tgtcaatctg	ttcgtgaatg	agtcagtgc	caatgctaca	ctgattaatg	3180
aactggtgcg	caaaagcatt	gaagcaccag	tgaccccaaa	tactgagata	gctgatgtat	3240
cctcaccaac	tagtgactat	gtcaagatcc	tggttcgcagc	tggtgctggc	accataactg	3300
tcgtttgtagt	tattttcatc	actgctgtag	taagatgtcg	ccaggcacca	caccttaagg	3360
ctgctcagaa	aaacatgcag	aattctgaat	gggtaccccc	aaaccagaa	aacaggcaga	3420
tgataatgat	gaagaaaaag	aaaaagaaga	agaagcattc	ccctaagaac	ctgctgctta	3480
atgttgtcac	tattgaagaa	actaaggcag	atgatgttga	cagtgtatga	aacagagtca	3540
cactagacct	tcctattgat	ctagaagagc	aaacaatggg	aaagtacaat	tgggtaacta	3600
cacctactac	tttcaagcct	gacagccctg	attttggccc	acactacaaa	tctgcctctc	3660
cacagcctgc	cttccaaatt	cagcctgaaa	ctccccgtaa	tttgaagcac	cacatcatcc	3720
aagaactgcc	tctcgataac	acctttgtgg	cctgtgactc	tatctccaat	tgttcctcaa	3780
gcagttcaga	tccttacagc	gtttctgact	gtggctatcc	agtgacaacc	ttcgagggtac	3840
ctgtgtccgt	acacaccaga	ccgactgatt	caaggacatg	aactattgaa	atctgcagtg	3900
agatgtaact	ttctaggaac	aacaaaatc	cattccccct	ccaaaaaatt	tcaatgattg	3960
tgatttcaaa	attaggtcaa	gatcattaat	tttgtaatct	agattttcca	ttataaaaagc	4020
aagcaaaaaat	catcttaaaa	atgatgtcct	agtgaacctt	gtgctttctt	tagctgtaat	4080
ctggcaatgg	aaatttataa	tttatggaag	agacagtgc	gcgcaataac	agagtactct	4140
catgctgttt	ctctgtttgc	tctgaatcaa	cagccatgat	gtaataataag	gctgtcttgg	4200
tgtatacact	tatggttaat	atatcagtca	tgaacatgc	aattacttgc	cctgtctgat	4260
tgttgaataa	ttaaaacatt	atctccagga	gtttggaagt	gagctgaact	agccaaacta	4320
ctctctgaaa	ggtatccagg	gcaagagaca	tttttaagac	cccaacaaa	caaaaaacaa	4380
aacaaaaaca	ctctggttca	gtgttttgaa	aatattgact	aacataatat	tgctgagaaa	4440
atcattttta	ttaccacca	ctctgcttaa	aagttgagtg	ggccggggcg	gggtggctcac	4500
gctgttaatt	ccagcacttt	gggaggccga	ggcgggtgga	tcacgaggtc	aggatattga	4560
gacctcctg	gctaacatgg	tgaaccccca	tctccactaa	aaatacaaaa	aattagctgg	4620
gcgtgggtgg	gggcgcctgt	agtcccagct	actcgggagg	ctgaggcagg	agaatggcgt	4680
gaacccggga	ggcggagctt	gcagtgcagc	gagatggcgc	cactgcactc	cagcctgggt	4740
gacagagcaa	gactctgtct	caaaaagaaa	aaaatgttca	gtgatagaaa	ataattttac	4800
taggttttta	tgttgattgt	actcatgctg	ttccactcct	tttaattatt	aaaaagttat	4860
ttttggctgg	gtgtgggtgg	tcatacctgt	aatcccagca	ctttggggagg	ccgaggcggg	4920
tggatcacct	gaggtcagga	gttcaagacc	agtctggcca	acat		4964

Table LIII(f). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 268) and 109P1D4 v.7 (SEQ ID NO: 269)
 Score = 5664 bits (2946), Expect = 0.0 Identities = 3000/3027 (99%) Strand = Plus / Plus

V.1	: 852	ttgttgtccgggacgtacatttttcgcggtcctgctagcatgcgtgggtgtccactctggc	911
V.7	: 837	ttgttgtccgggacgtacatttttcgcggtcctgctagtagtgcgtgggtgtccactctggc	896
V.1	: 912	gccaggagaaaaactacacatccgagaagaatgccagaaaacgtcctgataggcgac	971
V.7	: 897	gccaggagaaaaactacacatccgagaagaattccagaaaacgtcctgataggcaac	956
V.1	: 972	ttgttgaaagacctaacttgcgctgattccaaacaagtccttgacaactgctatgcag	1031
V.7	: 957	ttgttgaaagacctaacttgcgctgattccaaacaagtccttgacaactactatgcag	1016
V.1	: 1032	ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggc	1091
V.7	: 1017	ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggc	1076
V.1	: 1092	gagatcttcactactggcgctcgcattgatcgtagaaaattatgtgctggatcccaagg	1151
V.7	: 1077	gagatcttcactacggcgctcgcattgatcgtagaaaattatgtgctggatcccaagg	1136
V.1	: 1152	gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg	1211
V.7	: 1137	gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg	1196
V.1	: 1212	gttaagatacgttttctgatagaagatataaatgataatgcaccattgttcccagcaaca	1271
V.7	: 1197	gttaagatacgttttctgatagaagatataaatgataatgcaccattgttcccagcaaca	1256
V.1	: 1272	gttatcaacatatcaattccagagaactcggctataaactctaaatatactctcccagcg	1331
V.7	: 1257	gttatcaacatatcaattccagagaactcggctataaactctaaatatactctcccagcg	1316
V.1	: 1332	gctgttgatcctgacgtaggaataaacggagttcaaaactacgaactaattaagagtcaa	1391
V.7	: 1317	gctgttgatcctgacgtaggcataaacggagttcaaaactacgaactaattaagagtcaa	1376
V.1	: 1392	aacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgatt	1451
V.7	: 1377	aacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgatt	1436
V.1	: 1452	gttcaaaaggagtttagatagggagaaggatacctacgtgatgaaagtaaagggttgaa	1511
V.7	: 1437	gttcaaaaggagtttagatagggagaaggatacctatgtgatgaaagtaaagggttgaa	1496
V.1	: 1512	gatgggtggctttcctcaaagatccagtactgctattttgcaagtgaagtgttactgatata	1571
V.7	: 1497	gatgggtggctttcctcaaagatccagtactgctattttgcaagtaagtgttactgatata	1556
V.1	: 1572	aatgacaaccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgct	1631
V.7	: 1557	aatgacaaccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgct	1616

V.1 : 1632 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1691
|||||
V.7 : 1617 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1676

V.1 : 1692 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1751
|||||
V.7 : 1677 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1736

V.1 : 1752 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaacaccaaac 1811
|||||
V.7 : 1737 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaacaccaaac 1796

V.1 : 1812 cacaagttactggttttggcaagtgtggtgattgatgccagcaagagcaatggtgctg 1871
|||||
V.7 : 1797 cacaagttactggttttggcaagtgtggtgattgatgccagcaagagcaatggtgctg 1856

V.1 : 1872 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaac 1931
|||||
V.7 : 1857 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaac 1916

V.1 : 1932 cctgtcaatgacacagttgttctttcagaaaaattccactcaacacaaaaattgctctc 1991
|||||
V.7 : 1917 cctgtcaatgacacagttgttctttcagaaaaattccactcaacacaaaaattgctctc 1976

V.1 : 1992 ataactgtgacggataaggatgctggaccataatggcaggggtgacatgcttcacagatcat 2051
|||||
V.7 : 1977 ataactgtgacggataaggatgctggaccataatggcaggggtgacatgcttcacagatcat 2036

V.1 : 2052 gaaatccctttcagattaaggccagttatcagtaatcagttcctcctggagactgcagca 2111
|||||
V.7 : 2037 gaaatccctttcagattaaggccagttatcagtaatcagttcctcctggagaaatgcagca 2096

V.1 : 2112 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 2171
|||||
V.7 : 2097 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 2156

V.1 : 2172 aaacctcctttgaaatcagtcagcaatgctcttcatcaaagtgaagatgaaatgacaat 2231
|||||
V.7 : 2157 aaacctcctttgaaatcagtcagcaatgctcttcatcaaagtgaagatgaaatgacaat 2216

V.1 : 2232 gctccagttttcaccagctctttcgtaactgtttctattcctgagaataactctcctggc 2291
|||||
V.7 : 2217 gctccagttttcaccagctctttcgtaactgtttctattcctgagaataactctcctggc 2276

V.1 : 2292 atccagttgacgaaagtaagtgaatggatgcagacagtgggcctaagtctaagatcaat 2351
|||||
V.7 : 2277 atccagttgatgaaagtaagtgaacggatgcagacagtgggcctaagtctgagatcaat 2336

V.1 : 2352 tacctgctaggccctgatgctccacctgaattcagcctggattgtcgtacaggcatgctg 2411
|||||
V.7 : 2337 tacctgctaggccctgatgctccacctgaattcagcctggatcgtcgtacaggcatgctg 2396

V.1 : 2412 actgtagtgaagaaactagatagagaaaaaggagataaatattttattcacaattctggca 2471
|||||
V.7 : 2397 actgtagtgaagaaactagatagagaaaaaggagataaatattttattcacaattctggca 2456

V.1 : 2472 aaagataacgggtaccaccccttaaccagcaatgtcacagtctttgtaagcattattgat 2531
|||||
V.7 : 2457 aaagataatgggtaccaccccttaaccagcaatgtcacagtctttgtaagcattattgat 2516
|||||

V.1 : 2532 cagaatgacaatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaac 2591
|||||
V.7 : 2517 cagaatgacaatagcccagttttcactcacaatgaatacaaatctatgtcccagaaaac 2576
|||||

V.1 : 2592 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2651
|||||
V.7 : 2577 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2636
|||||

V.1 : 2652 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaaact 2711
|||||
V.7 : 2637 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaaact 2696
|||||

V.1 : 2712 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2771
|||||
V.7 : 2697 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2756
|||||

V.1 : 2772 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgcacaaagtaaccataaat 2831
|||||
V.7 : 2757 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgcacaaagtaaccataaat 2816
|||||

V.1 : 2832 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttat 2891
|||||
V.7 : 2817 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttacaactattcttat 2876
|||||

V.1 : 2892 gaattggttctaccgtccactaatccaggcacagtgggtctttcaggttaattgctggtgac 2951
|||||
V.7 : 2877 gaattggttctaccgtccactaatccaggcacagtgggtctttcaggttaattgctggtgac 2936
|||||

V.1 : 2952 aatgacactggcatgaatgcagagggttcgttacagcattgtaggaggaaacacaagagat 3011
|||||
V.7 : 2937 aatgacactggcatgaatgcagagggttcgttacagcattgtaggaggaaacacaagagat 2996
|||||

V.1 : 3012 ctgtttgcaatcgaccaagaacagggaacataacattgatggagaaatgtgatgttaca 3071
|||||
V.7 : 2997 ctgtttgcaatcgaccaagaacagggaacataacattgatggagaaatgtgatgttaca 3056
|||||

V.1 : 3072 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 3131
|||||
V.7 : 3057 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 3116
|||||

V.1 : 3132 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgatt 3191
|||||
V.7 : 3117 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcagtgaccaatgctacactgatt 3176
|||||

V.1 : 3192 aatgaactggtgcgcaaaagcactgaagcaccagtgaccccaataactgagatagctgat 3251
|||||
V.7 : 3177 aatgaactggtgcgcaaaagcattgaagcaccagtgaccccaataactgagatagctgat 3236
|||||

V.1 : 3252 gtatcctcaccaactagtactatgtcaagatcctggttgacagctgttgctggcaccata 3311
|||||
V.7 : 3237 gtatcctcaccaactagtactatgtcaagatcctggttgacagctgttgctggcaccata 3296
|||||

V.1 : 3312 actgtcgtttagttattttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3371
|||||
V.7 : 3297 actgtcgtttagttattttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3356
|||||
V.1 : 3372 aaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaaccagaaaaacagg 3431
|||||
V.7 : 3357 aaggctgctcagaaaaacatgcagaattctgaatgggctaccccaaaccagaaaaacagg 3416
|||||
V.1 : 3432 cagatgataatgatgaagaaaaaagaaaaagaagaagcattcccctaagaacttgctg 3491
|||||
V.7 : 3417 cagatgataatgatgaagaaaaaagaaaaagaagaagcattcccctaagaacttgctg 3476
|||||
V.1 : 3492 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgatggaacaga 3551
|||||
V.7 : 3477 cttaattgttgcactattgaagaaactaaggcagatgatgttgacagtgatggaacaga 3536
|||||
V.1 : 3552 gtcacactagaccttcctattgatctagaagagcaacaatgggaaagtacaattgggta 3611
|||||
V.7 : 3537 gtcacactagaccttcctattgatctagaagagcaacaatgggaaagtacaattgggta 3596
|||||
V.1 : 3612 actacacctactactttcaagcccgacagccctgatttggccgacactacaaatctgcc 3671
|||||
V.7 : 3597 actacacctactactttcaagcccgacagccctgatttggccgacactacaaatctgcc 3656
|||||
V.1 : 3672 tctccacagcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatc 3731
|||||
V.7 : 3657 tctccacagcctgccttccaaattcagcctgaaactcccctgaatttgaagcaccacatc 3716
|||||
V.1 : 3732 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaattgttcc 3791
|||||
V.7 : 3717 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaattgttcc 3776
|||||
V.1 : 3792 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgacgaccttcgag 3851
|||||
V.7 : 3777 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgacaaccttcgag 3836
|||||
V.1 : 3852 gtacctgtgtccgtacacaccagaccg 3878
|||||
V.7 : 3837 gtacctgtgtccgtacacaccagaccg 3863
|||||

Score = 1567 bits (815), Expect = 0.0Identities = 829/836 (99%) Strand = Plus /
Plus

V.1 : 3 ggtgggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttttt 62
|||||
V.7 : 1 ggtgggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaacctttttt 60
|||||
V.1 : 63 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgactttat 122
|||||
V.7 : 61 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgactttat 120
|||||
V.1 : 123 attaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcacat 182
|||||
V.7 : 121 attaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcacat 180
|||||

V.1 : 183 gatagttgttaccatgttttaggcattagtcacatcaacccctctcctctcccaaacttct 242
 |||||
 V.7 : 181 gatagttgttaccatgttttaggcgttagtcacatcaacccctctcctctcccaaacttct 240

V.1 : 243 cttcttcaaatcaaactttatttagtcctctcttataatgattccttgccctcgttttatc 302
 |||||
 V.7 : 241 cttcttcaaatcaaactttatttagtcctctcttataatgattccttgccctcgttttatc 300

V.1 : 303 cagatcaatttttttcactttgatgccagagctgaagaaatggactactgtataaatt 362
 |||||
 V.7 : 301 cagatcaatttttttcactttgatgccagagctgaagaaatggactattgtataaatt 360

V.1 : 363 attcattgccagagaataattgcattttaaacccatattataacaaagaataatgatta 422
 |||||
 V.7 : 361 attcattgccagagaataattgcattttaaacccatgttataacaaagaataatgatta 420

V.1 : 423 tattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatttt 482
 |||||
 V.7 : 421 tattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatttt 480

V.1 : 483 aattatttgtattctctttaactatcttggtatattaaagtattatcttttatatattta 542
 |||||
 V.7 : 481 aattatttgtattctctttaactatcttggtatattaaagtattatcttttatatattta 540

V.1 : 543 tcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatcttatt 602
 |||||
 V.7 : 541 tcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatcttatt 600

V.1 : 603 tcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttatca 662
 |||||
 V.7 : 601 tcatttatctttattcttaatgtacgaattcataatatttgattcagaacagatttatca 660

V.1 : 663 ctaattaacagagtgcaattatgctaacatctcatttactgattttaatttaaaacagt 722
 |||||
 V.7 : 661 ctaattaacagagtgcaattatgctaacatctcatttactgattttaatttaaaacagt 720

V.1 : 723 ttttgtaacatgcatgttttaggggttggtcttctaataatttcttcttctctctctct 782
 |||||
 V.7 : 721 ttttgtaacatgcatgttttaggggttggtcttctaataatttcttcttctctctctct 780

V.1 : 783 ctctctcttcttttggtcagtggtgtgctgggttaatacaacaaactgtaacaagtgt 838
 |||||
 V.7 : 781 ctctctcttcttttggtcagtggtgtgctgggttaatacaacaaactgtcacaagtgt 836

Table LIV(f). Peptide sequences of protein coded by 109P1D4 v.7 (SEQ ID NO: 270)

MFRVGFLIIS	SSSSLSPLLL	VSVVRVNTTN	CHKCLLSGTY	IFAVLLVCVV	FHSGAQEKNY	60
TIREIIPENV	LIGNLLKDLN	LSLIPNKS LT	TTMQFKLVYK	TGDVPLIRIE	EDTGEIFTTG	120
ARIDREKLCA	GIPRDEHCFY	EVEVAILPDE	IFRLVKIRFL	IEDINDNAPL	FPATVINISI	180
PENSAINSKY	TLPAAVDPDV	GINGVQNYEL	IKSQNIFGLD	VIETPEGDKM	PQLIVQKELD	240
REEKDTYVMK	VKVEDGGFPQ	RSSTAILQVS	VTDTNDNHPV	FKETEIEVSI	PENAPVGTSV	300
TQLHATDADI	GENAKIHFSF	SNLVSNIARR	LEHLNATTGL	ITIKEPLDRE	ETPNHKLVL	360
ASDGGLMPAR	AMVLVNVDV	NDNVPSIDIR	YIVNPVNDTV	VLSENIPLNT	KIALITVTDK	420
DADHNGRVTC	FTDHEIPFRL	RPVFSNQFLL	ENAAYL DYES	TKEYAIKLLA	ADAGKPPLNQ	480
SAMLFIKVKD	ENDNAPVFTQ	SFVTVSIPEN	NSPGIQLMKV	SATDADSGPN	AEINYLLGPD	540
APPEFSLDRR	TGMLTVVKKL	DREKEDKYLF	TILAKDNGVP	PLTSNVTVFV	SIIDQNDNSP	600
VFTHNEYKFX	VPENLPRHGT	VGLITVTDPD	YGDNSAVTLS	ILDENDFTI	DSQTGVIRPN	660

ISFDREKQES	YTFYVKAEDG	GRVSRSSSAK	VTINVVDVND	NKPVFIVPPY	NYSYELVLP	720
TNPGTVVQV	IAVDNDTGMN	AEVRSIVGG	NTRDLFAIDQ	ETGNITLMEK	CDVTDLGLHR	780
VLVKANDLGQ	PDSLFSVVIV	NLFVNESVTN	ATLINELVRK	SIEAPVTPNT	EIADVSSPTS	840
DYVKILVAAV	AGTITVVVVI	FITAVVRCRQ	APHLKAAQKN	MONSEWATPN	PENRQMIMMK	900
KKKKKKKHSP	KNLLLNVTI	EETKADDVDS	DGNRVTLDLP	IDLEEQTMGK	YNWVTTPTTF	960
KPDSPDLARH	YKSASPQPAF	QIQPETPLNL	KHHIIQELPL	DNTFVACDSI	SNCSSSSSDP	1020
YSVSDCGYPV	TTFEVPVSVH	TRPTDSRT				1048

Table LV(f). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 271) and 109P1D4 v.7 (SEQ ID NO: 272)
 Score = 1961 bits (5081), Expect = 0.0Identities = 992/1009 (98%), Positives = 995/1009 (98%)

V.1	: 3	LLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLTTAMQ	62
V.7	: 35	LLSGTYIFAVLL CVVFHSGAQEKNYTIREE+PENVLIG+LLKDLNLSLIPNKSLTT MQ	94
V.1	: 63	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	122
V.7	: 95	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	154
V.1	: 123	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	182
V.7	: 155	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	214
V.1	: 183	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	242
V.7	: 215	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	274
V.1	: 243	NDNHPVFKEITEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFNLVSNIAARRLFHL	302
V.7	: 275	NDNHPVFKEITEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFNLVSNIAARRLFHL	334
V.1	: 303	NATTGLITIKEPLDREETPNHKLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYIVN	362
V.7	: 335	NATTGLITIKEPLDREETPNHKLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYIVN	394
V.1	: 363	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLETA	422
V.7	: 395	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLE AA	454
V.1	: 423	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNSPG	482
V.7	: 455	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNSPG	514
V.1	: 483	IQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTILA	542
V.7	: 515	IQL KVSADADSGPNAEINYLLGPDAPPEFSLDRRTGMLTVVKKLDREKEDKYLFTILA	574
V.1	: 543	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYFYVPENLPRHGTVGLITVTDPDYGDN	602
V.7	: 575	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEY FYVPENLPRHGTVGLITVTDPDYGDN	634
V.1	: 603	SAVTLSILDENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	662
V.7	: 635	SAVTLSILDENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	694
V.1	: 663	VVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVQVIAVDNDTGMNAEVRSIVGGNTRD	722
V.7	: 695	VVDVNDNKPVFIVPP N SYELVLPSTNPGTVVQVIAVDNDTGMNAEVRSIVGGNTRD	754
V.1	: 723	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVIVNLFVNESVTNATLI	782
V.7	: 755	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVIVNLFVNESVTNATLI	814
V.1	: 783	NELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVIFITAVVRCRQAPHL	842
V.7	: 815	NELVRKS EAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVIFITAVVRCRQAPHL	874
V.1	: 843	KAAQKNQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNLFVTIEETKADDVDSGDR	902

KAAQKN QNSEWATPNPENRQMIMMKKKKKKHSKPNLLN VTIEETKADDVDSGDNR
 v.7 : 875 KAAQKNMQNSEWATPNPENRQMIMMKKKKKKHSKPNLLNVVTIEETKADDVDSGDNR 934
 VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLNSKHII 962
 v.1 : 903 VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLN KHII
 v.7 : 935 VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLNLKHII 994
 IQELPLDNTFVACDSISKCSSSSSDPYSVSDCGYPVTTTFFVPSVHTRP 1011
 v.1 : 963 IQELPLDNTFVACDSIS CSSSSSDPYSVSDCGYPVTTTFFVPSVHTRP
 v.7 : 995 IQELPLDNTFVACDSISNCSSSSDPYSVSDCGYPVTTTFFVPSVHTRP 1043

Table LII(g). Nucleotide sequence of transcript variant 109P1D4 v.8 (SEQ ID NO: 273)

ggtggtccag	tacctccaaa	gatatggaat	acactcctga	aatatcctga	aacctttttt	60
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attaatagct	attcttggtt	ttcttatcca	aagaaaaatc	ctctaataccc	cttttcacat	180
gatagtgtgt	accatgttta	ggcgtagtc	acatcaaccc	ctctcctctc	ccaaacttct	240
cttcttcaaa	tcaaacttta	ttagtccttc	ctttataatg	attccttgcc	tcctttttatc	300
cagatcaatt	ttttttcact	ttgatgccc	gagctgaaga	aatggactat	tgtataaatt	360
attcattgcc	aagagaataa	ttgcatttta	aacctatgtt	ataacaaaga	ataatgatta	420
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tgaaagacct	taacttgtcg	ctgattccaa	acaagtcctt	gacaactact	atgcagttca	1020
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aaaaggagtt	agatagggaa	gagaaggata	cctatgtgat	gaaagtaaa	ggtgaagatg	1500
gtggctttcc	tcaaagatcc	agtactgcta	ttttgcaagt	aagtgttact	gatacaaatg	1560
acaaccacc	agtctttaag	gagacagaga	ttgaagtcag	tataccagaa	aatgctcctg	1620
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cagttttcac	ccagtctttc	gtaactgttt	ctattcctga	gaataactct	cctggcatcc	2280
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caagaagaaa	taccaataac	acacacagaa	caaaaacat	caaaatctca	tatatgaaat	6060
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tattaaataa	cttatcaggc	atctcaatgg	ttactatcta	tgttagttaa	aatcaaatag	7080
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aattttgtgt	attcttattt	acttaacatt	ttacttttaa	ttatgtaaat	ttggttagaa	7980
aataataata	aatggttagt	gctattgtgt	aatggtagca	gttacaaaga	gcctctgcct	8040
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atgtaatcca	gaagcaaac	tgtatttaatt	gttctatttc	aggttctgta	ttgcatgttt	9000
tcttattaat	atatattaat	aaaagttatg	agaaat			9036

Table LIII(g). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 274) and 109P1D4 v.8 (SEQ ID NO: 275)
 Score = 5664 bits (2946), Expect = 0.0, Identities = 3000/3027 (99%) Strand = Plus / Plus

V.1	: 852	ttgttgtccgggacgtacattttcgcggtcctgctagcatgcgtggtgtccactctggc	911
V.8	: 837	ttgttgtccgggacgtacattttcgcggtcctgctagcatgcgtggtgtccactctggc	896
V.1	: 912	gcccaggagaaaaactacacatccgagaagaatgccagaaaacgtcctgataggcgac	971
V.8	: 897	gcccaggagaaaaactacacatccgagaagaattccagaaaacgtcctgataggcaac	956
V.1	: 972	ttgttgaaagaccttaacttgcgctgattccaaacaagtccttgacaactgctatgcag	1031
V.8	: 957	ttgttgaaagaccttaacttgcgctgattccaaacaagtccttgacaactactatgcag	1016
V.1	: 1032	ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggg	1091
V.8	: 1017	ttcaagctagtgtacaagaccggagatgtgccactgattcgaattgaagaggatactggg	1076
V.1	: 1092	gagatcttcactactggcgctcgattgatcgtgagaaattatgtgctggtatcccaagg	1151

V.8 : 1077 gagatcttcactaccggcgctcgcatgtgatcgtagaaaattatgtgctggtatcccaagg 1136

V.1 : 1152 gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg 1211
|||||

V.8 : 1137 gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg 1196

V.1 : 1212 gttaagatacgttttctgatagaagataaaatgataatgcaccattgttcccagcaaca 1271
|||||

V.8 : 1197 gttaagatacgttttctgatagaagataaaatgataatgcaccattgttcccagcaaca 1256

V.1 : 1272 gttatcaacatatcaattccagagaactcggctataaaactctaaatataactctcccagcg 1331
|||||

V.8 : 1257 gttatcaacatatcaattccagagaactcggctataaaactctaaatataactctcccagcg 1316

V.1 : 1332 gctgttgatcctgacgtaggaataaacggaggttcaaaactacgaactaattaagagtcaa 1391
|||||

V.8 : 1317 gctgttgatcctgacgtaggcataaacggaggttcaaaactacgaactaattaagagtcaa 1376

V.1 : 1392 aacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgatt 1451
|||||

V.8 : 1377 aacatttttggcctcgatgtcattgaaacaccagaaggagacaagatgccacaactgatt 1436

V.1 : 1452 gttcaaaaggagttagatagggagaaggatacctacgtgatgaaagttaaagggttgaa 1511
|||||

V.8 : 1437 gttcaaaaggagttagatagggagaaggatacctatgtgatgaaagttaaagggttgaa 1496

V.1 : 1512 gatggtggctttcctcaaagatccagtactgctattttgcaagtgaagtgttactgataca 1571
|||||

V.8 : 1497 gatggtggctttcctcaaagatccagtactgctattttgcaagtaagtgttactgataca 1556

V.1 : 1572 aatgacaaccacccagtcctttaaggagacagagattgaagtcagtataccagaaaatgct 1631
|||||

V.8 : 1557 aatgacaaccacccagtcctttaaggagacagagattgaagtcagtataccagaaaatgct 1616

V.1 : 1632 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1691
|||||

V.8 : 1617 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1676

V.1 : 1692 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1751
|||||

V.8 : 1677 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatttcacctc 1736

V.1 : 1752 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaagaaacaccaaac 1811
|||||

V.8 : 1737 aatgccaccactggacttatcacaatcaaagaaccactggatagggagaagaaacaccaaac 1796

V.1 : 1812 cacaagttactgggttttgcaagtgatgggtgattgatgccagcaagagcaatggtgctg 1871
|||||

V.8 : 1797 cacaagttactgggttttgcaagtgatgggtgattgatgccagcaagagcaatggtgctg 1856

V.1 : 1872 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1931
|||||

V.8 : 1857 gtaaatgttacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1916

V.1 : 1932 cctgtcaatgacacagttgttctttcagaaaatattccactcaacaccaaattgctctc 1991

V.8 : 1917 cctgtcaatgacacagttgttctttcagaaaaattccactcaacaccaaattgctctc 1976

V.1 : 1992 ataactgtgacggataaggatgCGGaccataatggcagggtgacatgcttcacagatcat 2051
|||||

V.8 : 1977 ataactgtgacggataaggatgCGGaccataatggcagggtgacatgcttcacagatcat 2036

V.1 : 2052 gaaatccctttcagattaaggccagtattcagtaatcagttcctcctggagactgcagca 2111
|||||

V.8 : 2037 gaaatccctttcagattaaggccagtattcagtaatcagttcctcctggagaatgcagca 2096

V.1 : 2112 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 2171
|||||

V.8 : 2097 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 2156

V.1 : 2172 aaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaat 2231
|||||

V.8 : 2157 aaacctcctttgaatcagtcagcaatgctcttcatcaaagtgaagatgaaaatgacaat 2216

V.1 : 2232 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2291
|||||

V.8 : 2217 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2276

V.1 : 2292 atccagttgacgaaagtaagtgcattggatgcagacagtgggcctaatactgataagatcaat 2351
|||||

V.8 : 2277 atccagttgatgaaagtaagtgcacggatgcagacagtgggcctaatactgagatcaat 2336

V.1 : 2352 tacctgctaggccctgatgctccacctgaattcagcctggattgtcgtacaggcatgctg 2411
|||||

V.8 : 2337 tacctgctaggccctgatgctccacctgaattcagcctggatcgtcgtacaggcatgctg 2396

V.1 : 2412 actgtagtgaagaaactagatagagaaaaaggataaatattttattcacaattctggca 2471
|||||

V.8 : 2397 actgtagtgaagaaactagatagagaaaaaggataaatattttattcacaattctggca 2456

V.1 : 2472 aaagataacggggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2531
|||||

V.8 : 2457 aaagataatggggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2516

V.1 : 2532 cagaatgacaatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaac 2591
|||||

V.8 : 2517 cagaatgacaatagcccagttttcactcacaatgaatacaaatctatgtcccagaaaac 2576

V.1 : 2592 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2651
|||||

V.8 : 2577 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2636

V.1 : 2652 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaact 2711
|||||

V.8 : 2637 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaact 2696

V.1 : 2712 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2771
|||||

V.8 : 2697 ggtgtcatccgaccaaataatttcatttgatagagaaaaacaagaatcttacactttctat 2756

V.1 : 2772 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2831
|||||
V.8 : 2757 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2816

V.1 : 2832 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttat 2891
|||||
V.8 : 2817 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttacaactattcttat 2876

V.1 : 2892 gaattggttctaccgtccactaatccaggcacagtgttcttcaggttaattgctgttgac 2951
|||||
V.8 : 2877 gaattggttctaccgtccactaatccaggcacagtgttcttcaggttaattgctgttgac 2936

V.1 : 2952 aatgacactggcatgaatgcagaggttcggttacagcattgtaggaggaacacaagagat 3011
|||||
V.8 : 2937 aatgacactggcatgaatgcagaggttcggttacagcattgtaggaggaacacaagagat 2996

V.1 : 3012 ctgtttgcaatcgaccaagaacagggaacataacattgatggagaaatgtgatgttaca 3071
|||||
V.8 : 2997 ctgtttgcaatcgaccaagaacagggaacataacattgatggagaaatgtgatgttaca 3056

V.1 : 3072 gaccttggtttacacagagtgttggtcaaagctaatagacttaggacagcctgattctctc 3131
|||||
V.8 : 3057 gaccttggtttacacagagtgttggtcaaagctaatagacttaggacagcctgattctctc 3116

V.1 : 3132 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgatt 3191
|||||
V.8 : 3117 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcagtgaccaatgctacactgatt 3176

V.1 : 3192 aatgaactggtgcgcaaaagcactgaagcaccagtgaccccaatactgagatagctgat 3251
|||||
V.8 : 3177 aatgaactggtgcgcaaaagcattgaagcaccagtgaccccaatactgagatagctgat 3236

V.1 : 3252 gtatcctcaccaactagtgtactatgtcaagatcctggttgagctgttgctggcaccata 3311
|||||
V.8 : 3237 gtatcctcaccaactagtgtactatgtcaagatcctggttgagctgttgctggcaccata 3296

V.1 : 3312 actgtcgttgtagttattttcatcactgtgttagtaagatgtcgccaggcaccacacctt 3371
|||||
V.8 : 3297 actgtcgttgtagttattttcatcactgtgttagtaagatgtcgccaggcaccacacctt 3356

V.1 : 3372 aaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaaccagaaaaacagg 3431
|||||
V.8 : 3357 aaggctgctcagaaaaacatgcagaattctgaatgggctaccccaaaccagaaaaacagg 3416

V.1 : 3432 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaactgtgtg 3491
|||||
V.8 : 3417 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaactgtgtg 3476

V.1 : 3492 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgtggaacacaga 3551
|||||
V.8 : 3477 cttaatgttgcactattgaagaaactaaggcagatgatgttgacagtgtggaacacaga 3536

V.1 : 3552 gtcacactagaccttcctattgatctagaagagcaacaatgggaaagtacaattgggta 3611
|||||
V.8 : 3537 gtcacactagaccttcctattgatctagaagagcaacaatgggaaagtacaattgggta 3596

V.1 : 3612 actacacctactactttcaagcccgacagccctgatttggcccgacactacaaatctgcc 3671
|||||
V.8 : 3597 actacacctactactttcaagcctgacagccctgatttggcccgacactacaaatctgcc 3656

V.1 : 3672 tctccacagcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatc 3731
|||||
V.8 : 3657 tctccacagcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatc 3716

V.1 : 3732 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcc 3791
|||||
V.8 : 3717 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaattgttcc 3776

V.1 : 3792 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgcagaccttcgag 3851
|||||
V.8 : 3777 tcaagcagttcagatccctacagcgtttctgactgtggctatccagtgcacaaccttcgag 3836

V.1 : 3852 gtacctgtgtccgtacacaccagaccg 3878
|||||
V.8 : 3837 gtacctgtgtccgtacacaccagaccg 3863

Score = 1567 bits (815), Expect = 0.0Identities = 829/836 (99%) Strand = Plus / Plus

V.1 : 3 ggtgggtccagttacctccaaagatatggaatacactcctgaaatatcctgaaaactttttt 62
|||||
V.8 : 1 ggtgggtccagttacctccaaagatatggaatacactcctgaaatatcctgaaaactttttt 60

V.1 : 63 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgactttat 122
|||||
V.8 : 61 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgactttat 120

V.1 : 123 attaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcacat 182
|||||
V.8 : 121 attaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccttttcacat 180

V.1 : 183 gatagttgttaccatgttttaggcatttagtcacatcaacccctctcctctcccaaacttct 242
|||||
V.8 : 181 gatagttgttaccatgttttaggcgttagtcacatcaacccctctcctctcccaaacttct 240

V.1 : 243 cttcttcaaatacaactttatttagtcctcctttataatgattccttgccctcggttttatc 302
|||||
V.8 : 241 cttcttcaaatacaactttatttagtcctcctttataatgattccttgccctccttttatc 300

V.1 : 303 cagatcaattttttttcaactttgatgccagagctgaagaaatggactactgtataaatt 362
|||||
V.8 : 301 cagatcaattttttttcaactttgatgccagagctgaagaaatggactattgtataaatt 360

V.1 : 363 attcattgccagagaataattgcattttaaacccatattataacaaagaataatgatta 422
|||||
V.8 : 361 attcattgccagagaataattgcattttaaacccatgttataacaaagaataatgatta 420

V.1 : 423 tattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatttt 482
|||||
V.8 : 421 tattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatttt 480

v.1 : 483 aattatttgtattctctttaactatcttggtatattaaagtattatcttttatatattta 542
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 481 aattatttgtattctctttaactatcttggtatattaaagtattatcttttatatattta 540

 v.1 : 543 tcaatggtggacacttttataggtagctctgtgtcatttttgatactgtaggtatcttatt 602
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 541 tcaatggtggacacttttataggtagctctgtgtcatttttgatactgtaggtatcttatt 600

 v.1 : 603 tcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttatca 662
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 601 tcatttatctttattcttaatgtacgaattcataatatttgattcagaacagatttatca 660

 v.1 : 663 ctaattaacagagtgtcaattatgctaacaatctcatttactgattttaatttaaaacagt 722
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 661 ctaattaacagagtgtcaattatgctaacaatctcatttactgattttaatttaaaacagt 720

 v.1 : 723 ttttgtaaactgcatgtttagggttggtcttcttaataatttcttctctctctctctct 782
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 721 ttttgtaaactgcatgtttagggttggtcttcttaataatttcttctctctctctctct 780

 v.1 : 783 ctctctctcttttggcagtggtgtgcggttaatacaacaaactgtacaagtg 838
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 v.8 : 781 ctctctctcttttggcagtggtgtgcggttaatacaacaaactgtcacaagtg 836

Table LIV(g). Peptide sequences of protein coded by 109P1D4 v.8 (SEQ ID NO: 276)

MFRVGFLLIIS	SSSSLSPLLL	VSVVRVNTTN	CHKCLLSGTY	IFAVLLVCVV	FHSGAQEKNY	60
TIREEIPENV	LIGNLLKDLN	LSLIPNKS LT	TTMQFKLVYK	TGDVPLIRIE	EDTGEIFTTG	120
ARIDREKLCA	GIPRDEHCFY	EVEVAILPDE	IFRLVKIRFL	IEDINDNAPL	FPATVINISI	180
PENSAINSKY	TLPAAVDPDV	GINGVQNYEL	IKSQNIFGLD	VIETPEGDKM	PQLIVQKELD	240
REEKDTYVMK	VKVEDGGFPQ	RSSTAILQVS	VTDTNDNHPV	FKETEIEVSI	PENAPVGTSV	300
TQLHATDADI	GENAKIHFSF	SNLVSNIARR	LFHLNATTGL	ITIKEPLDRE	ETPNHKKLLVL	360
ASDGGLMPAR	AMVLVNVTDV	NDNVPSIDIR	YIVNPNVNDTV	VLSENIPLNT	KIALITVTDK	420
DADHNGRVTC	FTDHEIPFRL	RPVFSNQFLL	ENAAYL DYES	TKEYAIKLLA	ADAGKPLNQ	480
SAMLFIKVKD	ENDNAPVFTQ	SFVTVSIPEN	NSPGIQLMKV	SATDADSGPN	AEINYLLGPD	540
APPEFSLDRR	TGMLTVVKKL	DREKEDKYLF	TILAKDNGVP	PLTSNVTVFV	SIIDQNDNSP	600
VFTHNEYKFY	VPENLPRHGT	VGLITVTPDP	YGDNSAVTLS	ILDENDDFTI	DSQTGVIRPN	660
ISFDREKQES	YTFYVKAEDG	GRVSRSSSAK	VTINVVDVND	NKPVFIVPPY	NYSYELVLP	720
TNPGTVVFQV	IADVNDTGMN	AEVRSIVGG	NTRDLFAIDQ	ETGNITLMEK	CDVTDLGLHR	780
VLVKANDLGQ	PDSLFSVVIV	NLFVNESVTN	ATLINELVRK	SIEAPVTPNT	EIADVSSPTS	840
DYVKILVAAV	AGTITVVVVI	FITAVVRCRQ	APHLKAAQKN	MONSEWATPN	PENRQMIMMK	900
KKKKKKKHSP	KNLLLNVVTI	EETKADDVDS	DGNRVTL DLP	IDLEEQTMGK	YNWVTPTTF	960
KPDSPDLARH	YKSASPQPAF	QIQPETPLNL	KHHIIQELPL	DNTFVACDSI	SNCSSSSSDP	1020
YSVSDCGYPV	TTFEVPVSVH	TRPSQRRVTF	HLPEGSQESS	SDGGLGDHDA	GSLTSTSHGL	1080
PLGYPQEEYF	DRATPSNRTE	GDGNSDPEST	FIPGLKKEIT	VQPTVEEASD	NCTQECLIYG	1140
HSDACWMPAS	LDHSSSSQAQ	ASALCHSPPL	SQASTQHHS	PVTQTIVLCH	SPPVTQTIAL	1200
CHSPPIQVS	ALHHSPLVQ	GTALHHSPPS	AQASALCYSP	PLAQAAAISH	SSSLPQVIAL	1260
HRSQAQSSVS	LQQGWVQGAN	GLCSVDQGVQ	GSATSQFYTM	SERLHPSDDS	IKVIPLTTFA	1320
PRQARPSRG	DSPIMETHPL					1340

Table LV(g). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 277) and 109P1D4 v.8 (SEQ ID NO: 278)
 Score = 1961 bits (5081), Expect = 0.0Identities = 992/1009 (98%), Positives = 995/1009 (98%)

v.1	: 3	LLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKS LTTAMQ	62
		LLSGTYIFAVLL CVVFHSGAQEKNYTIREE+PENVLIG+LLKDLNLSLIPNKS LTT MQ	
v.8	: 35	LLSGTYIFAVLLVCVVFHSGAQEKNYTIREEIPENVLIGNLLKDLNLSLIPNKS LTTTMMQ	94
v.1	: 63	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	122
		FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	
v.8	: 95	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	154

V.1	: 123	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	182
V.8	: 155	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	214
V.1	: 183	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	242
V.8	: 215	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	274
V.1	: 243	NDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSLVSNIAARRLFHL	302
V.8	: 275	NDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSLVSNIAARRLFHL	334
V.1	: 303	NATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYIVN	362
V.8	: 335	NATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPSIDIRYIVN	394
V.1	: 363	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLETA	422
V.8	: 395	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLE	454
V.1	: 423	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFVTVSIPENNSPG	482
V.8	: 455	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFVTVSIPENNSPG	514
V.1	: 483	IQLTKVSAMDADSGPNAKINYLGPDPAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTILA	542
V.8	: 515	IQL K V S A D A D S G P N A + I N Y L L G P D A P P E F S L D R T G M L T V V K K L D R E K E D K Y L F T I L A	574
V.1	: 543	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRHGTVGLITVTDPDYGDN	602
V.8	: 575	KDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYFYVPENLPRHGTVGLITVTDPDYGDN	634
V.1	: 603	SAVTLSDLENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	662
V.8	: 635	SAVTLSDLENDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVTIN	694
V.1	: 663	VVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	722
V.8	: 695	VVDVNDNKPVFIVPPN SYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	754
V.1	: 723	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNATLI	782
V.8	: 755	LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDLSFVSVIVNLFVNESVTNATLI	814
V.1	: 783	NELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAGTITV V V V I F I T A V V R C R Q A P H L	842
V.8	: 815	NELVRKSIEAPVTPNTEIADVSSPTS DYVKILVAAGTITV V V V I F I T A V V R C R Q A P H L	874
V.1	: 843	KAAQKNQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNFVTIEETKADDVSDG NR	902
V.8	: 875	KAAQKN QNSEWATPNPENRQMIMMKKKKKKKHSPKNLLN VTIEETKADDVSDG NR	934
V.1	: 903	VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLNSKH HI	962
V.8	: 935	VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQAFQIQPETPLN KH HI	994
V.1	: 963	IQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP	1011
V.8	: 995	IQELPLDNTFVACDSISNCSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP	1043

Table LI(h). Nucleotide sequence of transcript variant 109P1D4 v.9 (SEQ ID NO: 279)

cccctttctc	cccctctgtt	aagtcctcc	ccctcgccat	tcaaaagggc	tggctcggca	60
ctggtctcctt	gcagtcggcg	aactgtctgg	gcgggaggag	ccgtgagcag	tagctgcact	120
cagctgcccc	cgcggaag	aggaaggcaa	gcaaacaga	gtgcgcagag	tggcagtgcc	180
agcggcgaca	caggcagcac	aggcagcccc	ggctgacctga	atagcctcag	aaacaacctc	240
agcgactccg	gctgctctgc	ggactgcgag	ctgtggcggt	agagcccgct	acagcagtcg	300
cagtctccgt	ggagcggcg	gaagcctttt	ttctcccttt	cgtttacctc	ttcattctac	360

tctaaaggca	tcgttattag	gaaaatcctg	ttgtgaataa	gaaggattcc	acagatcaca	420
taccagagcg	gttttgcctc	agctgtcttc	aactttgtaa	tcttgtgaag	aagctgacaa	480
gcttggtgta	ttgcagtgc	ctatgaggac	tgaatgacag	tgggttttaa	ttcagatatt	540
tcaagtgttg	tgcgggttaa	tacaacaaac	tgtcacaaag	gtttgtgtgc	cgggacgtac	600
atthtcgcgg	tctgtctagt	atgctgtgtg	ttccactctg	gcgcccagga	gaaaaactac	660
accatccgag	aagaaattcc	agaaaacgtc	ctgataggca	acttgttgaa	agaccttaac	720
ttgtcgtgta	ttccaaacaa	gtccttgaca	actactatgc	agttcaagct	agtgatacaag	780
accggagatg	tgccactgat	tcgaattgaa	gaggatactg	gtgagatctt	cactaccggc	840
gctcgcattg	atcgtgagaa	attatgtgct	ggtatcccaa	gggatgagca	ttgcttttat	900
gaagtggagg	ttgccatttt	gccggatgaa	atatttagac	tgggttaagat	acgttttctg	960
atagaagata	taaatgataa	tgcaccattg	ttcccgacaa	cagttatcaa	catatcaatt	1020
ccagagaact	cggctataaa	ctctaaatat	actctcccag	cggctgttga	tcctgacgta	1080
ggcataaacg	gagttcaaaa	ctacgaacta	attaagagtc	aaaacatttt	tggcctcgat	1140
gtcattgaaa	ccacagaagg	agacaagatg	ccacaactga	ttgttcaaaa	ggagtttagat	1200
agggaagaga	aggataccta	tgtgatgaaa	gtaaagggtg	aagatgggtg	ctttcctcaa	1260
agatccagta	ctgctatttt	gcaagtaagt	gttactgata	caaatgacaa	ccaccagtc	1320
tttaaggaga	cagagattga	agtcagata	ccagaaaatg	ctcctgtagg	cacttcagtg	1380
acacagctcc	atgccacaga	tgtcgacata	ggtgaaaatg	ccaagatcca	cttctctttc	1440
agcaatctag	tctccaacat	tgccaggaga	ttatttcacc	tcaatgccac	cactggactt	1500
atcacaaatca	aagaaccact	ggatagggaa	gaaacaccaa	accacaagtt	actggttttg	1560
gcaagtgtatg	gtggattgat	gccagcaaga	gcaatggtgc	tggtaaatgt	tacagatgtc	1620
aatgataatg	tcccatccat	tgacataaga	tacatcgtca	atcctgtcaa	tgacacagtt	1680
gttctttcag	aaaatattcc	actcaacacc	aaaattgtct	tcataactgt	gacggataag	1740
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gatagagaaa	aagaggataa	atattttatt	acaattctgg	caaaagataa	tggggtacca	2220
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aacaaaccag	ttttcattgt	ccctccttac	aactattctt	atgaattggt	tctaccgtcc	2640
actaatccag	gcacagtggg	ctttcaggta	attgctgttg	acaatgacac	tggcatgaat	2700
gcagagggttc	gttacagcat	tgtaggagga	aacacaagag	atctgtttgc	aatcgacca	2760
gaaacaggca	acataacatt	gatggagaaa	tgtgatgtta	cagaccttgg	tttacacaga	2820
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aaaaagaaaa	agaagaagaa	gcattcccct	aagaacctgc	tgcttaatgt	tgtcactatt	3240
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aagcctgaca	gccctgattt	ggcccagac	tacaatctg	cctctccaca	gcctgccttc	3420
caaatccagc	ctgaaactcc	cctgaatttg	aagcaccaca	tcattccaaga	actgcctctc	3480
gataaacctt	ttgtggcctg	tgactctatc	tccaattggt	cctcaagcag	ttcagatccc	3540
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accagaccga	ctgattccag	gacatgaact	attgaaatct	gcagtgaag	gtaactttct	3660
aggaacaaca	aaattccatt	ccccttccaa	aaaatttcaa	tgattgtgat	ttcaaaatta	3720
ggctaagatc	attaattttg	taattctagat	ttccatttat	aaaagcaagc	aaaaatcatc	3780
ttaaaaatga	tgtcctagt	aaccttgtgc	tttctttagc	tgtaatctgg	caatggaaat	3840
ttaaaaatga	tgtcctagt	agtcagcgc	aataacagag	tactctcatg	ctgtttctct	3900
gtttgctctg	aatcaacagc	catgatgtaa	tataaggctg	tcttggtgta	tacacttatg	3960
gttaatatat	cagtcatgaa	acatgcaatt	acttgcctg	tctgattgtt	gaataattaa	4020
aacattatct	ccaggagttt	ggaagtgagc	tgaactagcc	aaactactct	ctgaaaggta	4080

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tccagggcaa gagacatttt taagacccca aacaaacaaa aaacaaaacc aaaacactct 4140
ggttcagtggt tttgaaaata ttgactaaca taatatgtgt gagaaaatca tttttattac 4200
ccaccactct gcttaaaagt tgagtgggcc gggcgcggtg gctcacgcct gtaattccag 4260
cactttggga ggccgagggc ggtggatcac gaggtcagga tattgagacc atcctggcta 4320
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gcctgtagtc ccagctactc gggaggctga ggcaggagaa tggcgtgaac ccgggagggc 4440
gagcttgca gtagccgaga tggegccact gcactccagc ctgggtgaca gagcaagact 4500
ctgtctcaaa aagaaaaaaa tggtcagtga tagaaaaata ttttactagg tttttatgtt 4560
gattgtactc atgctgttcc actcctttta attattaaaa agttattttt ggctgggtgt 4620
ggtggctcat acctgtaatc ccagcacttt gggaggccga ggcgggtgga tcacctgagg 4680
tcaggagtgc aagaccagtc tggccaacat

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Table LIII(h). Nucleotide sequence alignment of 109P1D4 v.1 (SEQ ID NO: 280) and 109P1D4 v.9 (SEQ ID NO: 281)
 Score = 5664 bits (2946), Expect = 0.0Identities = 3000/3027 (99%) Strand = Plus / Plus

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V.1 : 852 ttgttgtccgggacgtacattttcgcggtcctgctagcatgctggtgttccactctggc 911
      |||
V.9 : 583 ttgttgtccgggacgtacattttcgcggtcctgctagtagtgcgtggtgttccactctggc 642

V.1 : 912 gccaggagaaaaactacaccatccgagaagaatgccagaaaacgtcctgataggcgac 971
      |||
V.9 : 643 gccaggagaaaaactacaccatccgagaagaattccagaaaacgtcctgataggcaac 702

V.1 : 972 ttgttgaaagaccttaacttgtcgctgattccaaacaagtccttgacaactgctatgcag 1031
      |||
V.9 : 703 ttgttgaaagaccttaacttgtcgctgattccaaacaagtccttgacaactactatgcag 762

V.1 : 1032 ttcaagctagtgtagaagaccggagatgtgccactgattcgaattgaaggagatactggt 1091
      |||
V.9 : 763 ttcaagctagtgtagaagaccggagatgtgccactgattcgaattgaaggagatactggt 822

V.1 : 1092 gagatcttcactactggcgctcgattgatcgtagaaaattatgtgctgggtatcccaagg 1151
      |||
V.9 : 823 gagatcttcactaccggcgctcgattgatcgtagaaaattatgtgctgggtatcccaagg 882

V.1 : 1152 gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg 1211
      |||
V.9 : 883 gatgagcattgcttttatgaagtggaggttgccattttgccggatgaaatatttagactg 942

V.1 : 1212 gttaagatacggttttctgtagaagatataaatgataatgcaccattgttcccagcaaca 1271
      |||
V.9 : 943 gttaagatacggttttctgtagaagatataaatgataatgcaccattgttcccagcaaca 1002

V.1 : 1272 gttatcaacatatcaattccagagaactcggtataaactctaaatatactctcccagcg 1331
      |||
V.9 : 1003 gttatcaacatatcaattccagagaactcggtataaactctaaatatactctcccagcg 1062

V.1 : 1332 gctgttgatcctgacgtaggaataaacggagttcaaaactacgaactaattaagagtcaa 1391
      |||
V.9 : 1063 gctgttgatcctgacgtaggcataaacggagttcaaaactacgaactaattaagagtcaa 1122

V.1 : 1392 aacatTTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAAGTGATT 1451
      |||
V.9 : 1123 aacatTTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAAGTGATT 1182

V.1 : 1452 gttcaaaaggagtttagatagggagaaggatacctacgtgatgaaagtaaagggttgaa 1511
      |||

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V.9 : 1183 gttcaaaaggagttagataggggaagagaaggatacctatgtgatgaaagtaaagggtgaa 1242

V.1 : 1512 gatggtggcctttcctcaaagatccagtactgctattttgcaagtgaagtgttactgataca 1571
|||||

V.9 : 1243 gatggtggcctttcctcaaagatccagtactgctattttgcaagtaagtgttactgataca 1302

V.1 : 1572 aatgacaaccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgct 1631
|||||

V.9 : 1303 aatgacaaccaccagtcctttaaggagacagagattgaagtcagtataaccagaaaatgct 1362

V.1 : 1632 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1691
|||||

V.9 : 1363 cctgtaggcacttcagtgacacagctccatgccacagatgctgacataggtgaaaatgcc 1422

V.1 : 1692 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatctcacctc 1751
|||||

V.9 : 1423 aagatccacttctctttcagcaatctagtctccaacattgccaggagattatctcacctc 1482

V.1 : 1752 aatgccaccactggacttatcacaatcaagaaccactggataggggaagaacaccaaac 1811
|||||

V.9 : 1483 aatgccaccactggacttatcacaatcaagaaccactggataggggaagaacaccaaac 1542

V.1 : 1812 cacaagttactggttttggcaagtgatgggtgattgatgccagcaagagcaatgggtgctg 1871
|||||

V.9 : 1543 cacaagttactggttttggcaagtgatgggtgattgatgccagcaagagcaatgggtgctg 1602

V.1 : 1872 gttaaattgtacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1931
|||||

V.9 : 1603 gttaaattgtacagatgtcaatgataatgtcccatccattgacataagatacatcgtaaat 1662

V.1 : 1932 cctgtcaatgacacagttgttctttcagaaaaattccactcaacacaaaaattgctctc 1991
|||||

V.9 : 1663 cctgtcaatgacacagttgttctttcagaaaaattccactcaacacaaaaattgctctc 1722

V.1 : 1992 ataactgtgacggataaggatgcggaccataatggcaggggtgacatgcttcacagatcat 2051
|||||

V.9 : 1723 ataactgtgacggataaggatgcggaccataatggcaggggtgacatgcttcacagatcat 1782

V.1 : 2052 gaaatccctttcagattaaggccagttatcagtaatcagttcctcctggagactgcagca 2111
|||||

V.9 : 1783 gaaatccctttcagattaaggccagttatcagtaatcagttcctcctggagaatgcagca 1842

V.1 : 2112 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 2171
|||||

V.9 : 1843 tatcttgactatgagtcacaaaaagaatatgccattaaattactggctgcagatgctggc 1902

V.1 : 2172 aaacctcctttgaatcagtcagcaatgctcttcacaaagtgaagatgaaatgacaat 2231
|||||

V.9 : 1903 aaacctcctttgaatcagtcagcaatgctcttcacaaagtgaagatgaaatgacaat 1962

V.1 : 2232 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2291
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V.9 : 1963 gctccagttttcaccagtcctttcgtaactgtttctattcctgagaataactctcctggc 2022

V.1 : 2292 atccagttgacgaaagtaagtgaatggatgcagacagtgggcctaagtctaagatcaat 2351

|||||
V.9 : 2023 atccagttgatgaaagtaagtgaacggatgcagacagtgggcctaattgctgagatcaat 2082

V.1 : 2352 tacctgctaggccctgatgctccacctgaattcagcctggattgtcgtagcaggtatgctg 2411
|||||
V.9 : 2083 tacctgctaggccctgatgctccacctgaattcagcctggatcgtagcaggtatgctg 2142

V.1 : 2412 actgtagtgaagaaactagatagagaaaaaggataaatattttattcacattctggca 2471
|||||
V.9 : 2143 actgtagtgaagaaactagatagagaaaaaggataaatattttattcacattctggca 2202

V.1 : 2472 aaagataacgggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2531
|||||
V.9 : 2203 aaagataatgggtaccacccttaaccagcaatgtcacagtctttgtaagcattattgat 2262

V.1 : 2532 cagaatgacaatagcccagttttcactcacaatgaatacaacttctatgtcccagaaaaac 2591
|||||
V.9 : 2263 cagaatgacaatagcccagttttcactcacaatgaatacaaatctatgtcccagaaaaac 2322

V.1 : 2592 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2651
|||||
V.9 : 2323 cttccaaggcatggtacagtaggactaatcactgtaactgatcctgattatggagacaat 2382

V.1 : 2652 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaact 2711
|||||
V.9 : 2383 tctgcagttacgctctccatttttagatgagaatgatgacttcaccattgattcacaaact 2442

V.1 : 2712 ggtgtcatccgaccaaataattttcatttgatagagaaaaacaagaatcttacactttctat 2771
|||||
V.9 : 2443 ggtgtcatccgaccaaataattttcatttgatagagaaaaacaagaatcttacactttctat 2502

V.1 : 2772 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2831
|||||
V.9 : 2503 gtaaaggctgaggatggtggtagagtatcacgttcttcaagtgccaaagtaaccataaat 2562

V.1 : 2832 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttccaactgttcttat 2891
|||||
V.9 : 2563 gtggttgatgtcaatgacaacaaaccagttttcattgtccctccttacaactattcttat 2622

V.1 : 2892 gaattggttctaccgtccactaatccaggcacagtggcttttcaggttaattgctgttgac 2951
|||||
V.9 : 2623 gaattggttctaccgtccactaatccaggcacagtggcttttcaggttaattgctgttgac 2682

V.1 : 2952 aatgacactggcatgaatgcagaggttcgttacagcattgtaggaggaacacaaagagat 3011
|||||
V.9 : 2683 aatgacactggcatgaatgcagaggttcgttacagcattgtaggaggaacacaaagagat 2742

V.1 : 3012 ctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttaca 3071
|||||
V.9 : 2743 ctgtttgcaatcgaccaagaacaggcaacataacattgatggagaaatgtgatgttaca 2802

V.1 : 3072 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 3131
|||||
V.9 : 2803 gaccttggtttacacagagtgttggtcaaagctaatacttaggacagcctgattctctc 2862

v.1 : 3132 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcggtgaccaatgctacactgatt 3191
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 v.9 : 2863 ttcagtgttgtaattgtcaatctgttcgtgaatgagtcagtgaccaatgctacactgatt 2922

 v.1 : 3192 aatgaactggtgcgcaaaagcactgaagcaccagtgaccccaatactgagatagctgat 3251
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 v.9 : 2923 aatgaactggtgcgcaaaagcattgaagcaccagtgaccccaatactgagatagctgat 2982

 v.1 : 3252 gtatcctcaccaactagtactatgtcaagatcctggttcagctgttgctggcaccata 3311
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 v.9 : 2983 gtatcctcaccaactagtactatgtcaagatcctggttcagctgttgctggcaccata 3042

 v.1 : 3312 actgtcgttgtagttatttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3371
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 v.9 : 3043 actgtcgttgtagttatttcatcactgctgtagtaagatgtcgccaggcaccacacctt 3102

 v.1 : 3372 aaggctgctcagaaaaacaagcagaattctgaatgggctaccccaaacccagaaaaacagg 3431
 ||||||||||||||||||
 v.9 : 3103 aaggctgctcagaaaaacatgcagaattctgaatgggctaccccaaacccagaaaaacagg 3162

 v.1 : 3432 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacttgctg 3491
 ||||||||||||||||||
 v.9 : 3163 cagatgataatgatgaagaaaaagaaaaagaagaagaagcattcccctaagaacctgctg 3222

 v.1 : 3492 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgtggaacaga 3551
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 v.9 : 3223 cttaattttgtcactattgaagaaactaaggcagatgatgttgacagtgtggaacaga 3282

 v.1 : 3552 gtcacactagaccttcctattgatctagaagagcaaacaatgggaaagtacaattgggta 3611
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3283 gtcacactagaccttcctattgatctagaagagcaaacaatgggaaagtacaattgggta 3342

 v.1 : 3612 actacacctactactttcaagcccagacgcctgatttggcccgacactacaaatctgcc 3671
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3343 actacacctactactttcaagcctgacagccctgatttggcccgacactacaaatctgcc 3402

 v.1 : 3672 tctccacagcctgccttccaaattcagcctgaaactcccctgaattcgaagcaccacatc 3731
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3403 tctccacagcctgccttccaaattcagcctgaaactcccctgaatttgaagcaccacatc 3462

 v.1 : 3732 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaagtgttcc 3791
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3463 atccaagaactgcctctcgataaacacctttgtggcctgtgactctatctccaattgttcc 3522

 v.1 : 3792 tcaagcagttcagatccctacagcggtttctgactgtggctatccagtgacgaccttcgag 3851
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3523 tcaagcagttcagatccctacagcggtttctgactgtggctatccagtgacaaccttcgag 3582

 v.1 : 3852 gtacctgtgtccgtacacaccagaccg 3878
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||||
 v.9 : 3583 gtacctgtgtccgtacacaccagaccg 3609

Table LIV(h). Peptide sequences of protein coded by 109P1D4 v.9 (SEQ ID NO: 282)

MTVGFNSDIS	SVVRVNTTNC	HKCLLSGTYI	FAVLLVCVVF	HSGAQEKNYT	IREEIPENVL	60
IGNLLKDLNL	SLIPNKSLLT	TMQFKLVYKT	GDVPLIRIEE	DTGEIFTTGA	RIDREKLCAG	120
IPRDEHCFYE	VEVAILPDEI	FRLVKIRFLI	EDINDNAPLF	PATVINISIP	ENSAINSKYT	180

LPAAVDPDVG	INGVQNYELI	KSQNIFGLDV	IETPEGDKMP	QLIVQKELDR	EEKDTYVMKV	240
KVEDGGFPQR	SSTAILQVSV	TDTNDNHPVF	KETEIEVSIP	ENAPVGTSVT	QLHATDADIG	300
ENAKIHFSFS	NLVSNIARRL	FHLNATTGLI	TIKEPLDREE	TPNHKLLVLA	SDGGLMPARA	360
MVLNVNVDVN	DNVPSIDIRY	IVNPVNDTVV	LSENIPLNTK	IALITVTDKD	ADHNGRVTCF	420
TDHEIPFRLR	PVFSNQFLE	NAAYLDYEST	KEYAIKLLAA	DAGKPPLNQS	AMLFIKVKDE	480
NDNAPVFTQS	FVTVSIPENN	SPGIQLMKVS	ATDADSGPNA	EINYLLGPD	PPEFSLDRRT	540
GMLTVVKKLD	REKEDKYLFT	ILAKDNGVPP	LTSNVTVEVS	IIDQNDNSPV	FTHNEYKFYV	600
PENLPRHGT	GLITVTDPDY	GDNSAVTSLI	LDENDDFTID	SQTGVIRPNI	SFDREKQESY	660
TFYVKAEDGG	RVSRSSSAKV	TINVVDVNDN	KPVFIVPPYN	YSYELVLPST	NPGTVVFQVI	720
AVDNDTGMNA	EVRYISIVGGN	TRDLFAIDQE	TGNITLMEKC	DVTDLGLHRV	LVKANDLGQP	780
DSLESVVIVN	LEVNESVTNA	TLINELVRKS	IEAPVTPNTE	IADVSSPTSD	YVKILVAAVA	840
GTITVVVVIF	ITAVVRCRQA	PHLKAQKNM	QNSEWATPNP	ENRQMIMMK	KKKKKKHSPK	900
NLLNVVTIE	ETKADDVDS	GNRVTLDLPI	DLEEQTMGKY	NWVTPPTTFK	PDSPDLARHY	960
KSASPQPAFQ	IQPETPLNLK	HIIQELPLD	NTFVACDSIS	NCSSSSSDPY	SVSDCGYPVT	1020
TFEVPVSVHT	RPTDSRT					1037

Table LV(h). Amino acid sequence alignment of 109P1D4 v.1 (SEQ ID NO: 283) and 109P1D4 v.9 (SEQ ID NO: 284)
 Score = 1961 bits (5081), Expect = 0.0, Identities = 992/1009 (98%), Positives = 995/1009 (98%)

V.1	: 3	LLSGTYIFAVLLACVVFHSGAQEKNYTIREEMPENVLIGDLLKDLNLSLIPNKSLLTAMQ	62
		LLSGTYIFAVLL CVVFHSGAQEKNYTIREE+PENVLIG+LLKDLNLSLIPNKSLLT MQ	
V.9	: 24	LLSGTYIFAVLLVCVVFHSGAQEKNYTIREEIPENVLIGNLLKDLNLSLIPNKSLLTMMQ	83
V.1	: 63	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	122
		FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	
V.9	: 84	FKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIFRL	143
V.1	: 123	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	182
		VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	
V.9	: 144	VKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIKSQ	203
V.1	: 183	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	242
		NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	
V.9	: 204	NIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVTDT	263
V.1	: 243	NDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIARRLFHL	302
		NDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIARRLFHL	
V.9	: 264	NDNHPVFKETEIEVSIPENAPVGTSVTQLHATDADIGENAKIHFSFSNLVSNIARRLFHL	323
V.1	: 303	NATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVNVDVNDVPSIDIRYIVN	362
		NATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVNVDVNDVPSIDIRYIVN	
V.9	: 324	NATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVNVDVNDVPSIDIRYIVN	383
V.1	: 363	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLETA	422
		PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLE AA	
V.9	: 384	PVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCFTDHEIPFRLRPVFSNQFLENA	443
V.1	: 423	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNSPG	482
		YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNSPG	
V.9	: 444	YLDYESTKEYAIKLLAADAGKPPLNQSAMLFIKVKDENDNAPVFTQSFTVTSIPENNSPG	503
V.1	: 483	IQLTKVSAMDADSGPNAKINYLLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTILA	542
		IQL KVSADADSGPNA+INYLLGPDAPPEFSLD RTGMLTVVKKLDREKEDKYLFTILA	
V.9	: 504	IQLMKVSATDADSGPNAEINYLLGPDAPPEFSLDRRTGMLTVVKKLDREKEDKYLFTILA	563
V.1	: 543	KDNGVPPLTSNVTVEVSIIQNDNSPVFTHNEYNFYVPENLPRHGTGVLITVTDPDYGDN	602
		KDNGVPPLTSNVTVEVSIIQNDNSPVFTHNEY FYVPENLPRHGTGVLITVTDPDYGDN	
V.9	: 564	KDNGVPPLTSNVTVEVSIIQNDNSPVFTHNEYKFYVPENLPRHGTGVLITVTDPDYGDN	623
V.1	: 603	SAVTLISILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRRVSRSSSAKVTTIN	662
		SAVTLISILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRRVSRSSSAKVTTIN	
V.9	: 624	SAVTLISILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRRVSRSSSAKVTTIN	683
V.1	: 663	VVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	722
		VVDVNDNKPVFIVPP N SYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	
V.9	: 684	VVDVNDNKPVFIVPPNYSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYISIVGGNTRD	743

v.1 : 723 LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDSLFSVVIVNLFVNESVTNATLI 782
LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDSLFSVVIVNLFVNESVTNATLI
v.9 : 744 LFAIDQETGNITLMEKCDVTDLGLHRVLVKANDLGQPDSLFSVVIVNLFVNESVTNATLI 803

v.1 : 783 NELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVVIFITAVVRCRQAPHL 842
NELVRKS EAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVVIFITAVVRCRQAPHL
v.9 : 804 NELVRKSIEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVVIFITAVVRCRQAPHL 863

v.1 : 843 KAAQKNQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNLFVTIEETKADDVDSG NR 902
KAAQKN QNSEWATPNPENRQMIMMKKKKKKKHSPKNLLN VTIEETKADDVDSG NR
v.9 : 864 KAAQKNMQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLNVVTIEETKADDVDSG NR 923

v.1 : 903 VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNSKH HI 962
VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLN KH HI
v.9 : 924 VTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASQPAFQIQPETPLNLKH HI 983

v.1 : 963 IQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP 1011
IQELPLDNTFVACDSIS CSSSSSDPYSVSDCGYPVTTFEVPVSVHTRP
v.9 : 984 IQELPLDNTFVACDSISNCSSSSDPYSVSDCGYPVTTFEVPVSVHTRP 1032

CLAIMS:

1. A composition that comprises:
 - a) a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of Figure 2;
 - b) a peptide of Tables VIII-XXI;
 - c) a peptide of Tables XXII to XLV; or,
 - d) a peptide of Tables XLVI to XLIX.
2. A composition of claim 1, which elicits an immune response.
3. A protein of claim 2 that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence shown in Figure 2.
4. A protein of claim 2, which is bound by an antibody that specifically binds to a protein of Figure 2.
5. A composition of claim 2 wherein the composition comprises a cytotoxic T cell (CTL) polypeptide epitope or an analog thereof, from the amino acid sequence of a protein of Figure 2.
6. A composition of claim 5 further limited by a *proviso* that the epitope is not an entire amino acid sequence of Figure 2.
7. A composition of claim 2 further limited by a *proviso* that the polypeptide is not an entire amino acid sequence of a protein of Figure 2.
8. A composition of claim 2 that comprises an antibody polypeptide epitope from an amino acid sequence of Figure 2.
9. A composition of claim 8 further limited by a *proviso* that the epitope is not an entire amino acid sequence of Figure 2.
10. A composition of claim 8 wherein the antibody epitope comprises a peptide region of at least 5 amino acids of Figure 2 in any whole number increment up to the end of said peptide, wherein the epitope comprises an amino acid position selected from:
 - a) an amino acid position having a value greater than 0.5 in the Hydrophilicity profile of Figure 5,
 - b) an amino acid position having a value less than 0.5 in the Hydrophobicity profile of Figure 6;
 - c) an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;
 - d) an amino acid position having a value greater than 0.5 in the Average Flexibility profile of Figure 8;
 - e) an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9;
 - f) a combination of at least two of a) through e);
 - g) a combination of at least three of a) through e);
 - h) a combination of at least four of a) through e); or

- i) a combination of five of a) through e).
11. A polynucleotide that encodes a protein of claim 1.
12. A polynucleotide of claim 11 that comprises a nucleic acid molecule set forth in Figure 2.
13. A polynucleotide of claim 12 further limited by a *proviso* that the encoded protein is not an entire amino acid sequence of Figure 2.
14. A composition comprising a polynucleotide that is fully complementary to a polynucleotide of claim 11.
15. An 109P1D4 siRNA composition that comprises siRNA (double stranded RNA) that corresponds to the nucleic acid ORF sequence of the 109P1D4 protein or a subsequence thereof; wherein the subsequence is 19, 20, 21, 22, 23, 24, or 25 contiguous RNA nucleotides in length and contains sequences that are complementary and non-complementary to at least a portion of the mRNA coding sequence.
16. A polynucleotide of claim 13 that further comprises an additional nucleotide sequence that encodes an additional peptide of claim 1.
17. A method of generating a mammalian immune response directed to a protein of Figure 2, the method comprising:
exposing cells of the mammal's immune system to a portion of
a) a 109P1D4-related protein and/or
b) a nucleotide sequence that encodes said protein,
whereby an immune response is generated to said protein.
18. A method of generating an immune response of claim 17, said method comprising:
providing a 109P1D4-related protein that comprises at least one T cell or at least one B cell epitope; and,
contacting the epitope with a mammalian immune system T cell or B cell respectively, whereby the T cell or B cell is activated.
19. A method of claim 18 wherein the immune system cell is a B cell, whereby the activated B cell generates antibodies that specifically bind to the 109P1D4-related protein.
20. A method of claim 18 wherein the immune system cell is a T cell that is a cytotoxic T cell (CTL), whereby the activated CTL kills an autologous cell that expresses the 109P1D4-related protein.
21. A method of claim 18 wherein the immune system cell is a T cell that is a helper T cell (HTL), whereby the activated HTL secretes cytokines that facilitate the cytotoxic activity of a cytotoxic T cell (CTL) or the antibody-producing activity of a B cell.

corresponds to the nucleic acid ORF sequence of the 109P1D4 protein or a subsequence thereof; wherein the subsequence is 19, 20, 21, 22, 23, 24, or 25 contiguous RNA nucleotides in length and contains sequences that are complementary and non-complementary to at least a portion of the mRNA coding sequence.

30. A composition of claim 28, further comprising a physiologically acceptable carrier.
31. A pharmaceutical composition that comprises the composition of claim 28 in a human unit dose form.
32. A composition of claim 28 wherein the substance comprises an antibody or fragment thereof that specifically binds to a protein of Figure 2.
33. An antibody or fragment thereof of claim 32, which is monoclonal.
34. An antibody of claim 32, which is a human antibody, a humanized antibody or a chimeric antibody.
35. A non-human transgenic animal that produces an antibody of claim 32.
36. A hybridoma that produces an antibody of claim 33.
37. A composition of claim 28 wherein the substance reduces or inhibits the viability, growth or reproduction status of a cell that expresses a protein of Figure 2.
38. A composition of claim 28 wherein the substance increases or enhances the viability, growth or reproduction status of a cell that expresses a protein of Figure 2.
39. A composition of claim 28 wherein the substance is selected from the group comprising:
 - a) an antibody or fragment thereof, either of which immunospecifically binds to a protein of Figure 2;
 - b) a polynucleotide that encodes an antibody or fragment thereof, either of which immunospecifically binds to a protein of Figure 2;
 - c) a ribozyme that cleaves a polynucleotide having a 109P1D4 coding sequence, or a nucleic acid molecule that encodes the ribozyme; and, a physiologically acceptable carrier; and
 - d) human T cells, wherein said T cells specifically recognize a 109P1D4 peptide subsequence in the context of a particular HLA molecule;
 - e) a protein of Figure 2, or a fragment of a protein of Figure 2;
 - f) a nucleotide encoding a protein of Figure 2, or a nucleotide encoding a fragment of a protein of Figure 2;
 - g) a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of Figure 2;
 - h) a peptide of Tables VIII-XXI;
 - i) a peptide of Tables XXII to XLV;
 - j) a peptide of Tables XLVI to XLIX;

- k) an antibody polypeptide epitope from an amino acid sequence of Figure 2;
- l) a polynucleotide that encodes an antibody polypeptide epitope from an amino acid sequence of Figure 2; or
- m) an 109P1D4 siRNA composition that comprises siRNA (double stranded RNA) that corresponds to the nucleic acid ORF sequence of the 109P1D4 protein or a subsequence thereof; wherein the subsequence is 19, 20, 21, 22, 23, 24, or 25 contiguous RNA nucleotides in length and contains sequences that are complementary and non-complementary to at least a portion of the mRNA coding sequence.

40. A method of inhibiting viability, growth or reproduction status of cancer cells that express a protein of Figure 2, the method comprising:
administering to the cells the composition of claim 28, thereby inhibiting the viability, growth or reproduction status of said cells.

41. The method of claim 40, wherein the composition comprises an antibody or fragment thereof, either of which specifically bind to a 109P1D4-related protein.

42. The method of claim 40, wherein the composition comprises (i) a 109P1D4-related protein or, (ii) a polynucleotide comprising a coding sequence for a 109P1D4-related protein or comprising a polynucleotide complementary to a coding sequence for a 109P1D4-related protein.

43. The method of claim 40, wherein the composition comprises a ribozyme that cleaves a polynucleotide that encodes a protein of Figure 2.

44. The method of claim 40, wherein the composition comprises human T cells to said cancer cells, wherein said T cells specifically recognize a peptide subsequence of a protein of Figure 2 while the subsequence is in the context of the particular HLA molecule.

45. The method of claim 40, wherein the composition comprises a vector that delivers a nucleotide that encodes a single chain monoclonal antibody, whereby the encoded single chain antibody is expressed intracellularly within cancer cells that express a protein of Figure 2.

46. A method of delivering an agent to a cell that expresses a protein of Figure 2, said method comprising:
providing the agent conjugated to an antibody or fragment thereof of claim 32; and,
exposing the cell to the antibody-agent or fragment-agent conjugate.

47. A method of inhibiting viability, growth or reproduction status of cancer cells that express a protein of Figure 2, the method comprising:
administering to the cells the composition of claim 28, thereby inhibiting the viability, growth or reproduction status of said cells.

48. A method of targeting information for preventing or treating a cancer of a tissue listed in Table I to a subject in need thereof, which comprises:

detecting the presence or absence of the expression of a polynucleotide associated with a cancer of a tissue listed in Table I in a sample from a subject, wherein the expression of the polynucleotide is selected from the group consisting of:

- (a) a nucleotide sequence in Figure 2;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in Figure 2;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in Figure 2;

directing information for preventing or treating the cancer of a tissue listed in Table I to a subject in need thereof based upon the presence or absence of the expression of the polynucleotide in the sample.

49. The method of claim 48, wherein the information comprises a description of detection procedure or treatment for a cancer of a tissue listed in Table I.

50. A method for identifying a candidate molecule that modulates cell proliferation, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (i) the nucleotide sequence of SEQ ID NO:1;
 - (ii) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence set forth in Figure 3;
 - (iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence set forth in Figure 3; and
 - (iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and
- (b) determining the presence or absence of an interaction between the test molecule and the nucleotide sequence or protein,

whereby the presence of an interaction between the test molecule and the nucleotide sequence or protein identifies the test molecule as a candidate molecule that modulates cell proliferation.

51. The method of claim 50, wherein the system is an animal.

52. The method of claim 50, wherein the system is a cell.

53. The method of claim 50, wherein the test molecule comprises an antibody or antibody fragment that specifically binds the protein encoded by the nucleotide sequence of (i), (ii), (iii), or (iv).

54. A method for treating a cancer of a tissue listed in Table I in a subject, which comprises administering a candidate molecule identified by the method of claim 50 to a subject in need thereof, whereby the candidate molecule treats a cancer of a tissue listed in Table I in the subject.

55. A method for identifying a candidate therapeutic for treating a cancer of a tissue listed in Table I, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (i) the nucleotide sequence of SEQ ID NO:1;
- (ii) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence set forth in Figure 3;
- (iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence set forth in Figure 3; and
- (iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleotide sequence or protein,

whereby the presence of an interaction between the test molecule and the nucleotide sequence or protein identifies the test molecule as a candidate therapeutic for treating a cancer of a tissue listed in Table I.

56. The method of claim 55, wherein the system is an animal.

57. The method of claim 55, wherein the system is a cell.

58. The method of claim 55, wherein the test molecule comprises an antibody or antibody fragment that specifically binds the protein encoded by the nucleotide sequence of (i), (ii), (iii), or (iv).

Figure 1: 109P1D4 SSH sequence of 192 nucleotides. (SEQ ID NO: 1).

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1  GATCCTGGTT GCAGCTGTTG CTGGCACCAT AACTGTCGTT GTAGTTATTT TCATCACTGC
61 TGTAGTAAGA TGTCGCCAGG CACACACCTT AAGGCTGCTC AGAAAAACAT GCAGAATTCT
121 GAATGGGCTA CCCCAAACCC AGAAAACAGG CAGATGATAA AAAAAAAAAA AAAAAAAAAA
181 AAAAGCTTGA TC
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Figure 2:

Figure 2A. The cDNA (SEQ ID. NO. : 2) and amino acid sequence (SEQ ID. NO. : 3) of 109P1D4 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 846-3911 including the stop codon.

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1  ctggtgggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttt
61  ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtacttt
121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccctttttcac
181 atgatatgttgttaccatgttttaggcattagtcacatcaacccctctcctctcccaaactt
241 ctcttcttcaaatacaactttattagtcctctctttataatgattccttgccctcgtttta
301 tccagatcaattttttttctactttgatgccagagctgaagaaatggactactgtataaa
361 ttattcattgccagagaataattgcattttaaacccatattataacaaagaataatgat
421 tatattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatt
481 ttaattatttgtattctctttaactatcttggatatattaaagtattatcttttatatatt
541 tatcaatgggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta
601 tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat
661 cactaattaacagagtggtcaattatgctaacatctcatttactgattttaatttaaaaca
721 gtttttgttaacatgcatgttttaggggttggtctcttaataatttcttcttctctctct
781 ctctcctcttcttttggtcagtggtgtgcgggttaatacaacaaactgtaacaagtgtac
1  M D L L S G T Y I F A V L L A C V V F
841 ctggtATGGACTTGTGTCCGGGACGTACATTTTCGCGGTCCTGCTAGCATGCGTGGTGT
20  H S G A Q E K N Y T I R E E M P E N V L
901 TCCACTCTGGCGCCAGGAGAAAACTACACCATCCGAGAAGAAATGCCAGAAAACTGCC
40  I G D L L K D L N L S L I P N K S L T T
961 TGATAGGCGACTTGTGAAAGACCTTAACTTGTGCTGATTCCAAACAAGTCCTTGACAA
60  A M Q F K L V Y K T G D V P L I R I E E
1021 CTGCTATGCAGTTCAAGCTAGTGTAACAAGACCGGAGATGTGCCACTGATTGCAATTGAAG
80  D T G E I F T T G A R I D R E K L C A G
1081 AGGATACTGGTGAGATCTTCACTACTGGCGCTCGCATTGATCGTGAGAAATTATGTGCTG
100  I P R D E H C F Y E V E V A I L P D E I
1141 GTATCCCAAGGGATGAGCATTGCTTTTATGAAGTGGAGGTTGCCATTTTGCCGGATGAAA
120  F R L V K I R F L I E D I N D N A P L F
1201 TATTTAGACTGGTTAAGATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTTGT
140  P A T V I N I S I P E N S A I N S K Y T
1261 TCCCAGCAACAGTTATCAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATA
160  L P A A V D P D V G I N G V Q N Y E L I
1321 CTCTCCAGCGGCTGTTGATCCTGACGTAGGAATAAACGGAGTTCAAACTACGAACTAA
180  K S Q N I F G L D V I E T P E G D K M P
1381 TTAAGAGTCAAAACATTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGC
200  Q L I V Q K E L D R E E K D T Y V M K V
1441 CACAACTGATTGTTCAAAAGGAGTTAGATAGGGAAGAGAAGGATACCTACGTGATGAAAG
220  K V E D G G F P Q R S S T A I L Q V S V
1501 TAAAGGTTGAAGATGGTGGCTTTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTGAGTG
240  T D T N D N H P V F K E T E I E V S I P
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1561 TTACTGATACAAATGACAACCACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATAC
260 E N A P V G T S V T Q L H A T D A D I G
1621 CAGAAAATGCTCCTGTAGGCACCTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAG
280 E N A K I H F S F S N L V S N I A R R L
1681 GTGAAAATGCCAAGATCCACTTCTCTTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGAT
300 F H L N A T T G L I T I K E P L D R E E
1741 TATTTACCTCAATGCCACCACTGGACTTATCACAATCAAAGAACCACTGGATAGGGGAA
320 T P N H K L L V L A S D G G L M P A R A
1801 AAACACCAAACCACAAGTTACTGGTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAG
340 M V L V N V T D V N D N V P S I D I R Y
1861 CAATGGTGCTGGTAAATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGAT
360 I V N P V N D T V V L S E N I P L N T K
1921 ACATCGTCAATCCTGTCAATGACACAGTTGTTCTTTTCAGAAAATATTCCACTCAACACCA
380 I A L I T V T D K D A D H N G R V T C F
1981 AAATTGCTCTCATAACTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCT
400 T D H E I P F R L R P V F S N Q F L L E
2041 TCACAGATCATGAAATCCCTTTTCAGATTAAAGGCCAGTATTCAGTAATCAGTTCCTCCTGG
420 T A A Y L D Y E S T K E Y A I K L L A A
2101 AGACTGCAGCATATCTTGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTG
440 D A G K P P L N Q S A M L F I K V K D E
2161 CAGATGCTGGCAAACCTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATG
460 N D N A P V F T Q S F V T V S I P E N N
2221 AAAATGACAATGCTCCAGTTTTCACCCAGTCTTTTCGTAAGTGTTCCTATTCTCTGAGAATA
480 S P G I Q L T K V S A M D A D S G P N A
2281 ACTCTCCTGGCATCCAGTTGACGAAAGTAAGTGCAATGGATGCAGACAGTGGGCCTAATG
500 K I N Y L L G P D A P P E F S L D C R T
2341 CTAAGATCAATTACCTGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATTGTCGTA
520 G M L T V V K K L D R E K E D K Y L F T
2401 CAGGCATGCTGACTGTAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTATTCA
540 I L A K D N G V P P L T S N V T V F V S
2461 CAATTCTGGCAAAAGATAACGGGGTACCACCCCTTAACCAGCAATGTCACAGTCTTTGTAA
560 I I D Q N D N S P V F T H N E Y N F Y V
2521 GCATTATTGATCAGAATGACAATAGCCAGTTTTCAGTCAATGAATACAACCTTCTATG
580 P E N L P R H G T V G L I T V T D P D Y
2581 TCCAGAAAACCTTCCAAGGCATGGTACAGTAGGACTAATCACTGTAAGTATCCTGATT
600 G D N S A V T L S I L D E N D D F T I D
2641 ATGGAGACAATTCTGCAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTG
620 S Q T G V I R P N I S F D R E K Q E S Y
2701 ATTCACAACTGGTGTCTATCCGACCAAATATTTTCATTTGATAGAGAAAAACAAGAACTTT
640 T F Y V K A E D G G R V S R S S S A K V
2761 ACACTTTCTATGTAAAGGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAG
660 T I N V V D V N D N K P V F I V P P S N

2821 TAACCATAAAATGTGGTTGATGTCAATGACAACAAACCAGTTTTTCATTGTCCCTCCTTCCA
680 C S Y E L V L P S T N P G T V V F Q V I
2881 ACTGTTCTTATGAATTGGTTCTACCGTCCACTAATCCAGGCACAGTGGTCTTTCAGGTAA
700 A V D N D T G M N A E V R Y S I V G G N
2941 TTGCTGTTGACAATGACACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAA
720 T R D L F A I D Q E T G N I T L M E K C
3001 ACACAAGAGATCTGTTTGCAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAAT
740 D V T D L G L H R V L V K A N D L G Q P
3061 GTGATGTTACAGACCTTGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGC
760 D S L F S V V I V N L F V N E S V T N A
3121 CTGATTCTCTCTTCAGTGTGTAATTGTCAATCTGTTTCGTGAATGAGTCGGTGACCAATG
780 T L I N E L V R K S T E A P V T P N T E
3181 CTACACTGATTAATGAAGTGGTGCAGCAAGCACTGAAGCACCAGTGACCCCAAATACTG
800 I A D V S S P T S D Y V K I L V A A V A
3241 AGATAGCTGATGTATCCTCACCAACTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTG
820 G T I T V V V V I F I T A V V R C R Q A
3301 CTGGCACCATAACTGTCGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGG
840 P H L K A A Q K N K Q N S E W A T P N P
3361 CACCACACCTTAAGGCTGCTCAGAAAAACAAGCAGAATTCTGAATGGGCTACCCCAAACC
860 E N R Q M I M M K K K K K K K K H S P K
3421 CAGAAAACAGGCAGATGATAATGATGAAGAAAAAGAAAAAGAAGAAGCATTCCCTTA
880 N L L L N F V T I E E T K A D D V D S D
3481 AGAACTTGCTGCTTAATTTTGTCACTATTGAAGAACTAAGGCAGATGATGTTGACAGTG
900 G N R V T L D L P I D L E E Q T M G K Y
3541 ATGGAAACAGAGTCACACTAGACCTTCCTATTGATCTAGAAGAGCAAACAATGGGAAAGT
920 N W V T T P T T F K P D S P D L A R H Y
3601 ACAATTGGGTAACTACACCTACTACTTTCAAGCCCGACAGCCCTGATTTGGCCCGACACT
940 K S A S P Q P A F Q I Q P E T P L N S K
3661 ACAATCTGCCTCTCCACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCTGAATTCGA
960 H H I I Q E L P L D N T F V A C D S I S
3721 AGCACCACATCATCCAAGAACTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCT
980 K C S S S S S D P Y S V S D C G Y P V T
3781 CCAAGTGTTCCTCAAGCAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGA
1000 T F E V P V S V H T R P V G I Q V S N T
3841 CGACCTTCGAGGTACCTGTGTCCGTACACACCAGACCGGTAGGTATCCAAGTTTCTAACA
1020 T F *
3901 CAACTTTCTAActatttttttattattatttttcagttgatgtagaactttacaaaatcta
3961 ttgacttcaaagagggatcaaaacaatcatattctacagatgtacccaatagatatatgg
4021 attcaattaagtttggtagaagatgagaacaaaataactactgatttaggaaaattggat
4081 gcagaataataattatagtaggggcaattttgtctgtagatggcagtatgacaattcttg
4141 ctagagaatatattgaaaaaaacttcaacacaaaagggtttagcactgtcctcagtaacca
4201 ttgtgtgcatgaggatcagaatagtctgggctagatacatcacattaaagcttttcagaa

4261 tctgataaatagctctaaataactaatgatattgagaagcctagcttcacttgggaaaatc
4321 tgtggctgttcacagaaattcagcaccaagttattcccccatactctaccaggccttca
4381 ggtcctcataaagaaaagtgtcgttttcagattaggaactcaaaattattttggcgcac
4441 aaatctacagtcacacaatataacaagaatgggattagaaaaatgaaagcctactcattc
4501 tcatctttaagccagagaatgaaatatatatgaggtctctggatagctattttaaatattt
4561 gcatatttatgcaaggtattttgagcccttcagaagacattct

Figure 2B. The cDNA (SEQ ID. NO. : 4) and amino acid sequence (SEQ ID. NO. : 5) of 109P1D4 v.2.

The start methionine is underlined. The open reading frame extends from nucleic acid 503-3667 including the stop codon.

1 cccctttctccccctcggttaagtccc|ccccctcgccattcaaaagggctggctcgga
61 ctggctccttgagtcggcgaactgtcggggcgggaggagccgtgagcagtagctgcact
121 cagctgcccgcgcggcaaagaggaaggcaagccaaacagagtgcgcagagtggcagtgcc
181 agcggcgacacaggcagcacaggcagccgggctgcctgaatagcctcagaaacaacctc
241 agcgactccggctgctctgcggactgcgagctgtggcggtagagcccgtacagcagtcg
301 cagtctccgtggagcgggaggccttttttctccctttcgtttacctcttcattctac
361 tctaaaggcatcggtatttaggaaaatcctgttgcaataagaaggattccacagatcaca
421 taccggagagggttttgcctcagctgctctcaactttgtaatcttgtgaagaagctgacaa
1 M R T E R Q W V L I Q I F
481 gcttggctgattgcagagcactATGAGGACTGAACGACAGTGGGTTTTAATTCAGATATT
14 Q V L C G L I Q Q T V T S V P G M D L L
541 TCAAGTGTGTGCGGGTTAATAACAACAACTGTAACAAGTGACCTGGTATGGACTTGT
34 S G T Y I F A V L L A C V V F H S G A Q
601 GTCCGGGACGTACATTTTCGCGGTCCTGCTAGCATGCGTGGTGTTCCTCTGGCGCCCA
54 E K N Y T I R E E M P E N V L I G D L L
661 GGAGAAAACTACACCATCCGAGAAGAAATGCCAGAAAACGTCCTGATAGGCGACTTGT
74 K D L N L S L I P N K S L T T A M Q F K
721 GAAAGACCTTAACCTGTGCTGATTCCAAACAAGTCCTTGACAACTGCTATGCAGTTCAA
94 L V Y K T G D V P L I R I E E D T G E I
781 GCTAGTGATACAAGACCGGAGATGTGCCACTGATTGCAATTGAAGAGGATACTGGTGAGAT
114 F T T G A R I D R E K L C A G I P R D E
841 CTTCATACTGGCGCTCGCATTGATCGTGAGAAATTATGTGCTGGTATCCCAAGGGATGA
134 H C F Y E V E V A I L P D E I F R L V K
901 GCATTGCTTTTATGAAGTGGAGGTTGCCATTTTGCCGGATGAAATATTTAGACTGGTTAA
154 I R F L I E D I N D N A P L F P A T V I
961 GATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTGTTCCAGCAACAGTTAT
174 N I S I P E N S A I N S K Y T L P A A V
1021 CAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATACTCTCCCAGCGGCTGT
194 D P D V G I N G V Q N Y E L I K S Q N I
1081 TGATCCTGACGTAGGAATAAACGGAGTTCAAACTACGAACATAATTAAGAGTCAAAACAT
214 F G L D V I E T P E G D K M P Q L I V Q
1141 TTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAACGATTGTTCA
234 K E L D R E E K D T Y V M K V K V E D G

1201 AAAGGAGTTAGATAGGGAAGAGAAGGATACCTACGTGATGAAAGTAAAGGTTGAAGATGG
254 G F P Q R S S T A I L Q V S V T D T N D
1261 TGGCTTTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTGAGTGTTACTGATACAAATGA
274 N H P V F K E T E I E V S I P E N A P V
1321 CAACCAACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATACCAGAAAATGCTCCTGT
294 G T S V T Q L H A T D A D I G E N A K I
1381 AGGCACTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAGGTGAAAATGCCAAGAT
314 H F S F S N L V S N I A R R L F H L N A
1441 CCACTTCTCTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGATTATTTACCTCAATGC
334 T T G L I T I K E P L D R E E T P N H K
1501 CACCACTGGACTTATCACAATCAAAGAACCCTGGATAGGGAAGAAACACCAAACACAA
354 L L V L A S D G G L M P A R A M V L V N
1561 GTTACTGGTTTTTGCAAGTGATGGTGGATTGATGCCAGCAAGAGCAATGGTGTGGTAA
374 V T D V N D N V P S I D I R Y I V N P V
1621 TGTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGATACATCGTCAATCCTGT
394 N D T V V L S E N I P L N T K I A L I T
1681 CAATGACACAGTTGTCTTTTCAGAAAATATTCCACTCAACACCAAAATTGCTCTCATAAC
414 V T D K D A D H N G R V T C F T D H E I
1741 TGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCTTCACAGATCATGAAAT
434 P F R L R P V F S N Q F L L E T A A Y L
1801 CCCTTTCAGATTAAGGCCAGTATTTCAGTAATCAGTTCTCTCTGGAGACTGCAGCATATCT
454 D Y E S T K E Y A I K L L A A D A G K P
1861 TGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTGCAGATGCTGGCAAACC
474 P L N Q S A M L F I K V K D E N D N A P
1921 TCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATGAAAATGACAATGCTCC
494 V F T Q S F V T V S I P E N N S P G I Q
1981 AGTTTTACCCAGTCTTTCGTAACGTGTTCTATTCTCTGAGAATAACTCTCTGGCATCCA
514 L T K V S A M D A D S G P N A K I N Y L
2041 GTTGACGAAAGTAAGTGCAATGGATGCAGACAGTGGGCCTAATGCTAAGATCAATTACCT
534 L G P D A P P E F S L D C R T G M L T V
2101 GCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATTGTCGTACAGGCATGCTGACTGT
554 V K K L D R E K E D K Y L F T I L A K D
2161 AGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTTATTTCACAATTCTGGCAAAAGA
574 N G V P P L T S N V T V F V S I I D Q N
2221 TAACGGGGTACCACCCTTAACCAGCAATGTCACAGTCTTTGTAAGCATTATTGATCAGAA
594 D N S P V F T H N E Y N F Y V P E N L P
2281 TGACAATAGCCCAGTTTTCCTCACTCACAATGAATACAACCTCTATGTCCCAGAAAACCTTCC
614 R H G T V G L I T V T D P D Y G D N S A
2341 AAGGCATGGTACAGTAGGACTAATCACTGTAACCTGATCCTGATTATGGAGACAATTCTGC
634 V T L S I L D E N D D F T I D S Q T G V
2401 AGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTGATTTCACAAACTGGTGT
654 I R P N I S F D R E K Q E S Y T F Y V K

2461 CATCCGACCAATATTTTCATTGATAGAGAAAAACAAGAATCTTACACTTTCTATGTAAA
674 A E D G G R V S R S S S A K V T I N V V
2521 GGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAGTAACCATAAATGTGGT
694 D V N D N K P V F I V P P S N C S Y E L
2581 TGATGTCAATGACAACAAACCAGTTTTCATTGTCCCTCCTTCCAACGTTCCTTATGAATT
714 V L P S T N P G T V V F Q V I A V D N D
2641 GGTTCCTACCGTCCACTAATCCAGGCACAGTGGTCTTTTCAAGTAATTGCTGTTGACAATGA
734 T G M N A E V R Y S I V G G N T R D L F
2701 CACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAAACACAAGAGATCTGTT
754 A I D Q E T G N I T L M E K C D V T D L
2761 TGCAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAATGTGATGTTACAGACCT
774 G L H R V L V K A N D L G Q P D S L F S
2821 TGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGCCTGATTCTCTCTTCAG
794 V V I V N L F V N E S V T N A T L I N E
2881 TGTGTGAATTGTCAATCTGTTTCGTAATGAGTCGGTGACCAATGCTACACTGATTAAATGA
814 L V R K S T E A P V T P N T E I A D V S
2941 ACTGGTGCACAAAGCACTGAAGCACCAGTGACCCCAAATACTGAGATAGCTGATGTATC
834 S P T S D Y V K I L V A A V A G T I T V
3001 CTCACCAACTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTGCTGGCACCATAACTGT
854 V V V I F I T A V V R C R Q A P H L K A
3061 CGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGGCACCACCTTAAGGC
874 A Q K N K Q N S E W A T P N P E N R Q M
3121 TGCTCAGAAAAACAAGCAGAATTCTGAATGGGCTACCCCAAACCCAGAAAACAGGCAGAT
894 I M M K K K K K K K H S P K N L L L N
3181 GATAATGATGAAGAAAAAGAAAAAGAAGAAGCATTCCCCTAAGAACTGTGCTGCTTAA
914 F V T I E E T K A D D V D S D G N R V T
3241 TTTTGTCACTATTGAAGAACTAAGGCAGATGATGTTGACAGTGATGGAAACAGAGTCAC
934 L D L P I D L E E Q T M G K Y N W V T T
3301 ACTAGACCTTCCTATTGATCTAGAAGACCAAACAATGGGAAAGTACAATTGGGTAACACTAC
954 P T T F K P D S P D L A R H Y K S A S P
3361 ACCTACTACTTTCAAGCCCGACAGCCCTGATTTGGCCCGACACTACAAATCTGCCTCTCC
974 Q P A F Q I Q P E T P L N S K H H I I Q
3421 ACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCCTGAATTGGAAGCACCACATCATCCA
994 E L P L D N T F V A C D S I S K C S S S
3481 AGAACTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCTCCAAGTGTTCCTCAAG
1014 S S D P Y S V S D C G Y P V T T F E V P
3541 CAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGACGACCTTCGAGGTACC
1034 V S V H T R P T D S R T S T I E I C S E
3601 TGTGTCCGTACACACCAGACCGACTGATTCAGGACATCAACTATTGAAATCTGCAGTGA
1054 I *
3661 GATATAActttctaggaacaacaaaattccattccccttcaaaaaatttcaatgattgt
3721 gatttcaaaaattaggctaagatcattaattttgtaatctagatttccattataaaagca

3781 agcaaaaatcatcttaaaaatgatgtcctagtgaaacctgtgctttcttttagctgtaatc
3841 tggcaatggaaatttaaaatttatggaagagacagtgcagcacaataacagagtactctc
3901 atgctgtttctctgtttgctctgaatcaacagccatgatgtaataaaggctgtcttggt
3961 gtatacacttatgggttaatatatcagtcataaaacatgcaattacttgccctgtctgatt
4021 gttgaataattaaaacattatctccaggagtttggagtgagctgaactagccaaactac
4081 tctctgaaagggtatccagggaagagacatttttaagaccccaacaaacaaaaacaaa
4141 accaaaacactctgggtcagtggtttgaaaatattcactaacataatattgctgagaaaa
4201 tcattttttattaccaccactctgcttaaaagttagtggtggcgccggcggtggctcacg
4261 cctgtaatcccagcactttgggagccgagggcggtggatcacgaggtcaggagattgag
4321 accatcctggctaacacggtgaaaccccatctccactaaaaatacaaaaaattagcctgg
4381 cgtggtggcgccgctgtagtcacagctactcgggaggtgaggcaggagaatagcgtg
4441 aacccgggagggcgagcttgagtgagccgagatggcgccactgcactccagcctgggtg
4501 acagagcaagactctgtctcaaaaagaaaaaatgttcaatgatagaaaataattttact
4561 aggtttttatgttgattgtactcatgctgttccactccttttaattattaaaaagttatt
4621 tttggctgggtgtggtggctcacacctgtaatcccagcactttgggagggcgaggtgggt
4681 ggatcacctgaggtcaggagttcaagaccagtctggccaacat

Figure 2C. The cDNA (SEQ ID. NO. : 6) and amino acid sequence (SEQ ID. NO. : 7) of 109P1D4 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 846-4889 including the stop codon.

1 ctgggtggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttt
61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagtgttacttgtacttt
121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaatacccttttccac
181 atgatagttgttaccatgttttaggcattagtcacatcaacccctctcctctcccaaactt
241 ctcttcttcaaatacaactttatttagtccctcctttataatgattccttgccctggttta
301 tccagatcaattttttttctactttgatgccagagctgaagaaatggactactgtataaa
361 ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat
421 tatattttgtgattttgtaacaaataccctttattttcccttaactattgaattaaatatt
481 ttaattatttgtattctctttaactatcttgggtatattaaagtattatcttttatatatt
541 tatcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta
601 tttcatttatctttattcttaataatgtacgaattcataatatttgattcagaacaaatttat
661 cactaattaacagagtgatcaattatgctaacatctcatttactgattttaatttaaaaca
721 gtttttggttaacatgcatgttttaggggttggtcttctaataatttcttcttctctctct
781 ctctcctcttcttttgggtcagtggtgtgctgggttaatacaacaaactgtaacaagtgtac
1 M D L L S G T Y I F A V L L A C V V F
841 ctgggtATGGACTTGTGTCCGGGACGTACATTTTCGCGGTCCTGCTAGCATGCGTGGTGT
20 H S G A Q E K N Y T I R E E M P E N V L
901 TCCACTCTGGCGCCAGGAGAAAACTACACCATCCGAGAAGAAATGCCAGAAAACGTCC
40 I G D L L K D L N L S L I P N K S L T T
961 TGATAGGCGACTTGTGAAAGACCTTAACCTGTGCTGATTCCAAACAAGTCCTTGACAA
60 A M Q F K L V Y K T G D V P L I R I E E
1021 CTGCTATGCAGTTCAAGCTAGTGTACAAGACCGGAGATGTGCCACTGATTCGAATTGAAG

80 D T G E I F T T G A R I D R E K L C A G
1081 AGGATACTGGTGAGATCTTCACTACTGGCGCTCGCATTGATCGTGAGAAATTATGTGCTG
100 I P R D E H C F Y E V E V A I L P D E I
1141 GTATCCCAAGGGATGAGCATTGCTTTTATGAAGTGGAGGTTGCCATTTGCCGGATGAAA
120 F R L V K I R F L I E D I N D N A P L F
1201 TATTTAGACTGGTTAAGATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTGT
140 P A T V I N I S I P E N S A I N S K Y T
1261 TCCCAGCAACAGTTATCAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATA
160 L P A A V D P D V G I N G V Q N Y E L I
1321 CTCTCCAGCGGCTGTTGATCCTGACGTAGGAATAAACGGAGTTCAAACTACGAACTAA
180 K S Q N I F G L D V I E T P E G D K M P
1381 TTAAGAGTCAAAACATTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGC
200 Q L I V Q K E L D R E E K D T Y V M K V
1441 CACAACTGATTGTTCAAAAGGAGTTAGATAGGGAAGAGAAGGATACCTACGTGATGAAAG
220 K V E D G G F P Q R S S T A I L Q V S V
1501 TAAAGGTTGAAGATGGTGGCTTTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTGAGTG
240 T D T N D N H P V F K E T E I E V S I P
1561 TTAGTGATACAAATGACAACCACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATAC
260 E N A P V G T S V T Q L H A T D A D I G
1621 CAGAAAATGCTCCTGTAGGCACCTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAG
280 E N A K I H F S F S N L V S N I A R R L
1681 GTGAAAATGCCAAGATCCACTTCTCTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGAT
300 F H L N A T T G L I T I K E P L D R E E
1741 TATTTACCTCAATGCCACCACTGGACTTATCACAATCAAAGAACCACTGGATAGGGGAG
320 T P N H K L L V L A S D G G L M P A R A
1801 AAACACCAAACCACAAGTFACTGGTFTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAG
340 M V L V N V T D V N D N V P S I D I R Y
1861 CAATGGTGCTGGTAAATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGAT
360 I V N P V N D T V V L S E N I P L N T K
1921 ACATCGTCAATCCTGTCAATGACACAGTTGTTCTTTTCAGAAAATATTCCACTCAACACCA
380 I A L I T V T D K D A D H N G R V T C F
1981 AAATTGCTCTCATAACTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCT
400 T D H E I P F R L R P V F S N Q F L L E
2041 TCACAGATCATGAAATCCCTTTTCAGATTAAGGCCAGTATTCAGTAATCAGTTCCTCCTGG
420 T A A Y L D Y E S T K E Y A I K L L A A
2101 AGACTGCAGCATATCTTGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTG
440 D A G K P P L N Q S A M L F I K V K D E
2161 CAGATGCTGGCAAACCTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATG
460 N D N A P V F T Q S F V T V S I P E N N
2221 AAAATGACAATGCTCCAGTTTTCACCCAGTCTTTTCGTAAGTGTCTTCTATTCTCTGAGAATA
480 S P G I Q L T K V S A M D A D S G P N A
2281 ACTCTCCTGGCATCCAGTTGACGAAAGTAAGTGCAATGGATGCAGACAGTGGGCCTAATG

500 K I N Y L L G P D A P P E F S L D C R T
2341 CTAAGATCAATTACCTGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATTGTCGTA
520 G M L T V V K K L D R E K E D K Y L F T
2401 CAGGCATGCTGACTGTAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTTATTCA
540 I L A K D N G V P P L T S N V T V F V S
2461 CAATTCTGGCAAAAGATAACGGGGTACCACCCTTAACCAGCAATGTCACAGTCTTTGTAA
560 I I D Q N D N S P V F T H N E Y N F Y V
2521 GCATTATTGATCAGAATGACAATAGCCCCAGTTTTCACCTCACAATGAATACAACCTTCTATG
580 P E N L P R H G T V G L I T V T D P D Y
2581 TCCCAGAAAACCTTCCAAGGCATGGTACAGTAGGACTAATCACTGTAACCTGATCCTGATT
600 G D N S A V T L S I L D E N D D F T I D
2641 ATGGAGACAATTCTGCAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTG
620 S Q T G V I R P N I S F D R E K Q E S Y
2701 ATTCACAACTGGTGTCTATCCGACCAAATATTTTCAATTTGATAGAGAAAAACAAGAATCTT
640 T F Y V K A E D G G R V S R S S S A K V
2761 ACACTTTCTATGTAAAGGCTGAGGATGGTGGTAGAGTATCACGTCTTTCAAGTGCCAAAG
660 T I N V V D V N D N K P V F I V P P S N
2821 TAACCATAAATGTGGTTGATGTCAATGACAACAAACCAGTTTTTCATTGTCCCTCCTTCCA
680 C S Y E L V L P S T N P G T V V F Q V I
2881 ACTGTTCTTATGAATTGGTTCTACCGTCCACTAATCCAGGCACAGTGGTCTTTTCAGGTAA
700 A V D N D T G M N A E V R Y S I V G G N
2941 TTGCTGTTGACAATGACACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAA
720 T R D L F A I D Q E T G N I T L M E K C
3001 ACACAAGAGATCTGTTTGCAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAAT
740 D V T D L G L H R V L V K A N D L G Q P
3061 GTGATGTTACAGACCTTGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGC
760 D S L F S V V I V N L F V N E S V T N A
3121 CTGATTCTCTCTTCAGTGTGTGAATTGTCAATCTGTTTCGTTGAATGAGTCGGTGACCAATG
780 T L I N E L V R K S T E A P V T P N T E
3181 CTACACTGATTAAATGAACCTGGTGCAGCAAAAGCACTGAAGCACCAGTGACCCCAAATACTG
800 I A D V S S P T S D Y V K I L V A A V A
3241 AGATAGCTGATGTATCCTCACCACCTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTG
820 G T I T V V V V I F I T A V V R C R Q A
3301 CTGGCACCATAACTGTCGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGG
840 P H L K A A Q K N K Q N S E W A T P N P
3361 CACCACACCTTAAGGCTGCTCAGAAAAACAAGCAGAATTCTGAATGGGCTACCCCAAACC
860 E N R Q M I M M K K K K K K K K H S P K
3421 CAGAAAACAGGCAGATGATAATGATGAAGAAAAAGAAAAAGAGAAGAAGCATTCCCCCTA
880 N L L L N F V T I E E T K A D D V D S D
3481 AGAACTTGCTGCTTAATTTTGTCACTAFTGAAGAACTAAGGCAGATGATGTTGACAGTG
900 G N R V T L D L P I D L E E Q T M G K Y
3541 ATGGAAACAGAGTCACACTAGACCTTCCTATTGATCTAGAAGAGCAACAATGGGAAAGT

920 N W V T T P T T F K P D S P D L A R H Y
3601 ACAATTGGGTAACCTACACCTACTACTTTCAAGCCCGACAGCCCTGATTTGGCCCGACACT
940 K S A S P Q P A F Q I Q P E T P L N S K
3661 ACAAATCTGCCTCTCCACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCCTGAATTCGA
960 H H I I Q E L P L D N T F V A C D S I S
3721 AGCACCACATCATCCAAGAACTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCT
980 K C S S S S S D P Y S V S D C G Y P V T
3781 CCAAGTGTTCCTCAAGCAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGA
1000 T F E V P V S V H T R P P M K E V V R S
3841 CGACCTTCGAGGTACCTGTGTCCGTACACACCAGACCGCCAATGAAGGAGGTTGTGCGAT
1020 C T P M K E S T T M E I W I H P Q P Q R
3901 CTTGCACCCCCATGAAAGAGTCTACAACCTATGGAGATCTGGATTTCATCCCCAACACAGC
1040 K S E G K V A G K S Q R R V T F H L P E
3961 GGAAATCTGAAGGGAAAGTGGCAGGAAAGTCCCAGCGCGTGTACATTTACCTGCCAG
1060 G S Q E S S S D G G L G D H D A G S L T
4021 AAGGCTCTCAGGAAAGCAGCAGTGATGGTGGACTGGGAGACCATGATGCAGGCAGCCTTA
1080 S T S H G L P L G Y P Q E E Y F D R A T
4081 CCAGCACATCTCATGGCCTGCCCCCTTGGCTATCCTCAGGAGGAGTACTTTGATCGTGCTA
1100 P S N R T E G D G N S D P E S T F I P G
4141 CACCCAGCAATCGCACTGAAGGGGATGGCAACTCCGATCCTGAATCTACTTTTCATACCTG
1120 L K K A A E I T V Q P T V E E A S D N C
4201 GACTAAAGAAAGCTGCAGAAATAACTGTTCACCAACTGTGGAAGAGGCCTCTGACAACT
1140 T Q E C L I Y G H S D A C W M P A S L D
4261 GCACTCAAGAATGTCTCATCTATGGCCATTCTGATGCCTGTCTGGATGCCGGCATCTCTGG
1160 H S S S S Q A Q A S A L C H S P P L S Q
4321 ATCATTCCAGCTCTTCGCAAGCACAGGCCTCTGCTCTATGCCACAGCCCACCACTGTAC
1180 A S T Q H H S P R V T Q T I A L C H S P
4381 AGGCCTCTACTCAGCACCCACAGCCCACGAGTGACACAGACCATTGCTCTCTGCCACAGCC
1200 P V T Q T I A L C H S P P P I Q V S A L
4441 CTCCAGTGACACAGACCATCGCATTGTGCCACAGCCCACCAACCGATACAGGTGTCTGCTC
1220 H H S P P L V Q A T A L H H S P P S A Q
4501 TCCACCACAGTCCTCCTCTAGTGCAGGCTACTGCACTTCACCACAGCCCACCATCAGCAC
1240 A S A L C Y S P P L A Q A A A I S H S S
4561 AGGCCTCAGCCCTCTGCTACAGCCCTCCTTTAGCACAGGCTGCTGCAATCAGCCACAGCT
1260 P L P Q V I A L H R S Q A Q S S V S L Q
4621 CTCCTCTGCCACAGGTTATTTGCCCTCCATCGTAGTCAGGCCCAATCATCAGTCAGTTTGC
1280 Q G W V Q G A D G L C S V D Q G V Q G S
4681 AGCAAGGTTGGGTGCAAGGTGCTGATGGGCTATGCTCTGTTGATCAGGGAGTGCAAGGTA
1300 A T S Q F Y T M S E R L H P S D D S I K
4741 GTGCAACATCTCAGTTTTACACCATGTCTGAAAGACTTCATCCCAGTGATGATTCAATTA
1320 V I P L T T F T P R Q Q A R P S R G D S
4801 AAGTCATTCCTTTGACAACCTTCACTCCACGCCAACAGGCCAGACCGTCCAGAGGTGATT

1340 P I M E E H P L *

4861 CCCCATTATGGAAGAACATCCCTTGTAAGctaaaatagttacttcaaattttcagaaa
4921 agatgtatatagtcaaaatttaagatacaattccaatgagtattctgattatcagatttg
4981 taaataactatgtaaatagaaacagataccagaataaatctacagctagacccttagtca
5041 atagttaacccaaaaaattgcaatttggttaattcagaatgtgtatttaaaaagaaaagga
5101 atttaacaatttgcatccccctgtacagtaaggcttatcatgacagagcgactatttct
5161 gatgtacagtattttttgttggtttttatcatcatgtgcaatattactgatttggttccat
5221 gctgattgtgtggaaccagtatgtagcaaatggaaagcctagaaatatcttattttctaa
5281 gtttaccttttagtttacctaaacttttggttcagataacggttaaaagggtatacgtactcta
5341 gcctttttttgggctttctttttgatttttggttggttttcagbttttttgttggtgt
5401 tagtgagtctcccttcaaaatcgcagtaggtagtgtaaatactgcttggttggtgtctct
5461 ctgctgtcatgttttctaccttattccaatactatatgttgataaaatttgatatataca
5521 ttttcaataaagaatatgtataaactgtacagatctagatctacaacctatttctctact
5581 ctttagtagagttcgcagacacagaagtgcataaactgccctaattaagcaactatttggt
5641 aaaaagggcctctttttactttaatagtttagtgtaaagtacatcagaaataaagctgta
5701 tctgccattttaagcctgtagtcattattacttgggtctttacttctgggaatttgat
5761 gtaacagcctagaaaattaaaaggaggtggatgcatccaagcacgagtcacttaaaata
5821 tcgacggtaaactactattttgtagagaaactcaggaagatttaaatgttgatttgacag
5881 ctcaataggctgtttaccaaaggggtgttcagtaaaaataacaaatacatgtaactgtagat
5941 aaaaccatatactaaatctataagactaagggatttttggtattctagctcaacttactg
6001 aagaaaaccactaataacaacaagaatatcaggaagggaacttttcaagaaatgtaattat
6061 aaatctacatcaaacagaattttaaggaaaaatgcagagggagaaaataaggcacatgact
6121 gcttcttgtagtcaacaagaaataccaataacacacacagaacaaaaaccatcaaaatct
6181 catatatgaaataaaatatattcttctaagcaaagaaacagtactattcatagaaaacat
6241 tagttttcttctgttggtgtgttatttcttctgtatcctcttaactggccattatcttg
6301 tatgtgcacattttataaatgtacagaaacatcaccaacttaattttcttccatagcaaa
6361 actgagaaaaatacctgtttcagtataacactaaaccaagagacaattgatgtttaatgg
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6481 tgtaatgtataaacttgataatttaatttatgattaaactgtgtgtaattttgtaacataa
6541 actgtggtaattgcataatttcattgggtgaggatttccactgaatattgagaaagtttct
6601 tttcatgtgccagcagggttaagtagcggttttcagaatatacattattcccatccattgt
6661 aaagttccttaagtcatatttgactgggcgtgcagaataacttcttaacttttaactatc
6721 agagtttgatttaataaaattaataatgttttttctccttcgtggtgtaatgttccaag
6781 ggatttggagcactactggttttccagggtgcagtgaatcccgaaggactgatgatatttg
6841 aatgtttattaaattattatcatacaaatgtgttgatattgtggctattgttgatgttga
6901 aaatttttaacttggggaagattaagaaaagaaccaatagtgaacaaaatcagtgcttcc
6961 agtagattttagaacattctttgcctcaaaaaacctgcaaagatgatgtgagattttttc
7021 ttgtgttttaattattttcacattttctctctgcaaaactttagttttctgatgatctac
7081 acacacacacacacacacgtgcacacacacacacatttaaatgatataaaaagaagag
7141 gttgaaagattattaaataacttatcaggcatctcaatgggttactatctatgttagtgaa
7201 aatcaaataggactcaaagttggatatttgggatttttcttctgacagtataatttattg
7261 agttactagggaggttcttaaatcctcatatctggaaacttgtagcgttttgacacctt

7321 cctatagatgatataggaatgaaccaatacgcttttattaccctttctaactctgatttt
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 7441 taccagagaggctttgaatggaagcaggctgagagtagccaaagaggcaaggggtattag
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 7561 gaaacctgttacttctagggcttcagatctgatgatatctttttcatcacattacaagtt
 7621 atttctctgactgaatagacagtgggtataggttgacacagcacacaagtggctattgtga
 7681 tgtatgatgatgtagtcctacaactgcaaaacgtcttactgaaccaacaatcaaaaaat
 7741 gggtctgttttaaaaaggattttgtttgatttgaaattaaaacttcaagctgaatgactt
 7801 atatgagaataatacgttcaatcaaagtagttattctatctttgtgtccatattccattag
 7861 attgtgattattaattttctagctatgggtattactatatcacacttgtgagtatgtattc
 7921 aaatactaagtatcttatatgctacgtgcatacacattcttttcttaacctttacctgtg
 7981 ttttaactaatattgtgtcagtgatttaaaaattagcttttacatatgatattcacaatg
 8041 taataaatttagagagtaattttgtgtattcttatttacttaacattttacttttaatta
 8101 tgtaaatttggttagaaaataataataaatgggtagtgtctattgtgtaatggtagcagtt
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 8221 aaatagactaaacaaatcacaaattgttcagttctttaaattgtaattatgtcacacacac
 8281 aaaaaatccttttcaatcctgagaaaattaaaggcgttttactcacatgggtatttcaac
 8341 attagttttttgtttgtttctttttcatggtattactgaagggtgtgtatactccctaa
 8401 tacacatttatgaaaatctacttgttttaggcttttatttatactcttctgatttatattt
 8461 tttattataattattatttcttatcttcttcttttataatttttggaaaccaaatttat
 8521 agttagtttaggttaaactttttattatgaccattagaaactattttgaatgcttccaact
 8581 ggctcaattggccgggaaaacatgggagcaagagaagctgaaatatatttctgcaagaac
 8641 ctttctatattatgtgccaattaccacaccagatcaattttatgcagaggccttaaaata
 8701 ttctttcacagtagctttcttactaaccgtcatgtgcttttagtaaataatgattttta
 8761 aaagcagttcaagttgacaacagcagaaacagtaacaaaaaatctgctcagaaaaatgt
 8821 atgtgcacaaataaaaaaaattaatggcaattgttttagtgattgtaagtatactttttta
 8881 aagagtaaactgtgtgaaatttatactatccctgcttaaaatattaagatttttatgaaa
 8941 tatgtattttatgtttgtattgtgggaagattcctcctctgtgatatacacagcatctga
 9001 aagtgaacagtatcccaaagcagttccaacatgctttggaagtaagaaggttgactatt
 9061 gtatggccaaggatggcagtatgtaatccagaagcaaacttgatttaattgttctatttc
 9121 aggttctgtattgcatgttttcttattaatatattaataaaaagtattagagaaat

Figure 2D. The cDNA (SEQ ID. NO. : 8) and amino acid sequence (SEQ ID. NO. : 9) of 109P1D4 v.4. The start methionine is underlined. The open reading frame extends from nucleic acid 846-4859 including the stop codon.

1 ctggtgggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttt
 61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtacttt
 121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaattccccttttcac
 181 atgatagttgttaccatgttttaggcattagtcacatcaaccctctcctctcccaactt
 241 ctcttcttcaaatcaaactttatttagtccctcctttataatgattccttgccctggtttta
 301 tccagatcaattttttttcacttttgatgcccagagctgaagaaatggactactgtataaa
 361 ttattcattgccaagagaataattgcatttttaaccatattataacaaagaataatgat
 421 tatattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatt

481 ttaattatttgtattctctttaactatcttggtatattaaagtattatcttttatatatt
541 tatcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta
601 tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat
661 cactaattaacagagtgtcaattatgctaacatctcatttactgatttttaatttaaaca
721 gtttttgttaacatgcatgtttaggggttggtcttcttaataatttcttctctctctct
781 ctctctctctcttttggtcagtggtgtgcgggttaatacaacaaactgtaacaagtgtac
1 M D L L S G T Y I F A V L L A C V V F
841 ctgggtatgacttgttgcggtcgcggtcctgctagcatgctggtgt
20 H S G A Q E K N Y T I R E E M P E N V L
901 TCCACTCTGGCGCCAGGAGAAAACTACACCATCCGAGAAGAAATGCCAGAAAACGTCC
40 I G D L L K D L N L S L I P N K S L T T
961 TGATAGGCGACTTGTGAAAGACCTTAACCTGTCGCTGATTCCAAACAAGTCCTTGACAA
60 A M Q F K L V Y K T G D V P L I R I E E
1021 CTGCTATGCAGTTCAAGCTAGTGTACAAGACCGGAGATGTGCCACTGATTGGAATTGAAG
80 D T G E I F T T G A R I D R E K L C A G
1081 AGGATACTGGTGAGATCTTCACTACTGGCGCTCGCATTGATCGTGAGAAATTATGTGCTG
100 I P R D E H C F Y E V E V A I L P D E I
1141 GTATCCCAAGGGATGAGCATTGCTTTTATGAAGTGAGGTTGCCATTTTGCCGGATGAAA
120 F R L V K I R F L I E D I N D N A P L F
1201 TATTTAGACTGGTTAAGATACGTTTCTGATAGAAGATATAAATGATAATGCACCATTGT
140 P A T V I N I S I P E N S A I N S K Y T
1261 TCCCAGCAACAGTTATCAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATA
160 L P A A V D P D V G I N G V Q N Y E L I
1321 CTCTCCCAGCGGCTGTTGATCCTGACGTAGGAATAAACGGAGTTCAAACTACGAACATA
180 K S Q N I F G L D V I E T P E G D K M P
1381 TTAAGAGTCAAAACATTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGC
200 Q L I V Q K E L D R E E K D T Y V M K V
1441 CACAAC TGATTGTTCAAAAGGAGTTAGATAGGGAAGAGAAGGATACCTACGTGATGAAAG
220 K V E D G G F P Q R S S T A I L Q V S V
1501 TAAAGGTTGAAGATGGTGGCTTTCTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTGAGTG
240 T D T N D N H P V F K E T E I E V S I P
1561 T TACTGATACAAATGACAACCACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATAC
260 E N A P V G T S V T Q L H A T D A D I G
1621 CAGAAAATGCTCCTGTAGGCACCTTCACTGACACAGCTCCATGCCACAGATGCTGACATAG
280 E N A K I H F S F S N L V S N I A R R L
1681 GTGAAAATGCCAAGATCCACTTCTCTTTTCAAGCAATCTAGTCTCCAACATTGCCAGGAGAT
300 F H L N A T T G L I T I K E P L D R E E
1741 TATTTACCTCAATGCCACCACTGGACTTATCACAATCAAAGAACCACTGGATAGGGAAG
320 T P N H K L L V L A S D G G L M P A R A
1801 AAACACCAAACCACAAGTTACTGGTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAG
340 M V L V N V T D V N D N V P S I D I R Y
1861 CAATGGTGCTGGTAAATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGAT

360 I V N P V N D T V V L S E N I P L N T K
1921 ACATCGTCAATCCTGTCAATGACACAGTTGTTCTTTTCAGAAAATATTCCACTCAACACCA
380 I A L I T V T D K D A D H N G R V T C F
1981 AAATTGCTCTCATAACTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCT
400 T D H E I P F R L R P V F S N Q F L L E
2041 TCACAGATCATGAAATCCCTTTTCAGATTAAGGCCAGTATTCAGTAATCAGTTCCCTCCTGG
420 T A A Y L D Y E S T K E Y A I K L L A A
2101 AGACTGCAGCATATCTTGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTG
440 D A G K P P L N Q S A M L F I K V K D E
2161 CAGATGCTGGCAAACCTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATG
460 N D N A P V F T Q S F V T V S I P E N N
2221 AAAATGACAATGCTCCAGTTTTCACCCAGTCTTTTCGTAAGTGTTCCTATTCCTGAGAATA
480 S P G I Q L T K V S A M D A D S G P N A
2281 ACTCTCCTGGCATCCAGTTGACGAAAGTAAGTGCAATGGATGCAGACAGTGGGCCTAATG
500 K I N Y L L G P D A P P E F S L D C R T
2341 CTAAGATCAATTACCTGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATTGTCGTA
520 G M L T V V K K L D R E K E D K Y L F T
2401 CAGGCATGCTGACTGTAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTTATTCA
540 I L A K D N G V P P L T S N V T V F V S
2461 CAATTCTGGCAAAAGATAACGGGGTACCACCCTTAACCAGCAATGTCACAGTCTTTGTAA
560 I I D Q N D N S P V F T H N E Y N F Y V
2521 GCATTATTGATCAGAATGACAATAGCCCAGTTTTCCTCACAATGAATACAACCTTCTATG
580 P E N L P R H G T V G L I T V T D P D Y
2581 TCCCAGAAAACCTTCCAAGGCATGGTACAGTAGGACTAATCACTGTAAGTATCCTGATT
600 G D N S A V T L S I L D E N D D F T I D
2641 ATGGAGACAATTCTGCAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTG
620 S Q T G V I R P N I S F D R E K Q E S Y
2701 ATTCACAAACTGGTGTCTCCGACCAAAATATTTTCATTGATAGAGAAAAACAAGAATCTT
640 T F Y V K A E D G G R V S R S S S A K V
2761 ACACTTCTATGTAAAGGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAG
660 T I N V V D V N D N K P V F I V P P S N
2821 TAACCATAAATGTGGTTGATGTCAATGACAACAAACCAGTTTTCATTGTCCCTCCTTCCA
680 C S Y E L V L P S T N P G T V V F Q V I
2881 ACTGTTCTTATGAATTGGTTCTACCGTCCACTAATCCAGGCACAGTGGTCTTTTCAGGTAA
700 A V D N D T G M N A E V R Y S I V G G N
2941 TTGCTGTTGACAATGACACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAA
720 T R D L F A I D Q E T G N I T L M E K C
3001 ACACAAGAGATCTGTTTGCAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAAT
740 D V T D L G L H R V L V K A N D L G Q P
3061 GTGATGTTACAGACCTTGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGC
760 D S L F S V V I V N L F V N E S V T N A
3121 CTGATTCTCTCTTCAGTGTGTGAATTGTCAATCTGTTTCGTGAATGAGTCGGTGACCAATG

780 T L I N E L V R K S T E A P V T P N T E
3181 CTACACTGATTAATGAACTGGTGCGCAAAAGCACTGAAGCACCAGTGACCCCAAATACTG
800 I A D V S S P T S D Y V K I L V A A V A
3241 AGATAGCTGATGTATCCTCACCAACTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTG
820 G T I T V V V V I F I T A V V R C R Q A
3301 CTGGCACCATAACTGTCGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGG
840 P H L K A A Q K N K Q N S E W A T P N P
3361 CACCACACCTTAAGGCTGCTCAGAAAAACAAGCAGAATTCTGAATGGGCTACCCCAAACC
860 E N R Q M I M M K K K K K K K K H S P K
3421 CAGAAAACAGGCAGATGATAATGATGAAGAAAAGAAAAGAAGAAGCATTCCCTTA
880 N L L L N F V T I E E T K A D D V D S D
3481 AGAACTTGCTGCTTAATTTTGTCACTATTGAAGAACTAAGGCAGATGATGTTGACAGTG
900 G N R V T L D L P I D L E E Q T M G K Y
3541 ATGGAAACAGAGTCACACTAGACCTTCTTATGATCTAGAAGAGCAAACAATGGGAAAGT
920 N W V T T P T T F K P D S P D L A R H Y
3601 ACAATTGGGTAACACTACCTACTACTTTCAAGCCCGACAGCCCTGATTGGCCCGACACT
940 K S A S P Q P A F Q I Q P E T P L N S K
3661 ACAAATCTGCCTCTCCACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCTGAATTCGA
960 H H I I Q E L P L D N T F V A C D S I S
3721 AGCACCACATCATCAAGAAGTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCT
980 K C S S S S S D P Y S V S D C G Y P V T
3781 CCAAGTGTTCCTCAAGCAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGA
1000 T F E V P V S V H T R P P M K E V V R S
3841 CGACCTTCGAGGTACCTGTGTCCGTACACACCAGACCGCCAATGAAGGAGGTTGTGCGAT
1020 C T P M K E S T T M E I W I H P Q P Q S
3901 CTTCGACCCCATGAAAGAGTCTACAACATATGGAGATCTGGATTCTATCCCAACACAGT
1040 Q R R V T F H L P E G S Q E S S S D G G
3961 CCCAGCGGCGTGTACATTTCACCTGCCAGAAGGCTCTCAGGAAAGCAGCAGTGATGGTG
1060 L G D H D A G S L T S T S H G L P L G Y
4021 GACTGGGAGACCATGATGCAGGCAGCCTTACCAGCACATCTCATGGCCTGCCCCTTGGCT
1080 P Q E E Y F D R A T P S N R T E G D G N
4081 ATCCTCAGGAGGAGTACTTTGATCGTGCTACACCAGCAATCGCACTGAAGGGGATGGCA
1100 S D P E S T F I P G L K K A A E I T V Q
4141 ACTCCGATCCTGAATCTACTTTTCATACCTGGACTAAAGAAAGCTGCAGAAATAACTGTTC
1120 P T V E E A S D N C T Q E C L I Y G H S
4201 AACCAACTGTGGAAGAGGCCTCTGACAACTGCACTCAAGAATGTCTCATCTATGGCCATT
1140 D A C W M P A S L D H S S S S Q A Q A S
4261 CTGATGCCTGCTGGATGCCGGCATCTCTGGATCATTCCAGCTCTTCGCAAGCACAGGCCT
1160 A L C H S P P L S Q A S T Q H H S P R V
4321 CTGCTCTATGCCACAGCCCACTGTACAGGCCTCTACTCAGCACCACAGCCCAAGG
1180 T Q T I A L C H S P P V T Q T I A L C H
4381 TGACACAGACCATTGCTCTCTGCCACAGCCCTCCAGTGACACAGACCATCGCATTTGCC

1200 S P P P I Q V S A L H H S P P L V Q A T
4441 ACAGCCACCACCGATACAGGTGTCTGCTCTCCACCACAGTCCTCCTCTAGTGCAGGCTA
1220 A L H H S P P S A Q A S A L C Y S P P L
4501 CTGCACCTTCACCACAGCCCACCATCAGCACAGGCCTCAGCCCTCTGCTACAGCCCTCCTT
1240 A Q A A A I S H S S P L P Q V I A L H R
4561 TAGCACAGGCTGCTGCAATCAGCCACAGCTCTCCTCTGCCACAGGTTATTGCCCTCCATC
1260 S Q A Q S S V S L Q Q G W V Q G A D G L
4621 GTAGTCAGGCCCAATCATCAGTCAGTTTGCAGCAAGGTTGGGTGCAAGGTGCTGATGGGC
1280 C S V D Q G V Q G S A T S Q F Y T M S E
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1320 Q Q A R P S R G D S P I M E E H P L *
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4861 gctaaaatagttacttcaaattttcagaaaagatgtatatagtcaaaatthaagatacaa
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6721 ttttctccttcgtgttgttaatgttccaagggatttggagcatactgggtttccagggtgc
6781 atgtgaatcccgaaggactgatgatatttgaatgtttattaaattattatcatacaaatg
6841 tgttgatattgtggctattgttgatgttgaaaattttaaacttggggaagattaagaaaa
6901 gaaccaatagtgacaaaaatcagtgcttcagtagattttagaacattctttgcctcaaa
6961 aaacctgcaaagatgatgtgagattttttcttgtgttttaattattttcacattttctct
7021 ctgcaaaacttttagttttctgatgatctacacacacacacacacacagtgacacac
7081 acacacattttaaatgatataaaaagaagaggttgaaagattattaaataacttatcaggc
7141 atctcaatgggttactatctatgttagtgaaaatcaaataaggactcaaagttggatatttg
7201 ggatttttcttctgacagtataatttattgagttactagggaggttcttaaatcctcata
7261 tctggaaacttgtgacgttttgacacctttcctatagatgatataggaatgaaccaatac
7321 gcttttattacccttttctaactctgattttataatcagacttagattgtgtttagaatat
7381 taaatgactgggcaccctcttcttgggtttttaccagagaggtttgaatggaagcaggt
7441 gagagtagccaaagagggaaggggtattagcccagttattctcccctatgccttccttct
7501 ctttctaaagcgtccactaggtctggccttggaacctgttacttctagggttcagatct
7561 gatgatattcttttcatcacattacaagttatttctctgactgaatagacagtggtatag
7621 gttgacacagcacacaagtggctattgtgatgtatgatgtatgtagtccacaactgcaa
7681 aacgtcttactgaaccaacaatcaaaaaatggttctgttttaaaaaggattttgtttgat
7741 ttgaaataaaacttcaagctgaatgacttatatgagaataatacgttcaatcaaagtag
7801 ttattctattttgtgtccatattccattagattgtgtattattaattttctagctatggta
7861 ttactatatcacacttgtgagtatgtattcaataactaagtatcttatatgctacgtgca
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7981 aattagcttttacatatgatattacaatgtaataaatttagagagtaattttgtgtatt
8041 cttatttactttaacattttacttttaattatgtaaatttggttagaaaaataataaataat
8101 ggttagtgctattgtgtaatggtagcagttacaaagagcctctgccttcccaaactaata
8161 tttatcacacatgggtcattaaatgggaaaaaatagactaaacaaatcacaaattgttca
8221 gttcttaaaatgtaattatgtcacacacacaaaaaatccttttcaatcctgagaaaatta
8281 aaggcggttttactcacatggctatttcaacattagtttttttgtttgtttcttttcat
8341 ggtattactgaagggtgtgtatactccctaatacacatttatgaaaatctactgttttagg
8401 cttttatttatactcttctgatttatattttttattataattattatttcttatctttct
8461 tcttttatattttttggaaccaaatttatagttagtttaggtaaaactttttattatgac
8521 cattagaaactattttgaatgcttccaactggctcaattggccgggaaaacatgggagca
8581 agagaagctgaaatatatttctgcaagaacctttctatatattatgtgccaaattaccacacc
8641 agatcaattttatgcagaggccttaaaatattctttcacagtagctttcttacactaacc
8701 gtcattgtgcttttagtaaatatgattttttaaagcagttcaagttgacaacagcagaaac
8761 agtaacaaaaaatctgctcagaaaaatgtatgtgcacaaataaaaaaattaatggcaa
8821 ttgttttagtgattgtaagtatactttttaaagagtaaaactgtgtgaaatttatactatc
8881 cctgcttaaaatattaagatttttatgaaatatgtatttatgtttgtattgtgggaagat
8941 tcctcctctgtgatcatcacagcatctgaaagtgaacagtatcccaaagcagttccaac
9001 catgctttggaagtaagaaggttgactattgtatggccaaggatggcagtatgtaatcca

9061 gaagcaaaactgtattaattgttctatttcaggttctgtattgcatgttttcttattaat
9121 atatattaataaaaagttatgagaaat

Figure 2E. The cDNA (SEQ ID. NO. : 10) and amino acid sequence (SEQ ID. NO. : 11) of 109P1D4 v.5. The start methionine is underlined. The open reading frame extends from nucleic acid 846-4778 including the stop codon.

```
1 ctgggtggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaaactttt
61 ttttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtaacttt
121 atattaatagctattcttgtttttcttatccaaagaaaaatcctctaataccccctttcac
181 atgatagttgttaccatgttttaggcattagtcacatcaacccctctcctctcccaaactt
241 ctcttcttcaaatacaactttattagtcctctctttataatgattccttgctcgtttta
301 tccagatcaattttttttctactttgatgcccagagctgaagaaatggactactgtataaa
361 ttattcattgccaagagaataattgcattttaaacccatattataacaaagaataatgat
421 tatattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatt
481 ttaattatgttattctctttaactatcttggatatataaagtattatcttttatatatt
541 tatcaatggtggacacttttataggtactctgtgtcatttttgatactgtaggtatctta
601 tttcatttatctttattcttaatgtacgaattcataatatttgattcagaacaaatttat
661 cactaattaacagagtgtcaattatgctaacatctcatttactgattttaatttaaaaca
721 gtttttgttaacatgcatgttttaggggtggcttcttaataatttcttctctctctctct
781 ctctcctcttcttttggtcagtggtgtgcggttaatacaacaaactgtaacaagtgtac
1 M D L L S G T Y I F A V L L A C V V F
841 ctgggtATGGACTTGTGTCCGGGACGTACATTTTCGCGGTCCTGCTAGCATGCGTGGTGT
20 H S G A Q E K N Y T I R E E M P E N V L
901 TCCACTCTGGCGCCCAGGAGAAAACTACACCATCCGAGAAGAAATGCCAGAAAACGTCC
40 I G D L L K D L N L S L I P N K S L T T
961 TGATAGGCGACTTGTGAAAGACCTTAACTTGTGCTGATTCCAAACAAGTCCTTGACAA
60 A M Q F K L V Y K T G D V P L I R I E E
1021 CTGCTATGCAGTTCAAGCTAGTGTAAGACCGGAGATGTGCCACTGATTCTGAATTGAAG
80 D T G E I F T T G A R I D R E K L C A G
1081 AGGATACTGGTGAGATCTTCACTACTGGCGCTCGCATTGATCGTGAGAAATTATGTGCTG
100 I P R D E H C F Y E V E V A I L P D E I
1141 GTATCCCAAGGGATGAGCATTGCTTTTATGAAGTGGAGGTTGCCATTTTGCCGGATGAAA
120 F R L V K I R F L I E D I N D N A P L F
1201 TATTTAGACTGGTTAAGATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTGT
140 P A T V I N I S I P E N S A I N S K Y T
1261 TCCCAGCAACAGTTATCAACATATCAATTCAGAGAACTCGGCTATAAACTCTAAATATA
160 L P A A V D P D V G I N G V Q N Y E L I
1321 CTCTCCCAGCGGCTGTTGATCCTGACGTAGGAATAAACGGAGTTCAAAACTACGAACTAA
180 K S Q N I F G L D V I E T P E G D K M P
1381 TTAAGAGTCAAAACATTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGC
200 Q L I V Q K E L D R E E K D T Y V M K V
1441 CACAACCTGATTGTTCAAAAGGAGTTAGATAGGGAAGAGAAGGATACCTACGTGATGAAAG
220 K V E D G G F P Q R S S T A I L Q V S V
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1501 TAAAGGTTGAAGATGGTGGCTTTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTGAGTG
240 T D T N D N H P V F K E T E I E V S I P
1561 TTAAGGAGACAGAGATTGAAGTCAGTATAC
260 E N A P V G T S V T Q L H A T D A D I G
1621 CAGAAAATGCTCCTGTAGGCACTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAG
280 E N A K I H F S F S N L V S N I A R R L
1681 GTGAAAATGCCAAGATCCACTTCTCTTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGAT
300 F H L N A T T G L I T I K E P L D R E E
1741 TATTTTCACCTCAATGCCACCACTGGACTTATCACAATCAAAGAACCCTGGATAGGGAAG
320 T P N H K L L V L A S D G G L M P A R A
1801 AAACACCAAACCACAAGTTACTGGTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAG
340 M V L V N V T D V N D N V P S I D I R Y
1861 CAATGGTGCTGGTAAATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGAT
360 I V N P V N D T V V L S E N I P L N T K
1921 ACATCGTCAATCCTGTCAATGACACAGTTGTTCTTTTCAGAAAATATTCCACTCAACACCA
380 I A L I T V T D K D A D H N G R V T C F
1981 AAATGCTCTCATAACTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCT
400 T D H E I P F R L R P V F S N Q F L L E
2041 TCACAGATCATGAAATCCCTTTTCAGATTAAGGCCAGTATTTCAGTAATCAGTTCCTCCTGG
420 T A A Y L D Y E S T K E Y A I K L L A A
2101 AGACTGCAGCATATCTTGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTG
440 D A G K P P L N Q S A M L F I K V K D E
2161 CAGATGCTGGCAAACCTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATG
460 N D N A P V F T Q S F V T V S I P E N N
2221 AAAATGACAATGCTCCAGTTTTACCCAGTCTTTTCGTAAGTGTTCCTATTCTGAGAATA
480 S P G I Q L T K V S A M D A D S G P N A
2281 ACTCTCCTGGCATCCAGTTGACGAAAGTAAGTGCAATGGATGCAGACAGTGGGCCTAATG
500 K I N Y L L G P D A P P E F S L D C R T
2341 CTAAGATCAATTACCTGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATTGTCGTA
520 G M L T V V K K L D R E K E D K Y L F T
2401 CAGGCATGCTGACTGTAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTTATTCA
540 I L A K D N G V P P L T S N V T V F V S
2461 CAATTCTGGCAAAAGATAACGGGGTACCACCCCTTAACCAGCAATGTCACAGTCTTTGTAA
560 I I D Q N D N S P V F T H N E Y N F Y V
2521 GCATTATTGATCAGAATGACAATAGCCCAGTTTTCTACTCACAATGAATACAACCTTCTATG
580 P E N L P R H G T V G L I T V T D P D Y
2581 TCCCAGAAAACCTTCCAAGGCATGGTACAGTAGGACTAATCACTGTAAGTATGATCCTGATT
600 G D N S A V T L S I L D E N D D F T I D
2641 ATGGAGACAATTCTGCAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTG
620 S Q T G V I R P N I S F D R E K Q E S Y
2701 ATTCACAAACTGGTGTATCCGACCAAATATTTTCATTTGATAGAGAAAAACAAGAATCTT
640 T F Y V K A E D G G R V S R S S S A K V

2761 ACACCTTTCTATGTAAAGGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAG
660 T I N V V D V N D N K P V F I V P P S N
2821 TAACCATAAATGTGGTTGATGTCAATGACAACAAACCAGTTTTCATTGTCCCTCCTTCCA
680 C S Y E L V L P S T N P G T V V F Q V I
2881 ACTGTTCTTATGAATTGGTTCTACCGTCCACTAATCCAGGCACAGTGGTCTTTCAGGTAA
700 A V D N D T G M N A E V R Y S I V G G N
2941 TTGCTGTTGACAATGACACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAA
720 T R D L F A I D Q E T G N I T L M E K C
3001 ACACAAGAGATCTGTTTGAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAAT
740 D V T D L G L H R V L V K A N D L G Q P
3061 GTGATGTTACAGACCTTGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGC
760 D S L F S V V I V N L F V N E S V T N A
3121 CTGATTCTCTCTTCAGTGTGTAAATTGTCAATCTGTTTCGTGAATGAGTCGGTGACCAATG
780 T L I N E L V R K S T E A P V T P N T E
3181 CTACACTGATTAATGAACTGGTGCAGAAAAGCACTGAAGCACCAGTGACCCCAAATACTG
800 I A D V S S P T S D Y V K I L V A A V A
3241 AGATAGCTGATGTATCCTCACCAACTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTG
820 G T I T V V V V I F I T A V V R C R Q A
3301 CTGGCACCATAACTGTCGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGG
840 P H L K A A Q K N K Q N S E W A T P N P
3361 CACCACACCTTAAGGCTGCTCAGAAAAACAAGCAGAATTCTGAATGGGCTACCCCAAACC
860 E N R Q M I M M K K K K K K K K H S P K
3421 CAGAAAAACAGGCAGATGATAATGATGAAGAAAAAGAAAAAGAAGAAGCATTCCCCTA
880 N L L L N F V T I E E T K A D D V D S D
3481 AGAACTTGCTGCTTAATTTTGTCACTATTGAAGAACTAAGGCAGATGATGTTGACAGTG
900 G N R V T L D L P I D L E E Q T M G K Y
3541 ATGGAAACAGAGTCACACTAGACCTTCTCTATTGATCTAGAAGAGCAACAATGGGAAAGT
920 N W V T T P T T F K P D S P D L A R H Y
3601 ACAATTGGGTAACCTACACCTACTACTTTCAAGCCCGACAGCCCTGATTTGGCCCGACACT
940 K S A S P Q P A F Q I Q P E T P L N S K
3661 ACAAATCTGCCTCTCCACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCCTGAATTCGA
960 H H I I Q E L P L D N T F V A C D S I S
3721 AGCACCACATCATCCAAGAACTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCT
980 K C S S S S S D P Y S V S D C G Y P V T
3781 CCAAGTGTTCTCAAGCAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGA
1000 T F E V P V S V H T R P S Q R R V T F H
3841 CGACCTTCGAGGTACCTGTGTCCGTACACACCAGACCGTCCCAGCGCGTGTACATTTC
1020 L P E G S Q E S S S D G G L G D H D A G
3901 ACCTGCCAGAAGGCTCTCAGGAAAGCAGCAGTGATGGTGGACTGGGAGACCATGATGCAG
1040 S L T S T S H G L P L G Y P Q E E Y F D
3961 GCAGCCTTACCAGCACATCTCATGGCCTGCCCTTGGCTATCCTCAGGAGGAGTACTTTG
1060 R A T P S N R T E G D G N S D P E S T F

4021 ATCGTGCTACACCCAGCAATCGCACTGAAGGGGATGGCAACTCCGATCCTGAATCTACTT
1080 I P G L K K A A E I T V Q P T V E E A S
4081 TCATACCTGGACTAAAGAAAGCTGCAGAAATAACTGTTCAACCAACTGTGGAAGAGGCCT
1100 D N C T Q E C L I Y G H S D A C W M P A
4141 CTGACAACTGCACTCAAGAATGTCTCATCTATGGCCATTCTGATGCCTGCTGGATGCCGG
1120 S L D H S S S S Q A Q A S A L C H S P P
4201 CATCTCTGGATCATTCCAGCTCTTCGCAAGCACAGGCCTCTGCTCTATGCCACAGCCCAC
1140 L S Q A S T Q H H S P R V T Q T I A L C
4261 CACTGTACAGGCCTCTACTCAGCACCACAGCCCACGAGTGACACAGACCATTGCTCTCT
1160 H S P P V T Q T I A L C H S P P P I Q V
4321 GCCACAGCCCTCCAGTGACACAGACCATCGCATTGTGCCACAGCCCACCACCGATACAGG
1180 S A L H H S P P L V Q A T A L H H S P P
4381 TGTCTGCTCTCCACCACAGTCTCTCTAGTGCAGGCTACTGCACTTCACCACAGCCCAC
1200 S A Q A S A L C Y S P P L A Q A A A I S
4441 CATCAGCACAGGCCTCAGCCCTCTGCTACAGCCCTCCTTTAGCACAGGCTGCTGCAATCA
1220 H S S P L P Q V I A L H R S Q A Q S S V
4501 GCCACAGCTCTCCTCTGCCACAGGTTATTGCCCTCCATCGTAGTCAGGCCCAATCATCAG
1240 S L Q Q G W V Q G A D G L C S V D Q G V
4561 TCAGTTTGACAGCAAGGTTGGGTGCAAGGTGCTGATGGGCTATGCTCTGTTGATCAGGGAG
1260 Q G S A T S Q F Y T M S E R L H P S D D
4621 TGCAAGGTAGTGCAACATCTCAGTTTTACACCATGTCTGAAAGACTTCATCCCAGTGATG
1280 S I K V I P L T T F T P R Q Q A R P S R
4681 ATTC AATTAAGTCATTCTCTTTGACAACCTTCACTCCACGCCAACAGGCCAGACCGTCCA
1300 G D S P I M E E H P L *
4741 GAGGTGATTCCCCCATTATGGAAGAACATCCCTTGTAAGctaaaatagttacttcaa
4801 tttcagaaaagatgtatatagtcaaaatttaagatacaattccaatgagtattctgatta
4861 tcagatttgttaaataactatgtaaatagaaacagataaccagaataaatctacagctagac
4921 ccttagtcaatagttaacccaaaaattgcaatttggtttaattcagaatgtgtatttaaaa
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5041 actatttctgatgtacagtattttttgttgtttttatcatcatgtgcaatattactgatt
5101 tgtttccatgctgattgtgtggaaccagtatgttagcaaatggaaagcctagaaatatctt
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5401 gtatatacattttcaataaagaatatgtataaactgtacagatctagatctacaacctat
5461 tctctactctttagtagagttcgagacacagaagtgaataactgccctaattaagcaa
5521 ctatttgttaaaaaggcctctttttactttaatagtttagtgtaaagtacatcagaat
5581 aaagctgtatctgccattttaagcctgtagtcattattacttgggtctttacttctggg
5641 aatttgtatgtaacagcctagaaaattaaaaggaggtggatgcatccaaagcacgagtca
5701 cttaaaatatcgacggtaaactactattttgtagagaaactcaggaagatttaaatgttg
5761 atttgacagctcaataggctgttaccaaagggtgttcagtaaaaataacaatacatgta

5821 actgtagataaaaaccatataactaaatctataagactaagggatTTTTgttattctagctc
5881 aacttactgaagaaaaccactaataacaacaagaatatcaggaaggaactTTTcaagaaa
5941 tgtaattataaatctacatcaaacagaatTTtaaggaaaaatgcagagggagaaataagg
6001 cacatgactgcttcttgacgtcaacaagaataaccaataacacacacagaacaaaaacca
6061 tcaaaatctcatatgatgaataaaatataattcttctaagcaaagaaacagtactattcat
6121 agaaaacattagtttcttctgtgtgtgttatttcttctgtatcctcttaactggcc
6181 attatctgtatgtgcacattttataaatgtacagaaacatcaccaacttaattttcttc
6241 catagcaaaactgagaaaaatccttgtttcagtataacactaaaccaagagacaattgat
6301 gtttaatggggcggttgggtggggggggagtcataatctcctattgattaacttaga
6361 catagatTTTgtaatgtataaacttgatatttaatttatgattaaactgtgtgtaatttt
6421 gtaacataaaactgtggttaattgcataatttcattgggtgaggatttccactgaatattgag
6481 aaagtttctttcatgtgcccagcaggttaagtagcgTTTTcagaatatacattattccc
6541 atccattgtaaagttccttaagtcataatttgactgggcgtgcagaataacttcttaactt
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6661 tgttccaagggaTTTggagcatactgggtttccaggtgcatgtgaatcccgaaggactga
6721 tgatatttgaatgtttattaaattattatcatacaaagtgttgatattgtggctattgt
6781 tgatgttgaaaatTTTaaacttggggaagattaagaaaagaaccaatagtgacaaaaatc
6841 agtgcttccagtagattttagaacattcttgcctcaaaaaacctgcaaagatgatgtga
6901 gatTTTTcttgtgttttaattattttcacattttctctctgcaaaactttagttttctg
6961 atgatctacacacacacacacacacacacacacacacacacatttaaatgatataa
7021 aaagaagaggttgaaagattattaaataacttatcaggcatctcaatgggtactatctat
7081 gttagtgaaaatcaaataaggactcaaagttggatatttgggatttttcttctgacagtat
7141 aatttattgagttactagggaggttcttaaatcctcatatctggaaacttgtagcgtttt
7201 gacaccttctctatagatgatataggaatgaaccaatacgcttttattaccctttctaac
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7321 cttgggttttaccagagaggctttgaatggaagcaggctgagagtagccaaaggaggaag
7381 gggatttagcccagttattctccctatgccttcttctcttcttaagcgtccactaggt
7441 ctggccttggaacctgttacttctagggcttcagatctgatgatattcttttcatcaca
7501 ttacaagttatttctctgactgaatagacagtggtataggttgacacagcacacaagtg
7561 ctattgtgatgtatgatgtatgtagtcctacaactgcaaaacgtcttactgaaccaaca
7621 tcaaaaaatgggtctgttttaaaaaggattttgtttgatttgaaatataaacttcaagct
7681 gaatgacttatatgagaataataacgttcaatcaaagtagttattctattttgtgtccata
7741 ttccattagattgtgattattaattttctagctatgggtattactatatcacacttgtgag
7801 tatgtattcaataactaagtatcttatatgctacgtgcatacacattcttttctaaact
7861 ttacctgtgttttaactaatattgtgtcagtgattaaaaattagctttacatatgata
7921 tctacaatgtaataaatttagagagtaattttgtgtattcttatttacttaacattttac
7981 ttttaattatgtaaatttggttagaaaaataataaaatgggttagtgctattgtgtaatg
8041 gtagcagttacaagagcctctgccttcccaaactaatatttatcacacatgggtcattaa
8101 atgggaaaaaaatagactaaacaatcacaaattgttcagttcttaaaatgtaattatgt
8161 cacacacacaaaaaatccttttcaatcctgagaaaattaaaggcgttttactcacatggc
8221 tatttcaacattagtttttttgttttcttttcatgggtattactgaagggtgtgtat
8281 actccctaatacacatttatgaaaatctactgttttaggcttttatttatactcttctga

8341 tttatattttttattataattattattttcttatctttctcttttatattttttggaac
8401 caaatttatagtttagtttaggttaaactttttattatgaccattagaaactattttgaatg
8461 cttccaactggctcaattggccgggaaaacatgggagcaagagaagctgaaatatatttc
8521 tgcaagaacctttctatattatgtgccaattaccacaccagatcaattttatgcagaggc
8581 cttaaaatattctttcacagtagctttcttactaactaacgctcatgtgcttttagtaaata
8641 tgattttttaaaagcagttcaagttgacaacagcagaaacagtaacaaaaaatctgctca
8701 gaaaaatgtatgtgcacaaataaaaaaattaatggcaattgttttagtgattgtaagtga
8761 tacttttttaagagtaaaactgtgtgaaatttatactatccctgcttaaaatattaagatt
8821 tttatgaaatatgtatttatgtttgtattgtgggaagattcctcctctgtgatatacatc
8881 agcatctgaaagtgaacagtatcccaaagcagttccaacctgctttggaagtaagaagg
8941 ttgactattgtatggccaaggatggcagtatgtaatccagaagcaaacttgtattaattg
9001 ttctatttcagggttctgtattgcatgttttcttattaatatatattaataaaagtattga
9061 gaaat

Figure 2F. The cDNA (SEQ ID. NO. : 12) and amino acid sequence (SEQ ID. NO. : 13) of 109P1D4 v.6. The start methionine is underlined. The open reading frame extends from nucleic acid 614-3727 including the stop codon.

1 ggcagtcggcgaactgtctggcgaggagccgtgagcagtagctgcactcagctgccc
61 gcgcggcgaagaggaaggcaagccaaacagagtgcgcagagtggcagtgccagcggcgac
121 acaggcagcacaggcagcccggtgctgaatagcctcagaaacaacctcagcgactcc
181 ggctgctctgcggactgcgagctgtggcggtagagcccgctacagcagtcgcagctctccg
241 tggagcggcggaagcctttttctccctttcggtttacctcttcattctactctaaaggc
301 atcgttattagaggggtgcttaaaaagtacagatcaactggatggatgaatggatggaaga
361 ggatggaatatcttaacaaaacacattttccttaagtaaattcatgcatactccaaataa
421 aatacagaatgtgaagtatctctgaactgtgctgttgaaataggtagctactagctacat
481 gaaaatcctgttgtaataagaaggattccacagatcacataccagagcgggtttgcctc
541 agctgctctcaactttgtaatcttgtaagaagctgacaagcttggtgattgcagtgc
1 M T V G F N S D I S S V V R V N
601 ctatgaggactgaATGACAGTGGGTTTTAATTCAGATATTTCAAGTGTGTGCGGGTTAA
17 T T N C H K C L L S G T Y I F A V L L V
661 TACAACAACTGTCACAAGTGTGTTGTCCGGGACGTACATTTTCGCGGTCCTGCTAGT
37 C V V F H S G A Q E K N Y T I R E E I P
721 ATGCGTGGTGTTCCTCTGCGCCCCAGGAGAAAACTACACCATCCGAGAAGAAATTC
57 E N V L I G N L L K D L N L S L I P N K
781 AGAAAACGTCCTGATAGGCAACTTGTGAAAGACCTTAACCTGTGCGCTGATTCCAAACAA
77 S L T T T M Q F K L V Y K T G D V P L I
841 GTCCTTGACAACTACTATGCAGTTCAAGCTAGTGTAAGACCGGAGATGTGCCACTGAT
97 R I E E D T G E I F T T G A R I D R E K
901 TCGAATTGAAGAGGATACTGGTGAGATCTTCACTACCGGCGCTCGCATGATCGTGAGAA
117 L C A G I P R D E H C F Y E V E V A I L
961 ATTATGTGCTGGTATCCCAAGGGATGAGCATTGCTTTTATGAAGTGGAGGTTGCCATTTT
137 P D E I F R L V K I R F L I E D I N D N
1021 GCCCGATGAAATATTTAGACTGGTTAAGATACGTTTTCTGATAGAAGATATAAATGATAA

157 A P L F P A T V I N I S I P E N S A I N
1081 TGCACCATTTGTTCCCAGCAACAGTTATCAACATATCAATTCAGAGAACTCGGCTATAAA
177 S K Y T L P A A V D P D V G I N G V Q N
1141 CTCTAAATATACTCTCCCAGCGGCTGTTGATCCTGACGTAGGCATAAACGGAGTTCAAAA
197 Y E L I K S Q N I F G L D V I E T P E G
1201 CTACGAACTAATTAAGAGTCAAAACATTTTGGCCTCGATGTCATTGAAACACCAGAAGG
217 D K M P Q L I V Q K E L D R E E K D T Y
1261 AGACAAGATGCCACAACCTGATTGTTCAAAAGGAGTTAGATAGGGAAGAGAAGGATACCTA
237 V M K V K V E D G G F P Q R S S T A I L
1321 TGTGATGAAAGTAAAGGTTGAAGATGGTGGCTTTCTCTCAAAGATCCAGTACTGCTATTTT
257 Q V S V T D T N D N H P V F K E T E I E
1381 GCAAGTAAGTGTACTGATACAAATGACAACCACCCAGTCTTTAAGGAGACAGAGATTGA
277 V S I P E N A P V G T S V T Q L H A T D
1441 AGTCAGTATACCAGAAAATGCTCCTGTAGGCACCTTCAGTGACACAGCTCCATGCCACAGA
297 A D I G E N A K I H F S F S N L V S N I
1501 TGCTGACATAGGTGAAAATGCCAAGATCCACTTCTCTTTCAGCAATCTAGTCTCCAACAT
317 A R R L F H L N A T T G L I T I K E P L
1561 TGCCAGGAGATTATTTACCTCAATGCCACCCTGGACTTATCACAATCAAAGAACCCT
337 D R E E T P N H K L L V L A S D G G L M
1621 GGATAGGGAAGAAACACCAAACCACAAGTTACTGGTTTTGGCAAGTGATGGTGGATTGAT
357 P A R A M V L V N V T D V N D N V P S I
1681 GCCAGCAAGAGCAATGGTGCTGGTAAATGTTACAGATGTCAATGATAATGTCCCATCCAT
377 D I R Y I V N P V N D T V V L S E N I P
1741 TGACATAAGATACATCGTCAATCCTGTCAATGACACAGTTGTTCTTTTCAGAAAAATATTC
397 L N T K I A L I T V T D K D A D H N G R
1801 ACTCAACACCAAAATGCTCTCATAACTGTGACGGATAAGGATGCGGACCATAATGGCAG
417 V T C F T D H E I P F R L R P V F S N Q
1861 GGTGACATGCTTTCAGATCATGAAATTCCTTTTCAGATTAAGGCCAGTATTCAGTAATCA
437 F L L E N A A Y L D Y E S T K E Y A I K
1921 GTTCCTCCTGGAGAATGCAGCATATCTTGACTATGAGTCCACAAAAGAATATGCCATTAA
457 L L A A D A G K P P L N Q S A M L F I K
1981 ATTACTGGCTGCAGATGCTGGCAAACCTCCTTTGAATCAGTCAGCAATGCTCTTCATCAA
477 V K D E N D N A P V F T Q S F V T V S I
2041 AGTGAAAGATGAAAATGACAATGCTCCAGTTTTTCACCCAGTCTTTTCGTAAGTGTCTTCTAT
497 P E N N S P G I Q L M K V S A T D A D S
2101 TCCTGAGAATAACTCTCCTGGCATCCAGTTGATGAAAGTAAAGTGAACGGATGCAGACAG
517 G P N A E I N Y L L G P D A P P E F S L
2161 TGGGCCTAATGCTGAGATCAATTACCTGCTAGGCCCTGATGCTCCACCTGAATTCAGCCT
537 D R R T G M L T V V K K L D R E K E D K
2221 GGATCGTCGTACAGGCATGCTGACTGTAGTGAAGAACTAGATAGAGAAAAAGAGGATAA
557 Y L F T I L A K D N G V P P L T S N V T
2281 ATATTTATTACAAATCTGGCAAAAGATAATGGGGTACCACCCTTAACCAGCAATGTCAC

577 V F V S I I D Q N D N S P V F T H N E Y
2341 AGTCTTTGTAAGCATTATTGATCAGAATGACAATAGCCCAGTTTTCACCTACAATGAATA
597 K F Y V P E N L P R H G T V G L I T V T
2401 CAAATCTATGTCCCAGAAAACCTTCCAAGGCATGGTACAGTAGGACTAATCACTGTAAC
617 D P D Y G D N S A V T L S I L D E N D D
2461 TGATCCTGATTATGGAGACAATTCTGCAGTTACGCTCTCCATTTTAGATGAGAATGATGA
637 F T I D S Q T G V I R P N I S F D R E K
2521 CTTCAACCATGATTACAACTGGTGTCTCCGACCAATATTTCAATTTGATAGAGAAAA
657 Q E S Y T F Y V K A E D G G R V S R S S
2581 ACAAGAATCTTACACTTTCTATGTAAAGGCTGAGGATGGTGGTAGAGTATCACGTTCTTC
677 S A K V T I N V V D V N D N K P V F I V
2641 AAGTGCCAAAGTAACCATAAATGTGGTTGATGTCAATGACAACAAACCAGTTTTCATTGT
697 P P Y N Y S Y E L V L P S T N P G T V V
2701 CCCTCCTTACAACCTATTCTTATGAATTGGTTCTACCGTCCACTAATCCAGGCACAGTGGT
717 F Q V I A V D N D T G M N A E V R Y S I
2761 CTTTCAGGTAATTGCTGTTGACAATGACACTGGCATGAATGCAGAGGTTTCGTTACAGCAT
737 V G G N T R D L F A I D Q E . T G N I T L
2821 TGTAGGAGGAAACACAAGAGATCTGTTTGAATCGACCAAGAAACAGGCAACATAACATT
757 M E K C D V T D L G L H R V L V K A N D
2881 GATGGAGAAATGTGATGTTACAGACCTTGGTTTACACAGAGTGTGGTCAAAGCTAATGA
777 L G Q P D S L F S V V I V N L F V N E S
2941 CTTAGGACAGCCTGATTCTCTCTTCAGTGTGTGAATTGTCAATCTGTTTCGTGAATGAGTC
797 V T N A T L I N E L V R K S I E A P V T
3001 AGTGACCAATGCTACACTGATTAATGAAGTGGTGGCGAAAAGCATTGAAGCACCAGTGAC
817 P N T E I A D V S S P T S D Y V K I L V
3061 CCCAAATACTGAGATAGCTGATGTATCCTCACCAACTAGTGACTATGTCAAGATCCTGGT
837 A A V A G T I T V V V V I F I T A V V R
3121 TGCAGCTGTTGCTGGCACCATAACTGTGCTGTAGTTATTTTCATCACTGCTGTAGTAAG
857 C R Q A P H L K A A Q K N M Q N S E W A
3181 ATGTCGCCAGGCACCACACCTTAAGGCTGCTCAGAAAAACATGCAGAATTCTGAATGGGC
877 T P N P E N R Q M I M M K K K K K K K K
3241 TACCCCAAACCCAGAAAACAGGCAGATGATAATGATGAAGAAAAAGAAAAAGAAGAGAA
897 H S P K N L L L N F V T I E E T K A D D
3301 GCATTCCCTAAGAACCTGCTGCTTAATTTTGTCACTATTGAAGAACTAAGGCAGATGA
917 V D S D G N R V T L D L P I D L E E Q T
3361 TGTGACAGTGATGGAAACAGAGTCACACTAGACCTTCCTATTGATCTAGAAGAGCAAAC
937 M G K Y N W V T T P T T F K P D S P D L
3421 AATGGGAAAGTACAATTGGGTAACCTACTACTTTCAAGCCTGACAGCCCTGATTT
957 A R H Y K S A S P Q P A F Q I Q P E T P
3481 GGCCCCGACACTACAAATCTGCCTCTCCACAGCCTGCCTTCCAAATTCAGCCTGAAACTCC
977 L N L K H H I I Q E L P L D N T F V A C
3541 CCTGAATTTGAAGCACCACATCATCCAAGAACTGCCTCTCGATAACACCTTTGTGGCCTG

997 D S I S K C S S S S S D P Y S V S D C G
 3601 TGACTCTATCTCCAAGTGTTCCTCAAGCAGTTCAGATCCCTACAGCGTTTCTGACTGTGG
 1017 Y P V T T F E V P V S V H T R P T D S R
 3661 CTATCCAGTGACAACCTTCGAGGTACCTGTGTCCGTACACACCAGACCGACTGATTCCAG
 1037 T *
 3721 GACATGAactattgaaatctgcagtgagatgtaactttctaggaacaacaaaattccatt
 3781 ccccttccaaaaaatttcaatggattgtgatttcaaaattaggctaagatcattaattttt
 3841 gtaatctagatttccattataaaagcaagcaaaaatcatcttaaaaatgatgtcctagt
 3901 gaaccttgtgcttttcttagctgtaatctggcaatggaaatttaaaatttatggaagaga
 3961 cagtgcagcacaataacagagtactctcatgctgtttctctgtttgctctgaatcaacag
 4021 ccatgatgtaataaaggctgtcttggtgtatacacttatggttaatatatcagtcatga
 4081 aacatgcaattacttgcctgtctgattgttgtaataattaaaacattatcttccaggagt
 4141 ttggaagtgcagctgaactagccaaactactctctgaaagggtatccagggaagagacatt
 4201 tttaagaccccaacaaacaaaaacaaaaacactctgggtcagtggtttgaaaa
 4261 tattcactaacataatattgctgagaaaatcatttttattaccaccactctgcttaaaa
 4321 gttgagtgggcccggcgcggtgggtcacgcctgtaatcccagcactttgggagggcggag
 4381 cgggtggatcacgaggtcaggagattgagaccatcctggctaacacgggtgaaaccccatc
 4441 tccactaaaaatacaaaaaattagcctggcgtgggtggcgggcgctgtagtcccagctac
 4501 tcgggagggctgaggcaggagaatagcgtgaacccgggagggagcgttgagtgagccga
 4561 gatggcgccactctgcactccagcctgggtgacagagcaagaactctgtctcaaaaagaaa
 4621 aaaatgttcaatgatagaaaataattttactaggtttttatgttgattgtactcatgggtg
 4681 ttccactccttttaattattaaaaagttatttttggggtgggtgtgggtgcacaccgt
 4741 aatcccagcactttgggagggcgaggtgggtggatcacctgaggtcaggagttcaagacc
 4801 agtntggccaacatggcgaaaccccgtttt

Figure 2G. The cDNA (SEQ ID. NO. : 14) and amino acid sequence (SEQ ID. NO. : 15) of 109P1D4 v.7. The start methionine is underlined. The open reading frame extends from nucleic acid 735-3881 including the stop codon.

1 ggtgggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaacctttttt
 61 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtactttat
 121 attaatagctattcttgtttttcttatccaaagaaaaatcctctaattcccttttccacat
 181 gatagttgttaccatgtttaggcgttagtcacatcaacccctctcctctcccaaacttct
 241 cttcttcaaatcaaactttatttagtcctcctttataatgattccttgcctccttttatc
 301 cagatcaatttttttctactttgatgccagagctgaagaaatggactattgtataaatt
 361 attcattgccagagaataattgcatttttaaacccatgttataacaaagaataatgatta
 421 tattttgtgattttgtaacaaataaccctttattttcccttaactattgaattaaatatttt
 481 aattatttgtattctctttaactatcttgggtatattaaagtattatcttttatatattta
 541 tcaatgggtggacacttttataggtaactctgtgtcatttttgatactgtaggtatcttatt
 601 tcatttatctttattcttaattgtacgaattcataatatttgattcagaacagatttatca
 661 ctaattaacagagtggtcaattatgctaacatctcatttactgatttttaatttaaacagt
 1 M F R V G F L I I S S S S S L S
 721 ttttgtttaacatgcATGTTTAGGGTTGGCTTCTTAATAATTTCTTCTTCTTCTTCTCT
 17 P L L L V S V V R V N T T N C H K C L L

781 CTCCTCTTCTTTTGGTCAGTGTGTGCGGGTTAATACAACAACTGTCACAAGTGTGTTGT
37 S G T Y I F A V L L V C V V F H S G A Q
841 TGTCCGGGACGTACATTTTCGCGGTCTGCTAGTATGCGTGGTGTTCCTACTCTGGCGCCC
57 E K N Y T I R E E I P E N V L I G N L L
901 AGGAGAAAACTACACCATCCGAGAAGAAATTCAGAAAACGTCCTGATAGGCAACTTGT
77 K D L N L S L I P N K S L T T T M Q F K
961 TGAAAGACCTTAACCTTGTGCTGATTCCAAACAAGTCCTTGACAACTACTATGCAGTTCA
97 L V Y K T G D V P L I R I E E D T G E I
1021 AGCTAGTGTACAAGACCGGAGATGTGCCACTGATTCTGAATTGAAGAGGATACTGGTGAGA
117 F T T G A R I D R E K L C A G I P R D E
1081 TCTTCACTACCGCGCTCGCATTGATCGTGAGAAATTATGTGCTGGTATCCCAAGGGATG
137 H C F Y E V E V A I L P D E I F R L V K
1141 AGCATTGCTTTTATGAAGTGGAGGTTGCCATTTTGCCGGATGAAATATTTAGACTGGTTA
157 I R F L I E D I N D N A P L F P A T V I
1201 AGATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTGTTCCAGCAACAGTTA
177 N I S I P E N S A I N S K Y T L P A A V
1261 TCAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATACTCTCCAGCGGCTG
197 D P D V G I N G V Q N Y E L I K S Q N I
1321 TTGATCCTGACGTAGGCATAAACGGAGTTCAAACTACGAACTAATTAAGAGTCAAAACA
217 F G L D V I E T P E G D K M P Q L I V Q
1381 TTTTGGCCTCGATGTCATTGAAACACCAGAAGGAGACAAGATGCCACAACCTGATTGTTT
237 K E L D R E E K D T Y V M K V K V E D G
1441 AAAAGGAGTTAGATAGGGAAGAGAAGGATACCTATGTGATGAAAGTAAAGGTTGAAGATG
257 G F P Q R S S T A I L Q V S V T D T N D
1501 GTGGCTTCTCTCAAAGATCCAGTACTGCTATTTTGCAAGTAAGTGTACTGATACAAATG
277 N H P V F K E T E I E V S I P E N A P V
1561 ACAACCACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATACCAGAAAATGCTCCTG
297 G T S V T Q L H A T D A D I G E N A K I
1621 TAGGCACTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAGGTGAAAATGCCAAGA
317 H F S F S N L V S N I A R R L F H L N A
1681 TCCACTTCTCTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGATTATTTACCTCAATG
337 T T G L I T I K E P L D R E E T P N H K
1741 CCACCACTGGACTTATCACAATCAAAGAACCACTGGATAGGGAAGAAACACCAAACCACA
357 L L V L A S D G G L M P A R A M V L V N
1801 AGTTACTGGTTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAGCAATGGTGTGTTAA
377 V T D V N D N V P S I D I R Y I V N P V
1861 ATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGATACATCGTCAATCCTG
397 N D T V V L S E N I P L N T K I A L I T
1921 TCAATGACACAGTTGTTCTTTTCAGAAAATATTCCTCAACACCAAAATGCTCTCATAA
417 V T D K D A D H N G R V T C F T D H E I
1981 CTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCTTCACAGATCATGAAA
437 P F R L R P V F S N Q F L L E N A A Y L

2041 TTCCTTTTCAGATTAAGGCCAGTATTCAGTAATCAGTTCCTCCTGGAGAATGCAGCATATC
457 D Y E S T K E Y A I K L L A A D A G K P
2101 TTGACTATGAGTCCACAAAAGAATATGCCATTAAATTACTGGCTGCAGATGCTGGCAAAC
477 P L N Q S A M L F I K V K D E N D N A P
2161 CTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATGAAAATGACAATGCTC
497 V F T Q S F V T V S I P E N N S P G I Q
2221 CAGTTTTCACCCAGTCTTTTCGTAAGTGTCTTCTATTCTGAGAATAACTCTCCTGGCATCC
517 L M K V S A T D A D S G P N A E I N Y L
2281 AGTTGATGAAAGTAAGTGCAACGGATGCAGACAGTGGGCCTAATGCTGAGATCAATTACC
537 L G P D A P P E F S L D R R T G M L T V
2341 TGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATCGTCGTACAGGCATGCTGACTG
557 V K K L D R E K E D K Y L F T I L A K D
2401 TAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTTATTTCACAATTCTGGCAAAG
577 N G V P P L T S N V T V F V S I I D Q N
2461 ATAATGGGGTACCACCCTTAACCAGCAATGTCACAGTCTTTGTAAGCATTATTGATCAGA
597 D N S P V F T H N E Y K F Y V P E N L P
2521 ATGACAATAGCCAGTTTTCACCTCACAATGAATACAAATTCATGTCCCAGAAAACCTTC
617 R H G T V G L I T V T D P D Y G D N S A
2581 CAAGGCATGGTACAGTAGGACTAATCACTGTAACTGATCCTGATTATGGAGACAATTCTG
637 V T L S I L D E N D D F T I D S Q T G V
2641 CAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTGATTACAAACTGGTG
657 I R P N I S F D R E K Q E S Y T F Y V K
2701 TCATCCGACCAAATATTTTCATTTGATAGAGAAAAACAAGAATCTTACACTTTCTATGTAA
677 A E D G G R V S R S S S A K V T I N V V
2761 AGGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAGTAACCATAAATGTGG
697 D V N D N K P V F I V P P Y N Y S Y E L
2821 TTGATGTCAATGACAACAAACCAGTTTTTCATTGTCCCTCCTTACAACATTCTTATGAAT
717 V L P S T N P G T V V F Q V I A V D N D
2881 TGGTTCACCGTCCACTAATCCAGGCACAGTGGTCTTTCAGGTAATTGCTGTTGACAATG
737 T G M N A E V R Y S I V G G N T R D L F
2941 ACACTGGCATGAATGCAGAGGTTTCGTTACAGCATTGTAGGAGGAAACACAAGAGATCTGT
757 A I D Q E T G N I T L M E K C D V T D L
3001 TTGCAATCGACCAAGAAACAGGCAACATAACATTGATGGAGAAATGTGATGTTACAGACC
777 G L H R V L V K A N D L G Q P D S L F S
3061 TTGGTTTACACAGAGTGTGGTCAAAGCTAATGACTTAGGACAGCCTGATTCTCTCTTCA
797 V V I V N L F V N E S V T N A T L I N E
3121 GTGTTGTAATTGTCAATCTGTTTCGTGAATGAGTCAGTGACCAATGCTACACTGATTAATG
817 L V R K S I E A P V T P N T E I A D V S
3181 AACTGGTGCGCAAAGCATTGAAGCACCAGTGACCCCAAATACTGAGATAGCTGATGTAT
837 S P T S D Y V K I L V A A V A G T I T V
3241 CCTCACCAACTAGTGACTATGTCAAGATCCTGGTTGCAGCTGTTGCTGGCACCATAACTG
857 V V V I F I T A V V R C R Q A P H L K A

3301 TCGTTGTAGTTATTTTCATCACTGCTGTAGTAAGATGTCGCCAGGCACCCACACCTTAAGG
 877 A Q K N M Q N S E W A T P N P E N R Q M
 3361 CTGCTCAGAAAAACATGCAGAATTCTGAATGGGCTACCCCAAACCCAGAAAAACAGGCAGA
 897 I M M K K K K K K K H S P K N L L L N
 3421 TGATAATGATGAAGAAAAAGAAAAAGAAGAAGCATTCCCCTAAGAACCTGCTGCTTA
 917 V V T I E E T K A D D V D S D G N R V T
 3481 ATGTTGTCACTATTGAAGAACTAAGGCAGATGATGTTGACAGTGATGGAAACAGAGTCA
 937 L D L P I D L E E Q T M G K Y N W V T T
 3541 CACTAGACCTTCCTATTGATCTAGAAGAGCAAACAATGGGAAAGTACAATTGGGGTAACTA
 957 P T T F K P D S P D L A R H Y K S A S P
 3601 CACCTACTACTTTCAAGCCTGACAGCCCTGATTGCGCCGACACTACAAATCTGCCTCTC
 977 Q P A F Q I Q P E T P L N L K H H I I Q
 3661 CACAGCCTGCCTTCCAAATTCAGCCTGAAACTCCCCTGAATTTGAAGCACCACATCATCC
 997 E L P L D N T F V A C D S I S N C S S S
 3721 AAGAACTGCCTCTCGATAACACCTTTGTGGCCTGTGACTCTATCTCCAATTGTTCTCTCAA
 1017 S S D P Y S V S D C G Y P V T T F E V P
 3781 GCAGTTCAGATCCCTACAGCGTTTCTGACTGTGGCTATCCAGTGACAACCTTCGAGGTAC
 1037 V S V H T R P T D S R T *
 3841 CTGTGTCCGTACACACCAGACCGACTGATTCCAGGACATGAactattgaaatctgcagtg
 3901 agatgtaactttctaggaacaacaaaattccattccccttccaaaaatttcaatgattg
 3961 tgatttcaaaattaggctaagatcattaattttgtaatctagatttccattataaaagc
 4021 aagcaaaaatcatcttaaaaatgatgtccttagtgaaccttggtgttctttagctgtaat
 4081 ctggcaatggaaatttaaaatttatggaagagacagtgcagcgcaataacagagtactct
 4141 catgctgtttctctgtttgctctgaatcaacagccatgatgtaatataaggctgtcttgg
 4201 tgtatacacttatggttaatatatcagtcataacatgcaattacttgcctgtctgat
 4261 tgttgtaataatataaacattatctccaggagtttggaagtgcagtgtaactagccaaacta
 4321 ctctctgaaaggatccaggggcaagagacatttttaagaccccaaaacaaaaaaacaa
 4381 aacaaaaacactctggttcagtgttttgaaaatattgactaacataatattgctgagaaa
 4441 atcatttttattaccaccactctgcttaaaagttgagtgggcgggcggtggtcac
 4501 gcctgtaattccagcactttgggagggcgaggcggttgatcacgaggtcaggatattga
 4561 gaccatcctggctaacatggtgaaaccccatctccactaaaaatacaaaaaatttagctgg
 4621 gcgtggtggcgggcgccctgtagtcccagctactcgggaggctgaggcaggagaatggcgt
 4681 gaacccgggaggcgaggcttgagtgagccgagatggcgccactgcactccagcctgggt
 4741 gacagagcaagactctgtctcaaaaagaaaaaatgttcagtgatagaaaataattttac
 4801 taggtttttatgttgattgtactcatgctgttccactccttttaattattaaaaagttat
 4861 ttttggtggtgtggtggtcatacctgtaatcccagcactttgggaggccgaggcggtg
 4921 tggatcacctgaggtcaggagttcaagaccagtctggccaacat

Figure 2H. The cDNA (SEQ ID. NO. : 16) and amino acid sequence (SEQ ID. NO. : 17) of 109P1D4 v.8. The start methionine is underlined. The open reading frame extends from nucleic acid 735-4757 including the stop codon.

1 ggtggtccagtacctccaaagatatggaatacactcctgaaatatcctgaaacctttttt
 61 ttttcagaatcctttaataagcagttatgtcaatctgaaagttgcttacttgtactttat

121 attaatagctattcttgtttttcttatccaaagaaaaatcctctaatacccccttttcacat
181 gatagttgttaccatgttttagcggttagtcacatcaaccctctcctctcccaaacttct
241 cttcttcaaatcaaaactttattagtcctctctttataatgattccttgccctcttttatc
301 cagatcaattttttttcactttgatgccagagctgaagaaatggactattgtataaatt
361 attcattgccagagaataattgcattttaaacccatgttataacaaagaataatgatta
421 tattttgtgatttgaacaaataccctttattttcccttaactattgaattaaatatttt
481 aattatttgtattctctttaactatcttggatatattaaagtattatcttttatatattta
541 tcaatgggtggacacttttataggtactctgtgtcatttttgatactgtaggatatcttatt
601 tcatttatctttattcttaatgtacgaattcataatatttgattcagaacagatttatca
661 ctaattaacagagtgtcaattatgtaacatctcatttactgattttaatttaaacagt
1 M F R V G F L I I S S S S L S
721 ttttggttaacatgcATGTTTAGGGTTGGCTTCTTAATAATTTCTTCTCTCTCTCTCT
17 P L L L V S V V R V N T T N C H K C L L
781 CTCCTCTTCTTTTGGTCAGTGTGTGCGGGTTAATACAACAACTGTCACAAGTGTTTGT
37 S G T Y I F A V L L V C V V F H S G A Q
841 TGTCCGGGACGTACATTTTCGCGGTCTGCTAGTATGCGTGGTGTTCCTCTGGCGCCC
57 E K N Y T I R E E I P E N V L I G N L L
901 AGGAGAAAACTACACCATCCGAGAAGAAATTCAGAAAACGTCCTGATAGGCAACTTGT
77 K D L N L S L I P N K S L T T T M Q F K
961 TGAAAGACCTTAACFTGTCGCTGATTCCAAACAAGTCCTTGACAACACTATGTCAGTTCA
97 L V Y K T G D V P L I R I E E D T G E I
1021 AGCTAGTGTACAAGACCGGAGATGTGCCACTGATTGGAATTGAAGAGGATACTGGTGAGA
117 F T T G A R I D R E K L C A G I P R D E
1081 TCTTCACTACCGCGCTCGCATTGATCGTGAGAAATTATGTGCTGGTATCCCAAGGGATG
137 H C F Y E V E V A I L P D E I F R L V K
1141 AGCATTGCTTTTATGAAGTGGAGGTTGCCATTTTGCCGGATGAAATATTTAGACTGGTTA
157 I R F L I E D I N D N A P L F P A T V I
1201 AGATACGTTTTCTGATAGAAGATATAAATGATAATGCACCATTTGTTCCCAGCAACAGTTA
177 N I S I P E N S A I N S K Y T L P A A V
1261 TCAACATATCAATTCCAGAGAACTCGGCTATAAACTCTAAATATACTCTCCCAGCGGCTG
197 D P D V G I N G V Q N Y E L I K S Q N I
1321 TTGATCCTGACGTAGGCATAAACGGAGTTCAAAACTACGAACTAATTAAGAGTCAAAACA
217 F G L D V I E T P E G D K M P Q L I V Q
1381 TTTTGGCCTCGATGTTCATTGAAACACCAGAAGGAGACAAGATGCCACAACCTGATTGTTT
237 K E L D R E E K D T Y V M K V K V E D G
1441 AAAAGGAGTTAGATAGGGAAGAGAAGGATACCTATGTGATGAAAGTAAAGGTTGAAGATG
257 G F P Q R S S T A I L Q V S V T D T N D
1501 GTGGCTTTCCTCAAAGATCCAGTACTGCTATTTTGCAAGTAAGTGTACTGATACAAATG
277 N H P V F K E T E I E V S I P E N A P V
1561 ACAACCACCCAGTCTTTAAGGAGACAGAGATTGAAGTCAGTATACCAGAAAATGCTCTCTG
297 G T S V T Q L H A T D A D I G E N A K I
1621 TAGGCACTTCAGTGACACAGCTCCATGCCACAGATGCTGACATAGGTGAAAATGCCAAGA

317 H F S F S N L V S N I A R R L F H L N A
1681 TCCACTTCTCTTTTCAGCAATCTAGTCTCCAACATTGCCAGGAGATTATTTTCACCTCAATG
337 T T G L I T I K E P L D R E E T P N H K
1741 CCACCCTGGACTTATCACAATCAAAGAACCCTGGATAGGGAAGAAACACCAAACCACA
357 L L V L A S D G G L M P A R A M V L V N
1801 AGTTACTGGTTTTTGGCAAGTGATGGTGGATTGATGCCAGCAAGAGCAATGGTGGCTGGTAA
377 V T D V N D N V P S I D I R Y I V N P V
1861 ATGTTACAGATGTCAATGATAATGTCCCATCCATTGACATAAGATACATCGTCAATCCTG
397 N D T V V L S E N I P L N T K I A L I T
1921 TCAATGACACAGTTGTTCTTTTCAGAAAATATTCCACTCAACACCAAAATTTGCTCTCATAA
417 V T D K D A D H N G R V T C F T D H E I
1981 CTGTGACGGATAAGGATGCGGACCATAATGGCAGGGTGACATGCTTCACAGATCATGAAA
437 P F R L R P V F S N Q F L L E N A A Y L
2041 TTCCTTTTCAGATTAAGGCCAGTATTCAGTAATCAGTTCCTCCTGGAGAATGCAGCATATC
457 D Y E S T K E Y A I K L L A A D A G K P
2101 TTGACTATGAGTCCACAAAAGAAATATGCCATTAAATTACTGGCTGCAGATGCTGGCAAAC
477 P L N Q S A M L F I K V K D E N D N A P
2161 CTCCTTTGAATCAGTCAGCAATGCTCTTCATCAAAGTGAAAGATGAAAATGACAATGCTC
497 V F T Q S F V T V S I P E N N S P G I Q
2221 CAGTTTTTCACCCAGTCTTTTCGTAACGTGTTTCTATTCTGAGAATAACTCTCCTGGCATCC
517 L M K V S A T D A D S G P N A E I N Y L
2281 AGTTGATGAAAGTAAGTGCAACGGATGCAGACAGTGGGCCTAATGCTGAGATCAATTACC
537 L G P D A P P E F S L D R R T G M L T V
2341 TGCTAGGCCCTGATGCTCCACCTGAATTCAGCCTGGATCGTCTACAGGCATGCTGACTG
557 V K K L D R E K E D K Y L F T I L A K D
2401 TAGTGAAGAACTAGATAGAGAAAAAGAGGATAAATATTATTACCAATTCTGGCAAAAG
577 N G V P P L T S N V T V F V S I I D Q N
2461 ATAATGGGGTACCACCCTTAACCAGCAATGTCACAGTCTTTGTAAGCATTATTGATCAGA
597 D N S P V F T H N E Y K F Y V P E N L P
2521 ATGACAATAGCCCAGTTTTTCACTCACAATGAATACAAATTCATGTCCCAGAAAACCTTC
617 R H G T V G L I T V T D P D Y G D N S A
2581 CAAGGCATGGTACAGTAGGACTAATCACTGTAACGTATCCTGATTATGGAGACAATTCTG
637 V T L S I L D E N D D F T I D S Q T G V
2641 CAGTTACGCTCTCCATTTTAGATGAGAATGATGACTTCACCATTTGATTACAAACTGGTG
657 I R P N I S F D R E K Q E S Y T F Y V K
2701 TCATCCGACCAAATATTTTCATTTGATAGAGAAAAACAAGAATCTTACACTTTCTATGTAA
677 A E D G G R V S R S S S A K V T I N V V
2761 AGGCTGAGGATGGTGGTAGAGTATCACGTTCTTCAAGTGCCAAAGTAACCATAAATGTGG
697 D V N D N K P V F I V P P Y N Y S Y E L
2821 TTGATGTCAATGACAACAAACCAGTTTTTCATTGTCCCTCCTTACAACTATTCTTATGAAT
717 V L P S T N P G T V V F Q V I A V D N D
2881 TGGTTCTACCGTCCACTAATCCAGGCACAGTGGTCTTTTCAGGTAATTGCTGTTGACAAATG

737 T G M N A E V R Y S I V G G N T R D L F
2941 A C A C T G G C A T G A A T G C A G A G G T T C G T T A C A G C A T T G T A G G A G G A A C A C A A G A G A T C T G T
757 A I D Q E T G N I T L M E K C D V T D L
3001 T T G C A A T C G A C C A A G A A A C A G G C A A C A T A A C A T T G A T G G A G A A A T G T G A T G T T A C A G A C C
777 G L H R V L V K A N D L G Q P D S L F S
3061 T T G G T T T A C A C A G A G T G T T G G T C A A A G C T A A T G A C T T A G G A C A G C C T G A T T C T C T C T T C A
797 V V I V N L F V N E S V T N A T L I N E
3121 G T G T T G T A A T T G T C A A T C T G T T C G T G A A T G A G T C A G T G A C C A A T G C T A C A C T G A T T A A T G
817 L V R K S I E A P V T P N T E I A D V S
3181 A A C T G G T G C G C A A A A G C A T T G A A G C A C C A G T G A C C C C A A A T A C T G A G A T A G C T G A T G T A T
837 S P T S D Y V K I L V A A V A G T I T V
3241 C C T C A C C A A C T A G T G A C T A T G T C A A G A T C C T G G T T G C A G C T G T T G C T G G C A C C A T A A C T G
857 V V V I F I T A V V R C R Q A P H L K A
3301 T C G T T G T A G T T A T T T T C A T C A C T G C T G T A G T A A G A T G T C G C C A G G C A C C A C A C C T T A A G G
877 A Q K N M Q N S E W A T P N P E N R Q M
3361 C T G C T C A G A A A A C A T G C A G A A T T C T G A A T G G G C T A C C C C A A A C C C A G A A A A C A G G C A G A
897 I M M K K K K K K K K K H S P K N L L L N
3421 T G A T A A T G A T G A A G A A A A G A A A A G A A G A A G A A G C A T T C C C C T A A G A A C C T G C T G C T T A
917 V V T I E E T K A D D V D S D G N R V T
3481 A T G T T G T C A C T A T T G A A G A A A C T A A G G C A G A T G A T G T T G A C A G T G A T G G A A C A G A G T C A
937 L D L P I D L E E Q T M G K Y N W V T T
3541 C A C T A G A C C T T C C T A T T G A T C T A G A A G A G C A A A C A A T G G G A A A G T A C A A T T G G G T A A C T A
957 P T T F K P D S P D L A R H Y K S A S P
3601 C A C C T A C T A C T T T C A A G C C T G A C A G C C C T G A T T T G G C C C G A C A C T A C A A A T C T G C C T C T C
977 Q P A F Q I Q P E T P L N L K H H I I Q
3661 C A C A G C C T G C C T T C C A A A T T C A G C C T G A A A C T C C C C T G A A T T T G A A G C A C C A C A T C A T C C
997 E L P L D N T F V A C D S I S N C S S S
3721 A A G A A C T G C C T C T C G A T A A C A C C T T T G T G G C C T G T G A C T C T A T C T C C A A T T G T T C C T C A A
1017 S S D P Y S V S D C G Y P V T T F E V P
3781 G C A G T T C A G A T C C C T A C A G C G T T T C T G A C T G T G G C T A T C C A G T G A C A A C C T T C G A G G T A C
1037 V S V H T R P S Q R R V T F H L P E G S
3841 C T G T G T C C G T A C A C A C C A G A C C G T C C C A G C G G C G T G T C A C A T T T C A C C T G C C A G A A G G C T
1057 Q E S S S D G G L G D H D A G S L T S T
3901 C T C A G G A A A G C A G C A G T G A T G G T G G A C T G G G A G A C C A T G A T G C A G G C A G C C T T A C C A G C A
1077 S H G L P L G Y P Q E E Y F D R A T P S
3961 C A T C C C A T G G C C T G C C C T T G G C T A T C C T C A G G A G A G T A C T T T G A T C G T G C T A C A C C C A
1097 N R T E G D G N S D P E S T F I P G L K
4021 G C A A T C G C A C T G A A G G G G A T G G C A A C T C C G A T C C T G A A T C T A C T T T C A T A C C T G G A C T A A
1117 K E I T V Q P T V E E A S D N C T Q E C
4081 A G A A A G A A A T A A C T G T T C A C C A A C T G T G G A A G A G G C C T C T G A C A A C T G C A C T C A A G A A T
1137 L I Y G H S D A C W M P A S L D H S S S
4141 G T C T C A T C T A T G G C A T T C T G A T G C C T G C T G G A T G C C G G C A T C T C T G G A T C A T T C C A G C T

1157 S Q A Q A S A L C H S P P L S Q A S T Q
4201 CTTCAACAAGCACAGGCCTCTGCTCTATGCCACAGCCCACCACTGTACAGGCCTCTACTC
1177 H H S P P V T Q T I V L C H S P P V T Q
4261 AGCACCACAGCCCACCACTGACACAGACCATTGTTCTCTGCCACAGCCCTCCAGTGACAC
1197 T I A L C H S P P P I Q V S A L H H S P
4321 AGACCATCGCATTGTGCCACAGCCCACCAACGATACAGGTGTCTGCTCTCCACCACAGTC
1217 P L V Q G T A L H H S P P S A Q A S A L
4381 CTCCTCTAGTGCAGGGTACTGCACCTTACCACAGCCCACCATCAGCACAGGCCTCAGCCC
1237 C Y S P P L A Q A A A I S H S S S L P Q
4441 TCTGCTACAGCCCTCCTTTAGCACAGGCTGCTGCAATCAGCCACAGCTCTTCTCTGCCAC
1257 V I A L H R S Q A Q S S V S L Q Q G W V
4501 AGGTTATTGCCCTCCATCGTAGTCAGGCCCAATCATCAGTCAGTTTGCAGCAAGGTTGGG
1277 Q G A N G L C S V D Q G V Q G S A T S Q
4561 TGCAAGGTGCTAATGGACTATGCTCTGTTGATCAGGGAGTGCAAGGTAGTGCAACATCTC
1297 F Y T M S E R L H P S D D S I K V I P L
4621 AGTTTACACCATGTCTGAAAGACTTCATCCCAGTGATGATTCAATTAAAGTCATTCCTT
1317 T T F A P R Q Q A R P S R G D S P I M E
4681 TGACAACCTTCGCTCCACGCCAACAGGCCAGACCGTCCAGAGGTGATTCCCCCATTATGG
1337 T H P L *
4741 AAACACATCCCTTGTAAagctaaaaatagttacttcaaattttcagaaaagatgtatatag
4801 tcaaaatttaagatacaattccaatgagattctgattatcagatttgtaaataactatg
4861 taaatagaaacagataccagaataaatctacagctagacccttagtcaatagttaacca
4921 aaaattgcaatttgtttaattcagaatgtgtatttataaaagaaaaggaatttaacaattt
4981 gcatcccctgtacagtaaggcttatcatgacagagcgactatttctgatgtacagtat
5041 tttttgtgtgttttatcatcatgtgcaatattactgatttggttccatgctgattgtgtg
5101 gaaccagtatgtagcaaatggaaagcctagaaatatcttattttctaagtttacctttag
5161 tttacctaacttttgttcagataatgttaaaagggtatacgtactctagccttttttggg
5221 gctttctttttgatttttgtttgtgtgttttcagttttttgtgtgttagtgagtcctc
5281 cttcaaaatacacagtaggttagtgaataactgcttgtttgtgtctctctgctgtcatgt
5341 tttctaccttattccaatactatatattgttgataaaatttgatatatacattttcaataaag
5401 aatatgtataaactgtacagatctagatctacaacctatttctctactcttttagtagagt
5461 tcgagacacagaagtgaataactgccotaattaagcaactatttgtaaaaagggcccc
5521 tttttactttaatagtttagtgtaaagtacatcagaaataaaactgtatctgacatttta
5581 agcctgtagtccattattacttgggtctttacttctgggaatttgtagtaacagcctag
5641 aaaattaaaaggagggtggatgcatccaaagcacgagtcacttaaaatatcgacggtaaac
5701 tactattttgtagagaaactcaggaagatttaaagtgtgatttgacagctcaataggctg
5761 ttaccaaagggtgttcagtaaaaataacaaatacatgtaactgtagataaaaccacatac
5821 taaatctataagactaagggtttttgttattctagctcaacttactgaagaaaaccact
5881 aataacaacaagaatatcaggaagggaacttttcaagaaatgtaattataaatctacatca
5941 aacagaattttaaggaaaaatgcagagggagaaataaggcacatgactgcttcttcgagt
6001 caagaagaaataccaataacacacacagaaacaaaaccatcaaatctcatatatgaaat
6061 aaaatatattcttctaagcaaaagaacagtactattcatagaaaacattagttttctcct

6121 gttgtctgttatttccttctttttatcctcttaactggccattatcttgtatgtgcacatt
6181 ttataaatgtacagaaacatcaccaacttgattttcttccatagcaaaactgagaaaata
6241 ccttgtttcagtataacactaaaccaagagacaattgatgtttaatggggcggttgggg
6301 ttgggggggagtcataatctcctatttgattaacttagacatagattttgtaatgtataac
6361 ttgatattttaatttatgattaaactgtaattttgtaacataaactgtggttaattgcataa
6421 tttcattggtgaggatttcctttgaaatttgagaaagtttcttttcattgtgccagcagg
6481 ttaagtagcgttttcagaatatacattattcccatccattgtaaagttccttaagtcata
6541 tttgactggggtgcagaataacttcttaactattaactatcagagtttgattaataaaa
6601 ttaattaattttttttctccttcgtgttgtaattgtccaagggtttggagcatactgg
6661 ttttccagggtgatgtgaatcccgaaggactgatgatatttgaatgtttattaaattatt
6721 atcacacaaatgtgttgatattgtggctattgttgatgttgaaaattgtaaacttgggga
6781 agattaagaaaagaaccaatagtgacaaaaatcagtgttccagtagattttagaacatt
6841 ctttgcctcaaaaaacctgcaaagatgatgtgagatttttcttgtgttttaattatttt
6901 cacattttctctctgcaaaccttttagttttctgatgatctacacacacacatacacacac
6961 acacacacacacgtgcacacacacacatttaaaggatataaaaaagaagggttgaaagat
7021 tattaataaacttatcaggcatctcaatggttactatctatgttagtgaaaatcaaatag
7081 gactcaaagttagtatatttgggatttttctctgacagtataatttattgagttactagg
7141 gaggttcttaaatcctcatatctggaaacttgtgaagttttgacacctttcctatagata
7201 taggaatgaaccaatacgtttttattaccctttctaactctgattttataatcagactta
7261 gattgtgtttagaatattaaatgactgggcaccctcttcttggtttttaccagagaggct
7321 ttgaatggaagcaggctgagagtagccaaaggaggcaagggtattagcccagttattctc
7381 ccctatgccttctcttccctaagcgtccactaggctctggccttggaatctgttacttcta
7441 cggcttcagatctgatgatatttttcatcacattacaagttatttcttcttgactgaata
7501 gacagtggatatagggtgacacagcacacaagtggctattgtgatgtatgatgtatgtagt
7561 cccacaactgcaaaacgtcttactgaagcaacaatcgaaaaatgggtctgttttaaaaag
7621 gattttgtttgatttgaaattaaaacttcaaactgaatgacttatatgagaataatatgt
7681 tcaatcaaagtagttatttctattttgtgtccatattccattagattgtgattattaattt
7741 tctagctatggtattactatatcacacttgtgagtatgtattcaaataactaagtatctta
7801 tatgtctacgtgcatacacattcttttcttaaaactttacctgtgttttaactaatattgtg
7861 tcagtgtattaaaaattagcttttcatatgatattctacaatgtaataaatttagagagt
7921 aattttgtgtattcttatttacttaacattttacttttaattatgtaaatgttggttagaa
7981 aataataataaatgggttagtgctattgtgtaatggtagcagttacaaagagcctctgcct
8041 toccaaactaatattttatcacacatggtcattaaatgggaaaaaaatagactaaacaaat
8101 cacaaattgttcagttctttaaagttaattatgtcacacacacaaaaaatccttttcaa
8161 tcttgagaaaattaaagggtgttttactcacatggatatttcaacattagtttttttgtt
8221 tgtttctttttcatgggtattactgaagggtgtatactccctaatacacatttatgaaaa
8281 tctacttgtttgactttttatttatactcttctgatttatatttttattataattatta
8341 tttcttatcttcttttataatttttggaaaccaaatttatagttagtttaggttaaacttt
8401 ttattatgaccattagaaactattttgaatgtttccaactggctcaattggctgggaaaa
8461 catgggaacaagagaagctgaaatatatttctgcaagaacctttctatattatgtgccaa
8521 ttaccacaccagatcaattttatgcagaggccttaaaatattctttcacagtagctttct
8581 tacactaaccgtcatgtgcttttagtaaatatgatttttaaaagcagttcaagttgacaa

8641 cagcagaaacagtaacaaaaaaatctgctcagaaaaatgtatgtgcacaaataaaaaaaa
8701 ttaatggcaattgttttagtgactgtaagtatactttttaagagtaaactgtgtgaaat
8761 ttatactatccctgcttaaaatattaagatttttatgaaatatgtatttatgtttgtatt
8821 gtgggaagattcctcctctgtgatatacatagcatctgaaagtgaacagtatcccaaag
8881 cagttccaagcatgctttggaagtaagaagggtgactattgtatggccaaggatggcagt
8941 atgtaatccagaagcaaaacttgtattaattgttctatttcagggttctgtattgcatgttt
9001 tcttattaatatatattaataaaagttatgagaaat

Figure 21. The cDNA (SEQ ID. NO. : 18) and amino acid sequence (SEQ ID. NO. : 19) of 109P1D4 v.9. The start methionine is underlined. The open reading frame extends from nucleic acid 514-3627 including the stop codon.

1 cccctttctccccctctgttaagtccctccccctcgccattcaaaagggctggctcggca
61 ctggctccttgagtcggcgaactgtctggcgaggagccgtgagcagtagctgcact
121 cagctgcccgcgcggcaagaggaaggcaagccaaacagagtgcgcagagtggcagtgcc
181 agcggcgacacaggcagcacaggcagccgggctgcctgaatagcctcagaaacaacctc
241 agcgactccggctgctctgaggactgcgagctgtggcggtagagcccgctacagcagtcg
301 cagtctccgtggagcggcggaagcctttttctccctttcgtttacctcttcattctac
361 tctaaaggcatcggtatttaggaaaatcctgttgaataagaaggattccacagatcaca
421 taccagagcggttttgcctcagctgctctcaactttgtaatcctgtgaagaagctgacaa
1 M T V G F N S D I
481 gcttggctgattgcagtgcaactatgaggactgaATGACAGTGGGTTTAAATTCAGATATT
10 S S V V R V N T T N C H K C L L S G T Y
541 TCAAGTGTGTGTCGGGTTAATACAACAACTGTCAAGTGTGTGTTGTCGGGACGTAC
30 I F A V L L V C V V F H S G A Q E K N Y
601 ATTTTCGCGTCTGCTAGTATGCGTGGTGTTCCTACTCTGGCGCCAGGAGAAAACTAC
50 T I R E E I P E N V L I G N L L K D L N
661 ACCATCCGAGAAGAAATTCAGAAAACGTCCTGATAGGCAACTTGTGAAAGACCTTAAC
70 L S L I P N K S L T T T M Q F K L V Y K
721 TTGTCGCTGATTCCAAACAAGTCCTTGACAACACTACTATGCAGTTCAAGCTAGTGACAAAG
90 T G D V P L I R I E E D T G E I F T T G
781 ACCGGAGATGTGCCACTGATTGCAATTGAAGAGGATACTGGTGAGATCTTCACTACCGGC
110 A R I D R E K L C A G I P R D E H C F Y
841 GCTCGCATTGATCGTGAGAAATTATGTGCTGGTATCCCAAGGGATGAGCATTTGCTTTTAT
130 E V E V A I L P D E I F R L V K I R F L
901 GAAGTGGAGGTTGCCATTTTGCCGGATGAAATATTTAGACTGGTTAAGATACGTTTCTG
150 I E D I N D N A P L F P A T V I N I S I
961 ATAGAAGATATAAATGATAATGCACCATTTGTTCCCAGCAACAGTTATCAACATATCAATT
170 P E N S A I N S K Y T L P A A V D P D V
1021 CCAGAGAACTCGGCTATAAACTCTAAATATACTCTCCAGCGGCTGTTGATCCTGACGTA
190 G I N G V Q N Y E L I K S Q N I F G L D
1081 GGCATAAACGGAGTTCAAACTACGAACATAATTAAGAGTCAAAACATTTTGGCCTCGAT
210 V I E T P E G D K M P Q L I V Q K E L D
1141 GTCATTGAAACACCAGAAGGAGACAAGATGCCACAACCTGATTGTTCAAAAGGAGTTAGAT

230 R E E K D T Y V M K V K V E D G G F P Q
1201 AGGGAAGAGAAGGATACCTATGTGATGAAAGTAAAGGTTGAAGATGGTGGCTTTCCTCAA
250 R S S T A I L Q V S V T D T N D N H P V
1261 AGATCCAGTACTGCTATTTTGCAAGTAAGTGTACTGATACAAATGACAACCACCCAGTC
270 F K E T E I E V S I P E N A P V G T S V
1321 TTTAAGGAGACAGAGATTGAAGTCAGTATACCAGAAAATGCTCCTGTAGGCACCTTCAGTG
290 T Q L H A T D A D I G E N A K I H F S F
1381 ACACAGCTCCATGCCACAGATGCTGACATAGGTGAAAATGCCAAGATCCACTTCTCTTTC
310 S N L V S N I A R R L F H L N A T T G L
1441 AGCAATCTAGTCTCCAACATTGCCAGGAGATTATTTTCACCTCAATGCCACCACCTGGACTT
330 I T I K E P L D R E E T P N H K L L V L
1501 ATCACAATCAAAGAACCACCTGGATAGGGAAGAAACACCAAACCACAAGTTACTGGTTTTCG
350 A S D G G L M P A R A M V L V N V T D V
1561 GCAAGTGTGGTGGATTGATGCCAGCAAGAGCAATGGTGTGTAATGTTACAGATGTC
370 N D N V P S I D I R Y I V N P V N D T V
1621 AATGATAATGTCCCATCCATTGACATAAGATACATCGTCAATCCTGTCAATGACACAGTT
390 V L S E N I P L N T K I A L I T V T D K
1681 GTTCTTTTCAGAAAATATTCCACTCAACACCAAAATTTGCTCTCATAACTGTGACGGATAAG
410 D A D H N G R V T C F T D H E I P F R L
1741 GATGCGGACCATAATGGCAGGGTGACATGCTTCACAGATCATGAAATTCCTTTTCAGATTA
430 R P V F S N Q F L L E N A A Y L D Y E S
1801 AGGCCAGTATTTCAGTAATCAGTTCCTCCTGGAGAATGCAGCATATCTTGACTATGAGTCC
450 T K E Y A I K L L A A D A G K P P L N Q
1861 ACAAAGAATATGCCATTAAATTACTGGCTGCAGATGCTGGCAAACCTCCTTTGAATCAG
470 S A M L F I K V K D E N D N A P V F T Q
1921 TCAGCAATGCTCTTCATCAAAGTGAAAGATGAAAATGACAATGCTCCAGTTTTTCACCCAG
490 S F V T V S I P E N N S P G I Q L M K V
1981 TCTTTTCGTAACCTGTTTCTATTCTGAGAATAACTCTCCTGGCATCCAGTTGATGAAAGTA
510 S A T D A D S G P N A E I N Y L L G P D
2041 AGTGCAACGGATGCAGACAGTGGGCCCTAATGCTGAGATCAATTACCTGCTAGGCCCTGAT
530 A P P E F S L D R R T G M L T V V K K L
2101 GCTCCACCTGAATTTCAGCCTGGATCGTCGTACAGGCATGCTGACTGTAGTGAAGAACTA
550 D R E K E D K Y L F T I L A K D N G V P
2161 GATAGAGAAAAAGAGGATAAATATTTTATTCACAATTCTGGCAAAAGATAATGGGGTACCA
570 P L T S N V T V F V S I I D Q N D N S P
2221 CCCTTAACCAGCAATGTCACAGTCTTTGTAAGCATTATTGATCAGAATGACAATAGCCCA
590 V F T H N E Y K F Y V P E N L P R H G T
2281 GTTTTCACCTCACAATGAATACAAATTCTATGTCCCAGAAAACCTTCCAAGGCATGGTACA
610 V G L I T V T D P D Y G D N S A V T L S
2341 GTAGGACTAATCACTGTAACCTGATCCTGATTATGGAGACAATTCTGCAGTTACGCTCTCC
630 I L D E N D D F T I D S Q T G V I R P N
2401 ATTTTAGATGAGAATGATGACTTCACCATTGATTCACAACTGGTGTATCCGACCAAAT

650 I S F D R E K Q E , S Y T F Y V K A E D G
2461 ATTTTCATTTGATAGAGAAAAACAAGAATCTTACACTTTCTATGTAAAGGCTGAGGATGGT
670 G R V S R S S S A K V T I N V V D V N D
2521 GGTAGAGTATCACGTTCTTCAAGTGCCAAAGTAACCATAAATGTGGTTGATGTCAATGAC
690 N K P V F I V P P Y N Y S Y E L V L P S
2581 AACAAACCAGTTTTTCATTGTCCCTCCTTACAACATTCTTATGAATTGGTTCTACCGTCC
710 T N P G T V V F Q V I A V D N D T G M N
2641 ACTAATCCAGGCACAGTGGTCTTTTCAGGTAATTGCTGTTGACAATGACACTGGCATGAAT
730 A E V R Y S I V G G N T R D L F A I D Q
2701 GCAGAGGTTTCGTTACAGCATTGTAGGAGGAAACACAAGAGATCTGTTTGCAATCGACCAA
750 E T G N I T L M E K C D V T D L G L H R
2761 GAAACAGGCAACATAACATTGATGGAGAAATGTGATGTTACAGACCTTGGTTTACACAGA
770 V L V K A N D L G Q P D S L F S V V I V
2821 GTGTTGGTCAAAGCTAATGACTTAGGACAGCCTGATTCTCTCTTCAGTGTGTAAATTGTC
790 N L F V N E S V T N A T L I N E L V R K
2881 AATCTGTTTCGTGAATGAGTCAGTGACCAATGCTACACTGATTAATGAACTGGTGCGCAA
810 S I E A P V T P N T E I A D V S S P T S
2941 AGCATTGAAGCACCAGTGACCCCAAATACTGAGATAGCTGATGTATCCTCACCAACTAGT
830 D Y V K I L V A A V A G T I T V V V V I
3001 GACTATGTCAAGATCCTGGTTGCAGCTGTTGCTGGCACCATAACTGTCGTTGTAGTTATT
850 F I T A V V R C R Q A P H L K A A Q K N
3061 TTCATCACTGCTGTAGTAAGATGTGCCAGGCACCACACCTTAAGGCTGCTCAGAAAAAC
870 M Q N S E W A T P N P E N R Q M I M M K
3121 ATGCAGAATTCTGAATGGGCTACCCCAAACCCAGAAAACAGGCAGATGATAATGATGAAG
890 K K K K K K H S P K N L L L N V V T I
3181 AAAAAGAAAAAGAAGAAGAAGCATTCCCCTAAGAACCTGCTGCTTAATGTTGTCACTATT
910 E E T K A D D V D S D G N R V T L D L P
3241 GAAGAACTAAGGCAGATGATGTTGACAGTGATGGAAACAGAGTCACACTAGACCTTCCT
930 I D L E E Q T M G K Y N W V T T P T T F
3301 ATTGATCTAGAAGAGCAAACAATGGGAAAGTACAATTGGGTAACCTACACCTACTACTTTT
950 K P D S P D L A R H Y K S A S P Q P A F
3361 AAGCCTGACAGCCCTGATTTGGCCCGACACTACAAATCTGCCTCTCCACAGCCTGCCTTC
970 Q I Q P E T P L N L K H H I I Q E L P L
3421 CAAATTCAGCCTGAAACTCCCCTGAATTTGAAGCACCACATCATCCAAGAACTGCCTCTC
990 D N T F V A C D S I S N C S S S S S D P
3481 GATAACACCTTTGTGGCTGTGACTCTATCTCCAATTGTTCTCAAGCAGTTGAGATCCC
1010 Y S V S D C G Y P V T T F E V P V S V H
3541 TACAGCGTTTCTGACTGTGGCTATCCAGTGACAACCTTCGAGGTACCTGTGTCCGTACAC
1030 T R P T D S R T *
3601 ACCAGACCGACTGATTCCAGGACATGAactattgaaatctgcagtgagatgtaactttct
3661 aggaacaacaaaattccattccccttccaaaaatttcaatgattgtgatttcaaaatta
3721 ggctaagatcattaattttgtaatctagatttccattataaaagcaagcaaaaatcatc

3781 ttaaaaatgatgtcctagtgaaaccttgctgtttcttttagctgtaatctggcaatggaaat
3841 ttaaaatttatggaagagacagtgacgcgaataacagagtactctcatgctgtttctct
3901 gtttgctctgaatcaacagccatgatgtaataaaggctgtcttggtgtatacacttatg
3961 gttaatatatcagtcatgaaacatgcaattacttgccctgtctgattggtgaataattaa
4021 aacattatctccaggagtttggaagtgcagctgaactagccaaactactctctgaaaggta
4081 tccaggggcaagagacatttttaagaccccaaaacaaaaacaaaaacaaaacactct
4141 ggttcagtggtttgaaaatattgactaacataatattgctgagaaaatcatttttattac
4201 ccaccactctgcttaaaagttagtggtggcgccggcggtggctcacgcctgtaattccag
4261 cactttgggagggcgaggcggtggatcacgaggtcaggatattgagaccatcctggcta
4321 acatggtgaaaccccatctccactaaaaatacaaaaaattagctggcggtggtggcgggc
4381 gcctgtagtcccagctactcgggaggtgagggcaggagaatggcgtgaacccgggagggcg
4441 gagcttgacgtgagccgagatggcgccactgcactccagcctgggtgacagagcaagact
4501 ctgtctcaaaaagaaaaaatgttcagtgatagaaaataattttactagggtttttatgtt
4561 gattgtactcatgctgttccactccttttaattattaaaaagttatttttggctgggtgt
4621 ggtggctcatacctgtaatccagcactttgggagggccgaggcggtggatcacctgagg
4681 tcaggagttcaagaccagtcctggccaacat

Figure 2J. 109P1D4 v.1, v.2 and v.3 SNP variants. Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above.

v.1				v.2				v.3**			
SNP_no	Position	Alleles	AA change***	SNP_no	Position	Alleles	AA change**	SNP_no	Pos.	Alleles	AA change***
1	55	A/C						1	55	A/C	
2	206	A/G						2	206	A/G	
3	223	C/G						3	223	C/G	
4	295	G/C						4	295	G/C	
5	352	C/T						5	352	C/T	
6	400	A/G						6	400	A/G	
7	654	A/G						7	654	A/G	
8	830	A/C		1	574	A/C	V24V	8	830	A/C	
9	889	C/T	A15V	2	633	C/T	A44V	9	889	C/T	A15V
10	947	G/T	M34I	3	691	G/T	M63I	10	947	G/T	M34I
11	969	G/A	D42N	4	713	G/A	D71N	11	969	G/A	D42N
12	1023	G/A	A60T	5	767	G/A	A89T	12	1023	G/A	A60T
13	1305	A/G	I154V	6	1049	A/G	I183V	13	1305	A/G	I154V
14	1490	C/T	Y215Y	7	1234	C/T	Y244Y	14	1490	C/T	Y215Y
15	1556	G/A	V237V	8	1300	G/A	V266V	15	1556	G/A	V237V
16	1719	G/A	V292I	9	1463	G/A	V321I	16	1719	G/A	V292I
17	2057	C/T	I404I	10	1801	C/T	I433I	17	2057	C/T	I404I
18	2104	C/A	T420N	11	1848	C/A	T449N	18	2104	C/A	T420N
19	2302	C/T	T486M	12	2046	C/T	T515M	19	2302	C/T	T486M
20	2317	T/C	M491T	13	2061	T/C	M520T	20	2317	T/C	M491T
21	2343	A/G	K500E	14	2087	A/G	K529E	21	2343	A/G	K500E
22	2394	T/C	C517R	15	2138	T/C	C546R	22	2394	T/C	C517R
23	2480	C/T	N545N	16	2224	C/T	N574N	23	2480	C/T	N545N
24	2573	C/A	N576K	17	2317	C/A	N605K	24	2573	C/A	N576K
25	2878	C/A	S678Y	18	2622	C/A	S707Y	25	2878	C/A	S678Y
26	2884	G/A	C680Y	19	2628	G/A	C709Y	26	2884	G/A	C680Y
27	3170	G/A	S775S	20	2914	G/A	S804S	27	3170	G/A	S775S
28	3214	C/T	T790I	21	2958	C/T	T819I	28	3214	C/T	T790I
29	3391	A/T	K849M	22	3135	A/T	K878M	29	3391	A/T	K849M
30	3486	T/C	L881L	23	3230	T/C	L910L	30	3486	T/C	L881L
31	3498	T/G	F885V	24	3242	T/G	F914V	31	3498	T/G	F885V
32	3635	C/T	P930P	25	3379	C/T	P959P	32	3635	C/T	P930P
33	3718	C/T	S958L	26	3462	C/T	S987L	33	3718	C/T	S958L
34	3785	G/T	K980N	27	3529	G/T	K1009N	34	3785	G/T	K980N
35	3842	G/A	T999T	28	3586	G/A	T1028T	35	3842	G/A	T999T
36	3924	T/G		29	3639	C/G	S1046S TOP*	36	3898	G/A	R1018Q*
37	3947	C/T		30	3664	A/G	I1054M*	37	4337	G/A	S1164S*
38	4146	G/A		31	3714	T/C	*	38	4408	G/C	R1188P*
39	4206	T/G		32	3882	A/G	*	39	4426	C/T	A1194V*
40	4351	T/A		33	4176	C/G	*	40	4483	C/T	P1213L*
41	4452	C/A		34	4378	T/A	*	41	4528	C/G	A1228G*
				35	4383	T/C	*	42	4623	C/T	P1260S*
				36	4499	T/C	*	43	4704	G/A	D1287N*
				37	4508	A/G	*	44	4709	G/A	G1288G*
				38	4515	T/C	*	45	4728	G/C	G1295R*
				39	4676	T/C	*	46	4824	A/G	T1327A*
								47	4875	G/A	E1344K*
								48	4876	A/C	K1344T*
								49	4875-6	GA/A C	A1344T*

*Note: SNP not corresponding to those in v.1

**Note: more SNP in the 3' untranslated region are as following: 5151 C/T, 5318 C/T, 5350 T/G, 5357 T/C, 5377 T/G, 5424 G/A, 5651 T/C, 5695 G/A, 5705 C/A, 5889 G/A, 5948 T/C, 5998 C/A, 6136 C/G, 6250 T/C, 6274 G/T, 6342 A/G, 6579 A/T, 6580 C/T, 6711 T/A, 6748 G/T, 6863 T/C, 6906 T/G, 7058 A/C, 7306 C/A, 7565 C/T, 7578 G/C, 7627 C/T, 7700 T/C, 7725

C/G, 7728 A/T, 7734 A/G, 7789 G/A, 7815 C/T, 8315 C/T, 8331 C/A, 8430 G/A, 8572 C/T, 8593 C/T, 8608 G/A, 8862 T/C and 9030 C/G.

***Note: Amino acid that does not change is omitted.

Figure 2K. 109P1D4 v.6, v.7 and v.8 SNP variants. Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above.

v.6				v.7				v.8**			
SNP_no	Position	Alleles	AA change***	SNP_no	Position	Alleles	AA change***	SNP_no	Position	Alleles	AA change***
				1	204	G/A	*	1	204	G/A	*
				2	221	C/G	*	2	221	C/G	*
				3	293	C/G	*	3	293	C/G	*
				4	350	T/C	*	4	350	T/C	*
				5	398	G/A	*	5	398	G/A	*
1	597	T/A		6	652	G/A	*	6	652	G/A	*
2	720	T/C	V36A	7	874	T/C	V47A	7	874	T/C	V47A
3	778	T/G	I55M	8	932	T/G	I66M	8	932	T/G	I66M
4	800	A/G	N63D	9	954	A/G	N74D	9	954	A/G	N74D
5	854	A/G	T81A	10	1008	A/G	T92A	10	1008	A/G	T92A
6	937	C/T	T108T	11	1091	C/T	T119T	11	1091	C/T	T119T
7	1136	A/G	I175V	12	1290	A/G	I186V	12	1290	A/G	I186V
8	1321	T/C	Y236Y	13	1475	T/C	Y247Y	13	1475	T/C	Y247Y
9	1387	A/G	V258V	14	1541	A/G	V269V	14	1541	A/G	V269V
10	1550	G/A	V313I	15	1704	G/A	V324I	15	1704	G/A	V324I
11	1888	T/C	I425I	16	2042	T/C	I436I	16	2042	T/C	I436I
12	1935	A/C	N441T	17	2089	A/C	N452T	17	2089	A/C	N452T
13	2133	T/C	M507T	18	2287	T/C	M518T	18	2287	T/C	M518T
14	2148	C/T	T512M	19	2302	C/T	T523M	19	2302	C/T	T523M
15	2174	G/A	E521K	20	2328	G/A	E532K	20	2328	G/A	E532K
16	2225	C/T	R538C	21	2379	C/T	R549C	21	2379	C/T	R549C
17	2311	C/T	N566N	22	2465	C/T	N577N	22	2465	C/T	N577N
18	2404	A/C	K597N	23	2558	A/C	K608N	23	2558	A/C	K608N
19	2709	A/C	Y699S	24	2863	A/C	Y710S	24	2863	A/C	Y710S
20	2715	A/G	Y701C	25	2869	A/G	Y712C	25	2869	A/G	Y712C
21	3001	A/G	S796S	26	3155	A/G	S807S	26	3155	A/G	S807S
22	3045	T/C	I811T	27	3199	T/C	I822T	27	3199	T/C	I822T
23	3222	T/A	M870K	28	3376	T/A	M881K	28	3376	T/A	M881K
24	3317	C/T	L902L	29	3471	C/T	L913L	29	3471	C/T	L913L
25	3329	T/G	F906V	30	3483	G/T	V917F	30	3483	G/T	V917F
26	3466	T/C	P951P	31	3620	T/C	P962P	31	3620	T/C	P962P
27	3549	T/C	L979S	32	3703	T/C	L990S	32	3703	T/C	L990S
28	3616	G/T	K1001N	33	3770	T/G	N1012K	33	3770	T/G	N1012K
29	3673	A/G	T1020T	34	3827	A/G	T1031T	34	3827	A/G	T1031T
30	3726	G/C	Stop1038S	35	3880	G/C	Stop1049S	35	4205	A/G	S1157S*
31	3751	G/A	M1046I	36	3905	G/A	M1057I	36	4276	C/G	P1181R*
32	3801	T/C		37	3955	T/C		37	4294	T/C	V1187A*
33	3970	A/G		38	4123	G/A		38	4351	C/T	P1206L*
34	4265	C/G		39	4417	G/C		39	4396	G/C	G1221A*
								40	4491	T/C	S1253P*
								41	4572	A/G	N1280D*
								42	4577	A/G	G1281G*
								43	4596	G/C	G1288R*
								44	4692	G/A	A1320T*
								45	4743	A/G	T1337A*
								46	4744	C/A	T1337K*
								47	4743-4	AC/GA	T1337E*

*Note: SNP not corresponding to those in v.6.

**Note: more SNP in the 3' untranslated region are as following: 5019 T/C, 5186 T/C, 5218 G/T, 5225 T/C, 5245 G/T, 5292 A/G, 5519 C/T, 5563 A/G, 5573 A/C, 5757 G/A, 5816 C/T, 5866 C/A, 6004 G/C, 6118 C/T, 6142 T/G, 6210 G/A, 6441 T/A, 6442 T/C, 6573 A/T, 6610 T/G, 6725 C/T, 6768 G/T, 6994 G/T, 7176 A/C, 7428 T/C, 7441 C/G, 7490 T/C, 7563 C/T, 7588 G/C, 7591 A/T, 7597 G/A, 7652 A/G, 7678 T/C, 8179 T/C, 8195 A/C, 8294 A/G, 8432 T/C, 8453 T/C, 8468 A/G, 8722 C/T and 8890 G/C

***Note: Amino acid that does not change is omitted.

Figure 3:

Figure 3A. Amino acid sequence 109P1D4 v.1 (SEQ ID NO: 20). The 109P1D4 v.1 protein has 1021 amino acids.

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1 MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLTTA
61 MQFKLVYKTG DVPLIRIEED TGRIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF
121 RLVKIRFLIE DINDNAPLFP ATVINISIPE NSAINSKYTL PAAVDPDVGI NGVQNYELIK
181 SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKOTYVMKVK VEDGGFPQRS STAILQVSVT
241 DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF
301 HLNATTGLIT IKEPLDREET PNHKLLVLAS DGGLMPARAM VLVNVTDVND NVPSIDIRYI
361 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLEET
421 AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS
481 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDL EKEDKYLFTI
541 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG
601 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT
661 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVVFQVIA VDNDTGMNAE VRYSIVGGNT
721 RDLFAIDQET GNITLMEKCD VTDLGLHRVL VKANDLGQPD SLFSVVIVNL FVNESVTNAT
781 LINELVRKST EAPVTPNTEI ADVSSPTS DY VKILVAAGVAG TITVVVVIFI TAVVRCRQAP
841 HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVSDG
901 NRVTLDLPID LEEQTMGKYN WVTPTTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH
961 HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PVGIQVSNIT
1021 F

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Figure 3B. Amino acid sequence 109P1D4 v.2 (SEQ ID NO: 21). The 109P1D4 v.2 protein has 1054 amino acids.

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1 MRTERQWVLI QIFQVLCGLI QOTVTSVPGM DLLSGTYIFA VLLACVVFHS GAQEKNYTIR
61 EEMPENVLIG DLLKDLNLSL IPNKSLTTAM QFKLVYKTGD VPLIRIEEDT GEIFTTGARI
121 DREKLCAGIP RDEHCFYEV VAILPDEIFR LVKIRFLIED INDNAPLFPA TVINISIPEN
181 SAINSKYTL PAAVDPDVGIN GVQNYELIKS QNIFGLDVIE TPEGDKMPQL IVQKELDREE
241 KOTYVMKVKV EDGGFPQRSS TAILQVSVTD TNDNHPVFKE TEIEVSIPEN APVGTSVTQL
301 HATDADIGEN AKIHFSFSNL VSNIAARRLFH LNATTGLITI KEPLDREETP NHKLLVLASD
361 GGLMPARAMV LVNVTDVNDN VPSIDIRYIV NPVNDTVVLS ENIPLNTKIA LITVTDKDA
421 HNGRVTCFTD HEIPFRLRPV FSNQFLETA AYLDYESTKE YAIKLLAADA GKPPPLNQSAM
481 LFIKVKDEND NAPVFTQSFV TVSIPENNNSP GIQLTKVSAM DADSGPNAKI NYLLGPDAPP
541 EFSLDCRTGM LTVVKKLDRE KEDKYLFTIL AKDNGVPPLT SNVTVFVSII DQNDNSPVFT
601 HNEYNFYVPE NLPRHGTVGL ITVTDPDYGD NSAVTSLILD ENDDFTIDSQ TGVIRPNISF
661 DREKQESYTF YVKAEDGGRV SRSSSAKVTI NVVDVNDNKP VFIVPPSNCS YELVLPSTNP
721 GTVVVFQVIAV DNDTGMNAEV RYSIVGGNTR DLFAIDQETG NITLMEKCDV TDLGLHRVLV
781 KANDLGQPD LFSVVIVNLF VNESVTNATL INELVRKSTE APVTPNTEIA DVSSPTS DYV
841 KILVAAGVAG ITVVVVIFIT AVVRCRQAPH LKAAQKNKQN SEWATPNPEN RQMIMMKKKK
901 KKKKHSPKNL LNFVTIEET KADDVSDGN RVTLDLPIDL EEQTMGKYNW VTTPTTFKPD
961 SPDLARHYKS ASPQPAFQIQ PETPLNSKH HIIQELPLDNT FVACDSISKC SSSSSDPYSV
1021 SDCGYPVTTF EVPVSVHTRP TDSRTSTIEI CSEI

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Figure 3C. Amino acid sequence 109P1D4 v.3 (SEQ ID NO: 22). The 109P1D4 v.3 protein has 1347 amino acids.

1 MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLTTA
61 MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF
121 RLVKIRFLIE DINDNAPLFP ATVINISIFE NSAINSKYTL PAAVDPDVGI NGVQNYELIK
181 SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT
241 DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF
301 HLNATTGLIT IKEPLDREET PNHKLLVLAS DGGLMPARAM VLVNVTVDND NVPSIDIRYI
361 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLEET
421 AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS
481 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDL EKEDKYLFTI
541 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG
601 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT
661 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVQVIA VDNDTGMNAE VRYSIVGGNT
721 RDLFAIDQET GNITLMEKCD VTDLGLHRVL VKANDLGQPD SLFSVVIVNL FVNESVTNAT
781 LINELVRKST EAPVTPNTEI ADVSSPTSDY VKILVAAVAG TITVVVVIFI TAVVRCRQAP
841 HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVSDG
901 NRVTLDLPID LEEQTMGKYN WVTTPTTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH
961 HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PPMKEVVRSC
1021 TPMKESTTME IWIHPQPQRK SEGKVAGKSQ RRVTFHLPEG SQESSSDGGL GDHDAGSLTS
1081 TSHGLPLGYP QEYFDRATP SNRTEGDGNS DPESTFIPGL KKA AEITVQP TVEEASDNCT
1141 QECLYIGHSD ACWMPASLDH SSSSQAQASA LCHSPPLSQA STQHHSRPTV QTIALCHSPP
1201 VTQTIALCHS PPPIQVSALH HSPPLVQATA LHHSPPSAQA SALCYSPPLA QAAAISSSSP
1261 LPQVIALHRS QAQSSVSLQQ GWVQAGGLC SVDQGVQGSA TSQFYTMSEK LHPSSDSIKV
1321 IPLTTFTPRQ QARPSRGDSP IMEEHPL

Figure 3D. Amino acid sequence 109P1D4 v.4 (SEQ ID NO: 23). The 109P1D4 v.4 protein has 1337 amino acids.

1 MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLTTA
61 MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF
121 RLVKIRFLIE DINDNAPLFP ATVINISIFE NSAINSKYTL PAAVDPDVGI NGVQNYELIK
181 SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT
241 DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF
301 HLNATTGLIT IKEPLDREET PNHKLLVLAS DGGLMPARAM VLVNVTVDND NVPSIDIRYI
361 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLEET
421 AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS
481 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDL EKEDKYLFTI
541 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG
601 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT
661 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVQVIA VDNDTGMNAE VRYSIVGGNT
721 RDLFAIDQET GNITLMEKCD VTDLGLHRVL VKANDLGQPD SLFSVVIVNL FVNESVTNAT
781 LINELVRKST EAPVTPNTEI ADVSSPTSDY VKILVAAVAG TITVVVVIFI TAVVRCRQAP
841 HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVSDG
901 NRVTLDLPID LEEQTMGKYN WVTTPTTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH
961 HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PPMKEVVRSC

1021 TPMKESTTME IWIHPQPQSQ RRVTFHLPEG SQESSSDGGL GDHDAGSLTS TSHGLPLGYF
 1081 QEYFDRATP SNRTEGDGNS DPESTFIPGL KKAEEITVQP TVEEASDNCT QECLYIGHSD
 1141 ACWMPASLDH SSSSQAQASA LCHSPPLSQA STQHHSRVRT QTIALCHSPP VTQTIALCHS
 1201 PPPIQVSALH HSPPLVQATA LHSPPSAQA SALCYSPPLA QAAAISHSSP LPQVIALHRS
 1261 QAQSSVSLQQ GWVQGADGLC SVDQGVQGS TSQFYTMSE LHPSDDSIKV IPLTTFTPRQ
 1321 QARPSRGDSP IMEEHPL

Figure 3E. Amino acid sequence 109P1D4 v.5 (SEQ ID NO: 24). The 109P1D4 v.5 protein has 1310 amino acids.

1 MDLLSGTYIF AVLLACVVFH SGAQEKNTYI REEMPENVLI GDLLKDLNLS LIPNKSLTTA
 61 MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF
 121 RLVKIRFLIE DINDNAPLEF ATVINISIEP NSAINSKYTL PAAVDPDVGI NGVQNYELIK
 181 SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT
 241 DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF
 301 HLNATTGLIT IKEPLDREET PNHKLLVLAS DGGLMPARAM VLVNVTDVND NVPSIDIRYI
 361 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLLET
 421 AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS
 481 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDRE EKEDKYLFTI
 541 LAKDNGVPPV TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYD
 601 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT
 661 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVFQVIA VDNDTGMNAE VRYSIVGGNT
 721 RDLFAIDQET GNITLMEKCD VTDLGLHRLV VKANDLGQPD SLFSVVIVNL FVNESVTNAT
 781 LINELVKRST EAPVTPNTEI ADVSSPTSDY VKILVAAGVAG TITVVVVFIF TAVVRCRQAP
 841 HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVDSG
 901 NRVTLDELPID LEEQTMGKYN WVTPTTFKP DSPDLARHYK SASQPAPFQI QPETPLNSKH
 961 HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PSQRRVTFHL
 1021 PEGSQESSSD GGLGDHDAGS LTSTSHGLPL GYPQEYFDR ATPSNRTEGD GNSDPESTFI
 1081 PGLKKAABIT VQPTVEEASD NCTQECLYIG HSDACWMPAS LDHSSSSQAQ ASALCHSPPL
 1141 SQASTQHHSR RVTQTIALCH SPPVTQTIAL CHSPPIQVS ALHHSPPPLVQ ATALHHSPPS
 1201 AQASALCYSP PLAQAAAISH SSPLPQVIAL HRSQAQSSVS LQQGWVQAD GLCSVDQGVQ
 1261 GSATSQFYTM SERLHPSDDS IKVIPLTTFT PRQARPSRG DSPIMEEHPL

Figure 3F. Amino acid sequence 109P1D4 v.6 (SEQ ID NO: 25). The 109P1D4 v.6 protein has 1037 amino acids.

1 MTVGFNSDIS SVVRVNTTNC HKCLLSGTYI FAVLLVCVVF HSGAQEKNTYI IREEIPENVL
 61 IGNLLKDLNL SLIPNKSLTT TMQFKLVYKT GDVPLIRIEE DTGEIFTTGA RIDREKLCAG
 121 IPRDEHCFYE VEVAILPDEI FRLVKIRFLI EDINDNAPLEF PATVINISIP ENSAINSKYT
 181 LPAAVDPDVG INGVQNYELI KSNIFGLDV IETPEGDKMP QLIVQKELDR EEKDTYVMKV
 241 KVEDGGFPQR SSTAILQVSV TDTNDNHPVF KETEIEVSIP ENAPVGTSVT QLHATDADIG
 301 ENAKIHFSFS NLVSNIAARRL FHLNATTGLI TIKEPLDREE TPNHKLLVLA SDGGLMPARA
 361 MVLVNVTDVN DNVPSIDIRY IVNPVNDTVV LSENIPLNTK IALITVTDKD ADHNGRVTCF
 421 TDHEIPFRLR PVFSNQFLE NAAYLDYEST KEYAIKLLAA DAGKPPLNQS AMLFIKVKDE
 481 NDNAPVFTQS FVTVSIPENN SPGIQLMKVS ATDADSGPNA EINYLLGPD APEFSLDRRT
 541 GMLTVVKKLD REKEDKYLFT ILAKDNGVPP LTSNVTVFVS IIDQNDNSPV FTHNEYKFYV

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601 PENLPRHGTV GLITVTPDPY GDNSAVTLSI LDENDDFTID SQTGVIRPNI SFDREKQESY
661 TFFYVKAEDGG RVSRSSSSAK TINVVDVNDN KPVFIVPPYN YSYELVLPST NPGTVVPQVI
721 AVDNDTGMNA EVRYSIVGGN TRDLFAIDQE TGNITLMEKC DVTDLGLHRV LVKANDLGQP
781 DSLFSVVIVN LFNESVTINA TLINELVRKS IEAPVTPNTE IADVSSPTSD YVKILVAAVA
841 GTITVVVVIF ITAVVRCRQA PHLKAAQKNM QNSEWATPNP ENRQMIMMKK KKKKKKHSPK
901 NLLLNFTVIE ETKADDVDSG GNRVTLDLPI DLEEQTMGKY NWVTTPTTTFK PDSPLARHY
961 KSASPQPAFQ IQPETPLNLK HHIIQELPLD NTFVACDSIS KCSSSSSDPY SVSDCGYPVT
1021 TFEVPSVHT RPTDSRT

```

Figure 3G. Amino acid sequence 109P1D4 v.7 (SEQ ID NO: 26). The 109P1D4 v.7 protein has 1048 amino acids.

```

1 MFRVGFLIIS SSSSLSPLLL VSVVRVNTTN CHKCLLSGTY IFAVLLVCVV FHSGAQEKNY
61 TIREEIPENV LIGNLLKDLN LSLIPNKS LT TTMQFKLVYK TGDVPLIRIE EDTGEIFTTG
121 ARIDREKLCA GIPRDEHCFY EVEVAILPDE IFRLVKIRFL IEDINDNAPL FPATVINISI
181 PENSAINSKY TLPAAVDPDV GINGVQNYEL IKSQNIFGLD VIETPEGDKM PQLIVQKELD
241 REEKDTYVMK VKVEDGGFPQ RSSTAILQVS VTDNDNHPV FKETEIEVSI PENAPVGTSV
301 TQLHATDADI GENAKIHFSF SNLVSNIARR LFHLNATTGL ITIKEPLDRE ETPNHKLLVL
361 ASDGGLMPAR AMVLNVNTDV NDNVPSIDIR YIVNPVNDTV VLSENIPLNT KIALITVTDK
421 DADHNGRVTC FTDHEIPFRL RPVFSNQFL ENAAYLDYES TKEYAIKLLA ADAGKPPLNQ
481 SAMLPIKVKD ENDNAPVFTQ SFVTVSIPEN NSPGIQLMKV SATDADSGPN AEINYLLGPD
541 APPEFSLDRR TGMLTVVKKL DREKEDKYLE TILAKDNGVP PLTSNVTVFV SIIDQNDNSP
601 VFTHNEYKFY VPENLPRHGT VGLITVTPDP YGDNSAVTLS ILDENDDFTI DSQTGVIRPN
661 ISFDREKQES YTFYVKAEDG GRVSRSSSAK VTINVVDVND NKPVFIVPPY NYSYELVLPS
721 TNPGTVPVQV IAVDNDTGMN AEVRSIVGG NTRDLFAIDQ ETGNITLMEK CDVTDLGLHR
781 VLVKANDLGQ PDSLFSVVIV NLFVNESVTN ATLINELVRK SIEAPVTPNT EIAADVSSPTS
841 DYVKILVAAV AGTITVVVVI FITAVVRCRQ APHLKAAQKN MONSEWATPN PENRQMIMMK
901 KKKKKKKHSP KNLLNVVTI EETKADDVDS DGNRVTLDLPI IDLEEQTMGK YNWVTTPTTTF
961 KPDSPDLARH YKSASPQPAF IQPETPLNL KHHIIQELPL DNTFVACDSI SNCSSSSSDP
1021 YSVSDCGYPV TFEVPSVHT TRPTDSRT

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Figure 3H. Amino acid sequence 109P1D4 v.8 (SEQ ID NO: 27). The 109P1D4 v.8 protein has 1340 amino acids.

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1 MFRVGFLIIS SSSSLSPLLL VSVVRVNTTN CHKCLLSGTY IFAVLLVCVV FHSGAQEKNY
61 TIREEIPENV LIGNLLKDLN LSLIPNKS LT TTMQFKLVYK TGDVPLIRIE EDTGEIFTTG
121 ARIDREKLCA GIPRDEHCFY EVEVAILPDE IFRLVKIRFL IEDINDNAPL FPATVINISI
181 PENSAINSKY TLPAAVDPDV GINGVQNYEL IKSQNIFGLD VIETPEGDKM PQLIVQKELD
241 REEKDTYVMK VKVEDGGFPQ RSSTAILQVS VTDNDNHPV FKETEIEVSI PENAPVGTSV
301 TQLHATDADI GENAKIHFSF SNLVSNIARR LFHLNATTGL ITIKEPLDRE ETPNHKLLVL
361 ASDGGLMPAR AMVLNVNTDV NDNVPSIDIR YIVNPVNDTV VLSENIPLNT KIALITVTDK
421 DADHNGRVTC FTDHEIPFRL RPVFSNQFL ENAAYLDYES TKEYAIKLLA ADAGKPPLNQ
481 SAMLPIKVKD ENDNAPVFTQ SFVTVSIPEN NSPGIQLMKV SATDADSGPN AEINYLLGPD
541 APPEFSLDRR TGMLTVVKKL DREKEDKYLE TILAKDNGVP PLTSNVTVFV SIIDQNDNSP
601 VFTHNEYKFY VPENLPRHGT VGLITVTPDP YGDNSAVTLS ILDENDDFTI DSQTGVIRPN
661 ISFDREKQES YTFYVKAEDG GRVSRSSSAK VTINVVDVND NKPVFIVPPY NYSYELVLPS

```

721 TNP GTVVFQV IAVDNDTGMN AEVRSIVGG NTRDLFAIDQ ETGNITLMEK CDVTDLGLHR
781 VLVKANDLGQ PDSLFSVVIV NLFVNESVTN ATLINELVRK SIEAPVTPNT EIADVSSPTS
841 DYVKILVA AV AGTITVVVVI FITAVVRCRQ APLKAAQKN MONSEWATPN PENRQMIMMK
901 KKKKKKKHSP KNLLLNVTI EETKADDVDS DGNRVTL DLP IDLEEQTMGK YNWVTTPTTF
961 KPDS PDLARH YKSASPQPAF QIQPETPLNL KHHIIQELPL DNTFVACDSI SNCSSSSSDP
1021 YSVSDCGYPV TTFEVPVSVH TRPSQRRVTF HLEPGSQESS SDGGLGDHDA GSLTSTSHGL
1081 PLGYPQEEYF DRATPSNRTE GDGNSDPEST FIPGLKKEIT VQPTVEEASD NCTQECLYIG
1141 HSDACWMPAS LDHSSSSQAQ ASALCHSPPL SQASTQHHSP PVTQTIVLCH SPPVTQTIAL
1201 CHSPPIQVS ALHHSPLVQ GTALHHSPPS AQASALCYSP PLAQAAAISH SSSLPQVIAL
1261 HRSQAQSSVS LQQGWVQGAN GLCSVDQGVQ GSATSQFYTM SERLHPSDDS IKVIPLTTFA
1321 PRQARPSRG DSPIMETHPL

Figure 3I. Amino acid sequence 109P1D4 v.9 (SEQ ID NO: 28). The 109P1D4 v.9 protein has 1037 amino acids.

1 MTVGFNSDIS SVVRVNTTNC HKCLLSGTYI FAVLLVCVVF HSGAQEKNYT IREEIPENVL
61 IGNLLKDLNL SLIPNKSLTT TMQFKLVYKT GDVPLIRIEE DTGEIFTTGA RIDREKLCAG
121 IPRDEHCFYE VEVAILPDEI FRLVKIRFLI EDINDNAPLF PATVINISIP ENSAINSKYT
181 LPAAVDPDVG INGVQNYELI KSNIFGLDV IETPEGDKMP QLIVQKELDR EKKDTYVMKV
241 KVEDGGFPQR SSTA ILQVSV TDINDNHPVF KETEIEVSIP ENAPVGTSVT QLHATDADIG
301 ENAKIHFSFS NLVSN IARRL FHLNATTGLI TIKEPLDREE TPNHKLVLVA SDGGLMPARA
361 MVLVNVTDVN DNVPSIDIRY IVNPVNDTVV LSENIPLNTK IALITVTDKD ADHNGRVTCF
421 TDHEIPFRLR PVFSNQFLL E NAAYLDYEST KEYAIKLLAA DAGKPPLNQS AMLFIKVKDE
481 NDNAPVFTQS FVTVSIPENN SPGIQLMKVS ATDADSGPNA EINYLLGPDA PPEFSLDRRT
541 GMLTVVKKLD REKEDKYLEF ILAKDNGVPP LTSNVTVFVS IIDQNDNSPV FTHNEYKFYV
601 PENLPRHGTV GLITVTDPDY GDNSAVTLSI LDENDDFTID SQTGVIRPNI SFDREKQESY
661 TFYVKAEDGG RVSRS SAKV TINVVDVNDN KPVFIVPPYN YSYELVLPST NPGTVVFQVI
721 AVDNDTGMNA EVRSIVGGN TRDLFAIDQE TGNITLMEKC DVTDLGLHRV LVKANDLGQP
781 DSLFSVVIVN LFNESVTNA TLINELVRKS IEAPVTPNTE IADVSSPTS D YVKILVA AVA
841 GTITVVVVI F ITAVVRCRQA PHLKAAQKNM QNSEWATPNP ENRQMIMMK KKKKKKHSPK
901 NLLLNVTIE ETKADDVDS D GNRVTLDLPI DLEEQTMGKY NWTTPPTTFK PDS PDLARHY
961 KSASPQPAFQ IQPETPLNLK HHIIQELPLD NTFVACDSIS NCSSSSSDPY SVSDCGYPVT
1021 TFEVPVSVHT RPTDSRT

Figure 4: Alignment of 109P1D4 v.1 Protein (SEQ ID NO: 29) with protocadherin-11 (SEQ ID NO: 30)

protocadherin 11 X-linked isoform a precursor; protocadherin X;
 protocadherin-S [Homo sapiens]
 dbj|BAA90765.1| protocadherin-Xa [Homo sapiens]
 Length = 1021

Score = 2024 bits (5244), Expect = 0.0
 Identities = 1021/1021 (100%), Positives = 1021/1021 (100%)

```

Query: 1   MDLLSGTYIFAVLLACVVFHSGAQEKNTTIREEMPENVLIGDLLKDLNLSLIPNKSLTFTA 60
Sbjct: 1   MDLLSGTYIFAVLLACVVFHSGAQEKNTTIREEMPENVLIGDLLKDLNLSLIPNKSLTFTA 60

Query: 61  MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF 120
Sbjct: 61  MQFKLVYKTGDVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHCFYEVEVAILPDEIF 120

Query: 121  RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK 180
Sbjct: 121  RLVKIRFLIEDINDNAPLFPATVINISIPENSAINSKYTLPAAVDPDVGINGVQNYELIK 180

Query: 181  SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT 240
Sbjct: 181  SQNIFGLDVIETPEGDKMPQLIVQKELDREKDTYVMKVVEDGGFPQRSSTAILQVSVT 240

Query: 241  DTNDNHPVFKETEIEVSIPENAPVGTSTVQLHATDADIGENAKIHFSFNLVSNIRRLF 300
Sbjct: 241  DTNDNHPVFKETEIEVSIPENAPVGTSTVQLHATDADIGENAKIHFSFNLVSNIRRLF 300

Query: 301  HLNATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPISDIRYI 360
Sbjct: 301  HLNATTGLITIKEPLDREETPNHKLLVLASDGGMLPARAMVLNVTDVNDNVPISDIRYI 360

Query: 361  VNPVNDTVVLSENIPLNTKIALITVTDKADHNGRVTCTDHEIPFRLRPVFSNQFLLFET 420
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Query: 481  PGIQLTKVSAMDADSGPNAKINYLGPDAPPEFSLDCRTGMLTVVKKLDREKEDKYLFTI 540
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Query: 541  LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPELPRHGTVGLITVTDPPDYG 600
Sbjct: 541  LAKDNGVPPLTSNVTVFVSIIDQNDNSPVFTHNEYNFYVPELPRHGTVGLITVTDPPDYG 600

Query: 601  DNSAVTSLILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT 660
Sbjct: 601  DNSAVTSLILDENDDFTIDSQTGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSSAKVT 660

Query: 661  INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT 720
Sbjct: 661  INVVDVNDNKPVFIVPPSNCSYELVLPSTNPGTVVFQVIAVDNDTGMNAEVRYSIVGGNT 720

Query: 721  RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFSVVIIVNLFVNESVTNAT 780
Sbjct: 721  RDLFAIDQETGNITLMEKCDVTDGLHRVLVKANDLGQPDLSFSVVIIVNLFVNESVTNAT 780

Query: 781  LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVIFITAVVRCRQAP 840
Sbjct: 781  LINELVRKSTEAPVTPNTEIADVSSPTS DYVKILVAAVAGTITVVVIFITAVVRCRQAP 840

Query: 841  HLKAAQKNKQNSEWATPNPENRQMIMMKKKKKKKHSPKNLLLNFTIETKADDVDSGD 900
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Query: 901 NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQPAFQIQPETPLNSKH 960
NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQPAFQIQPETPLNSKH
Sbjct: 901 NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKSASPQPAFQIQPETPLNSKH 960

Query: 961 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTTFEVPVSVHTRPVGIQVSNTT 1020
HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTTFEVPVSVHTRPVGIQVSNTT
Sbjct: 961 HIIQELPLDNTFVACDSISKSSSSSDPYSVSDCGYPVTTTFEVPVSVHTRPVGIQVSNTT 1020

Query: 1021 F 1021
F
Sbjct: 1021 F 1021

Figure 5a: 109P1D4 variant 1
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

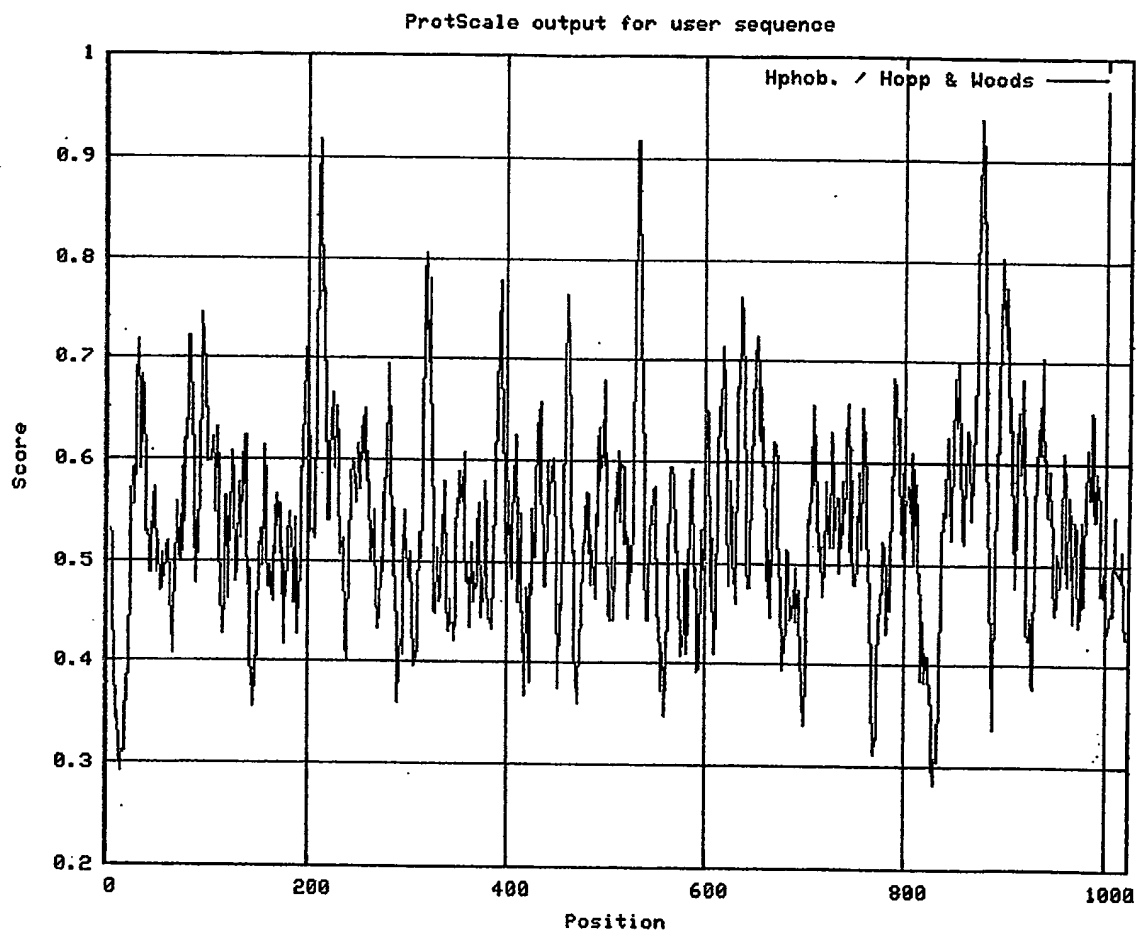


Figure 5b: 109P1D4 variant 2
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

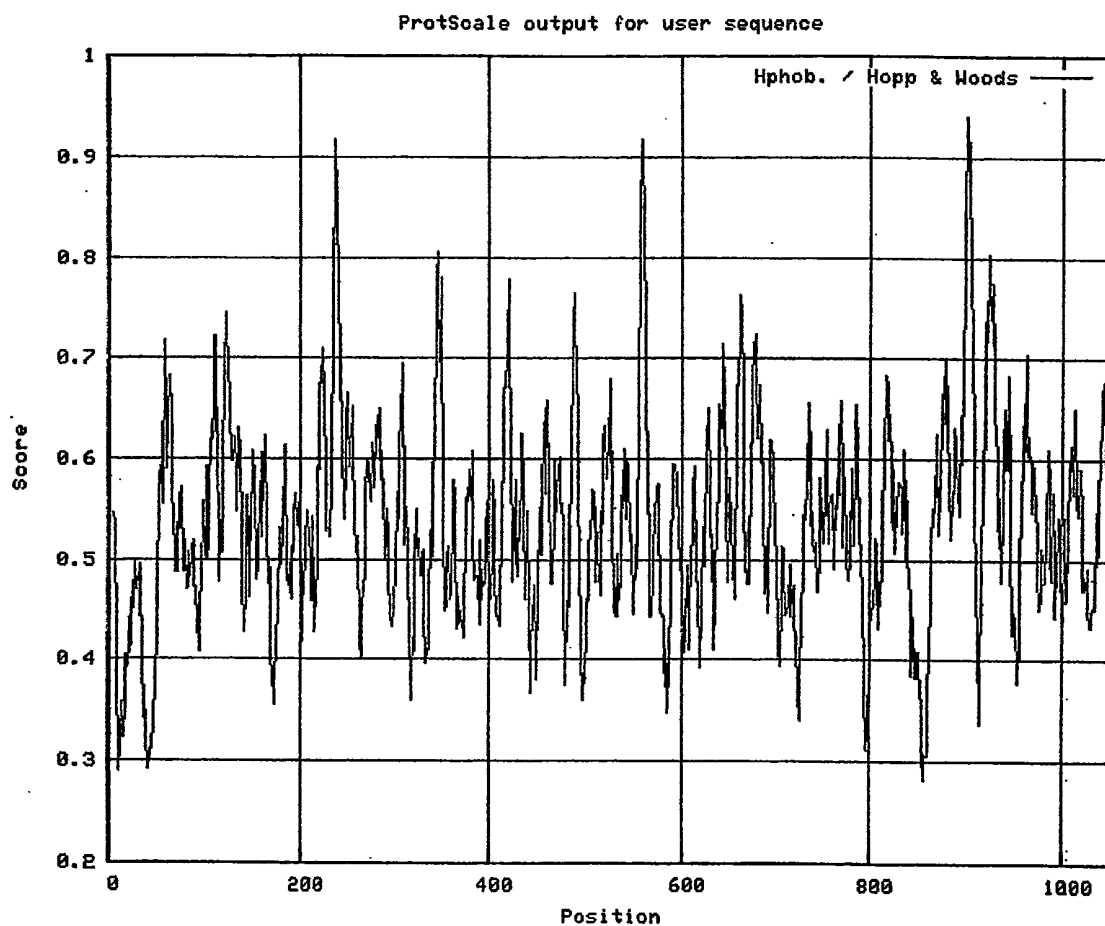


Figure 5c: 109P1D4 variant 3
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

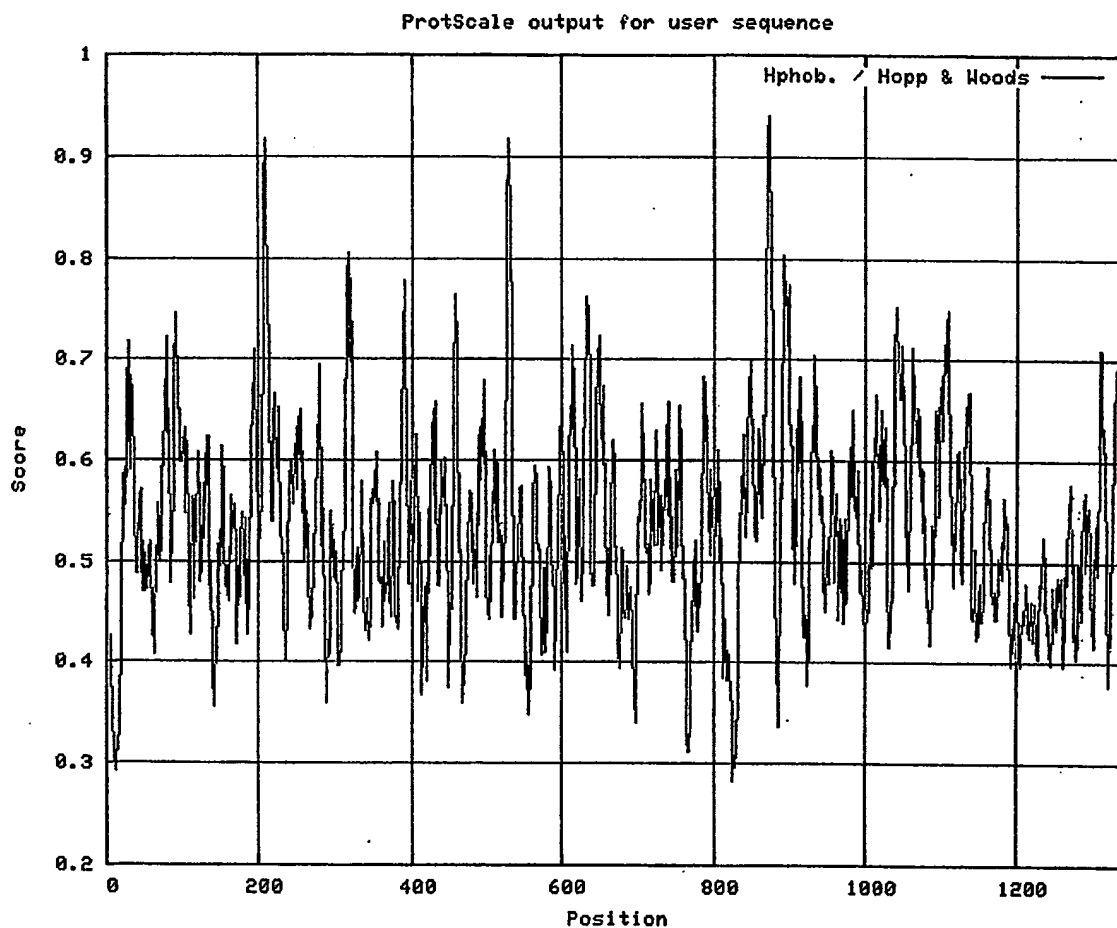


Figure 5d: 109P1D4 variant 4
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

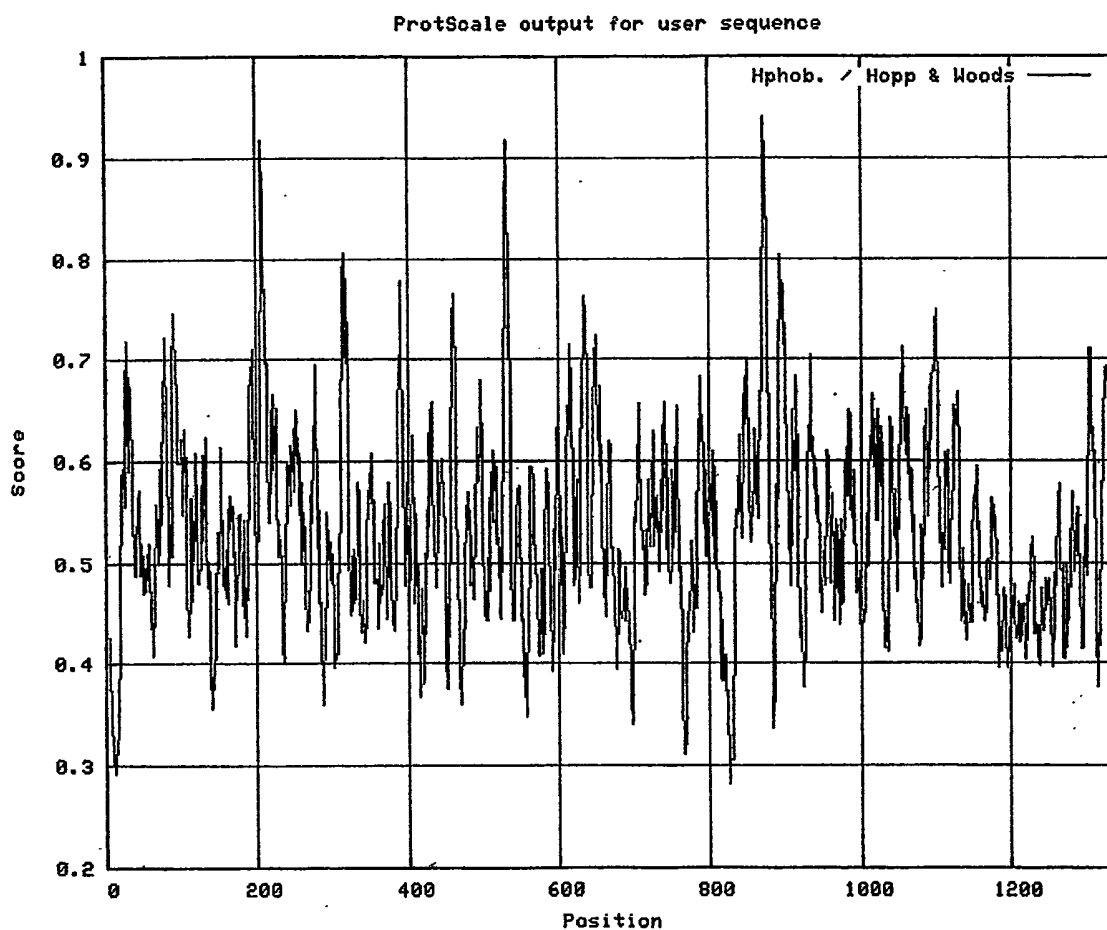


Figure 5e: 109P1D4 variant 5
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

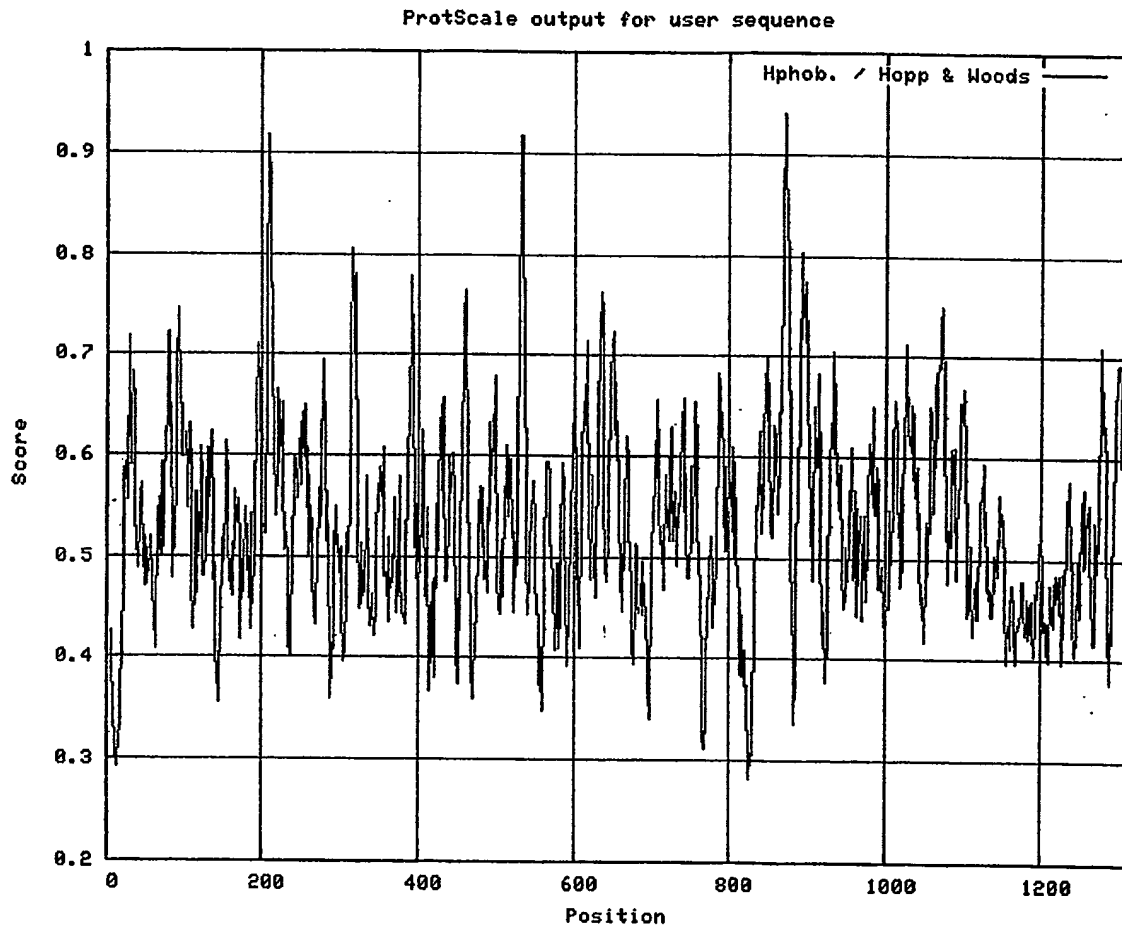


Figure 5f: 109P1D4 variant 6
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

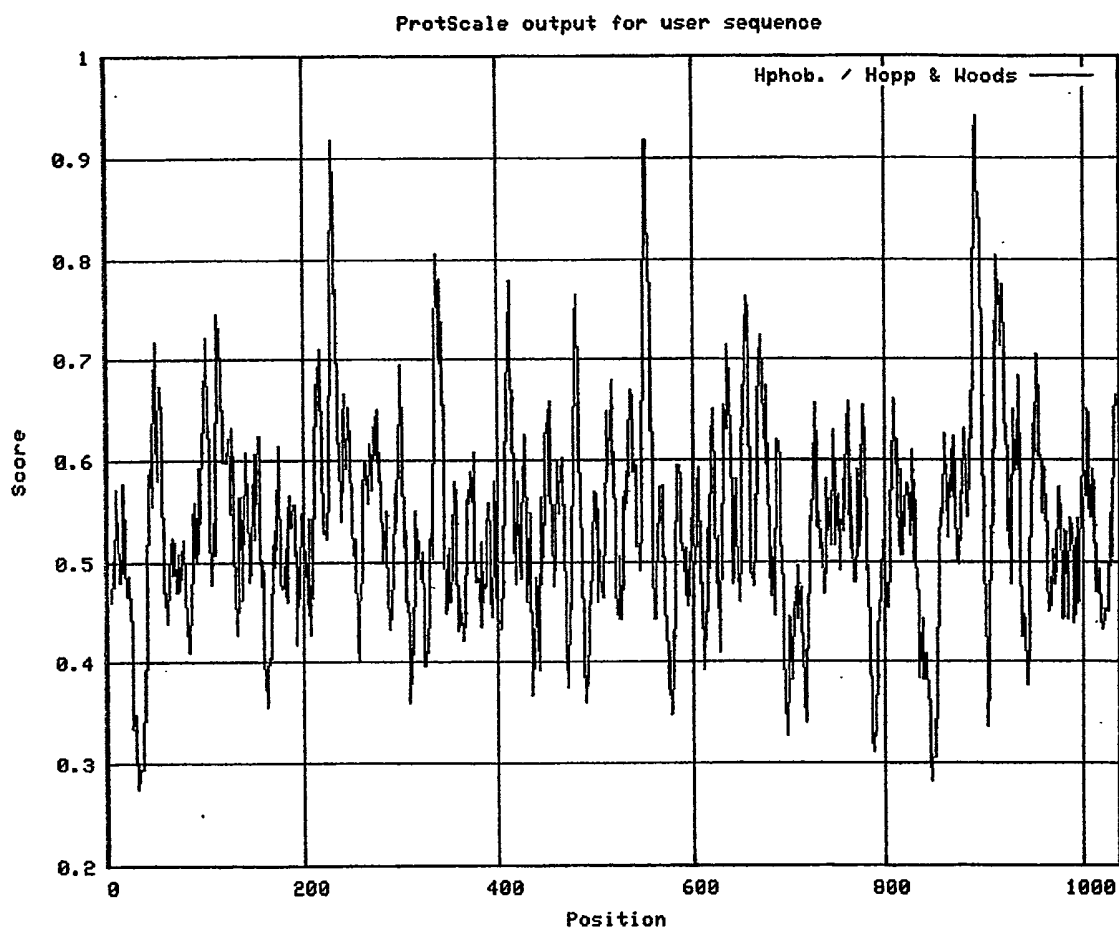


Figure 5g: 109P1D4 variant 7
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

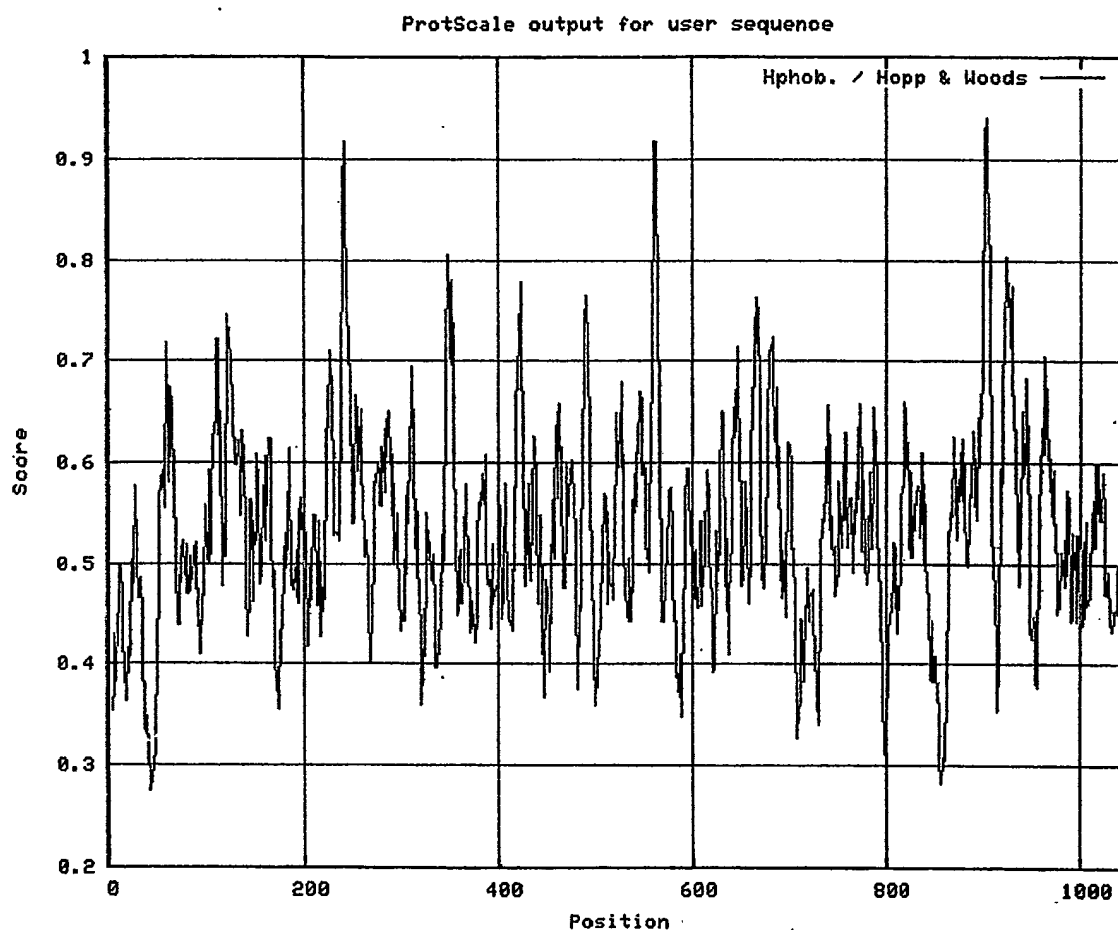


Figure 5h: 109P1D4 variant 8
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

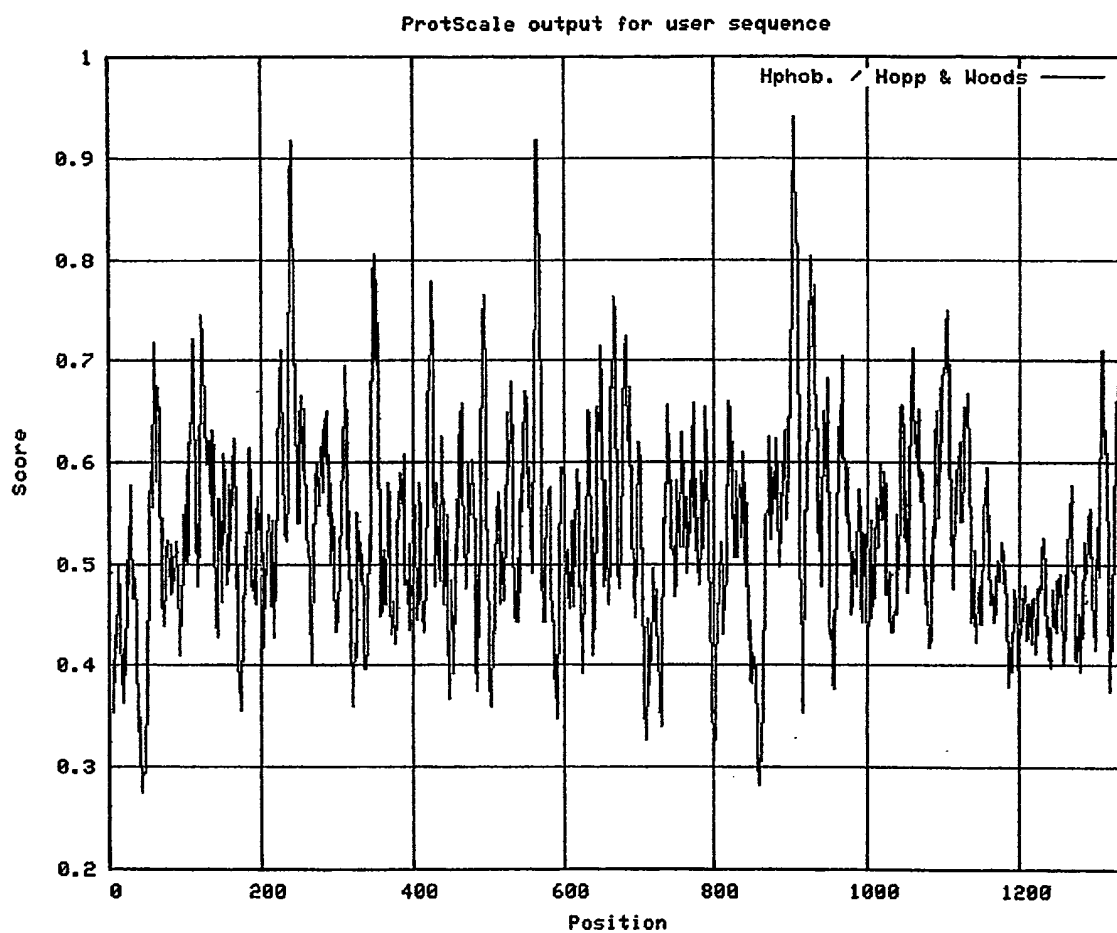


Figure 5i: 109P1D4 variant 9
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

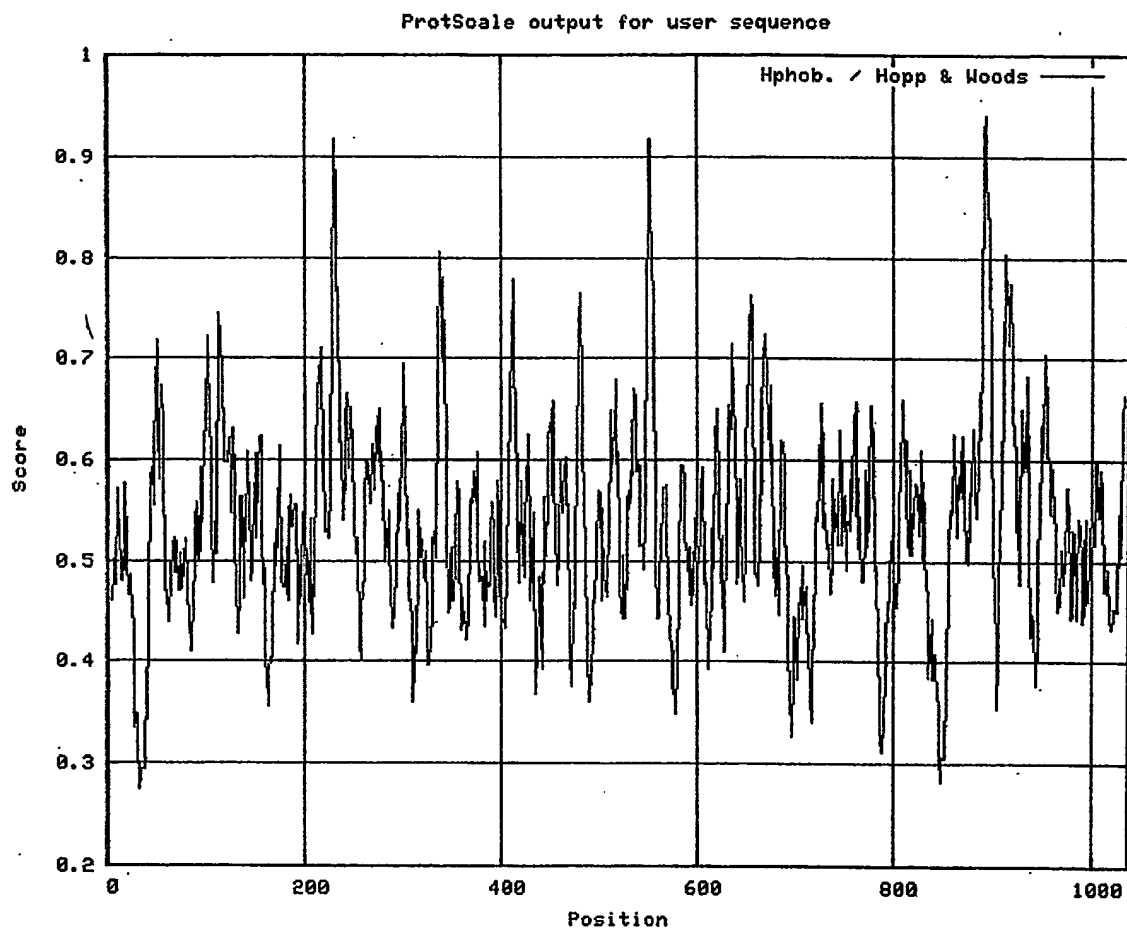


Figure 6a: 109P1D4 variant 1
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

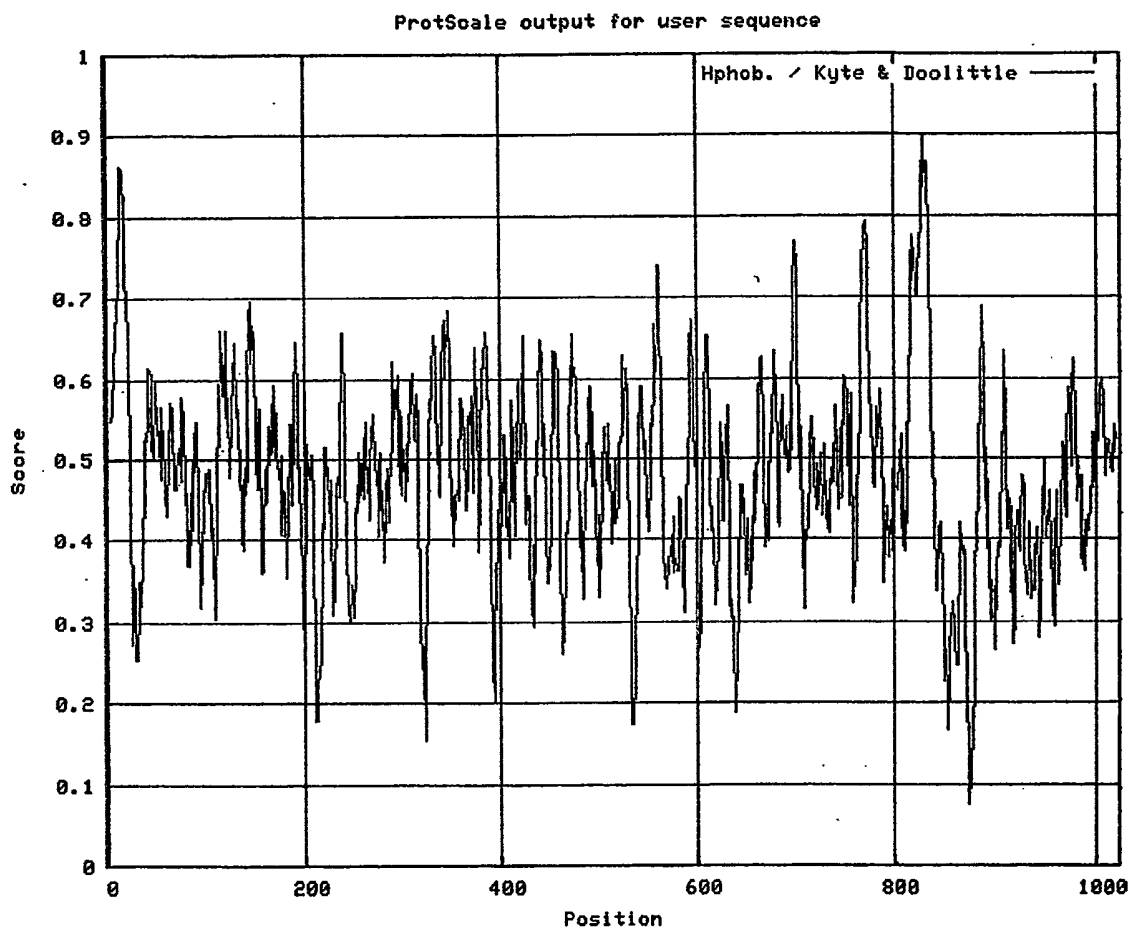


Figure 6b: 109P1D4 variant 2
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

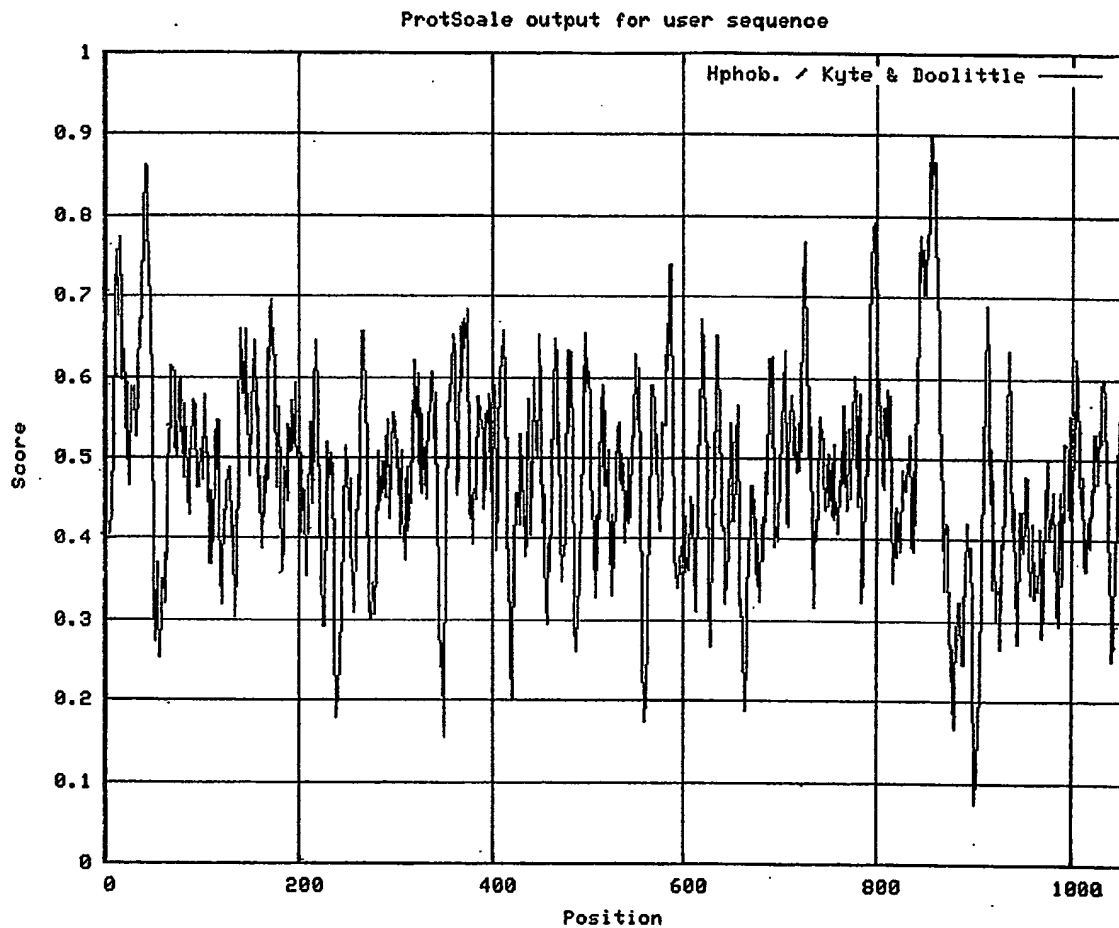


Figure 6c: 109P1D4 variant 3
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

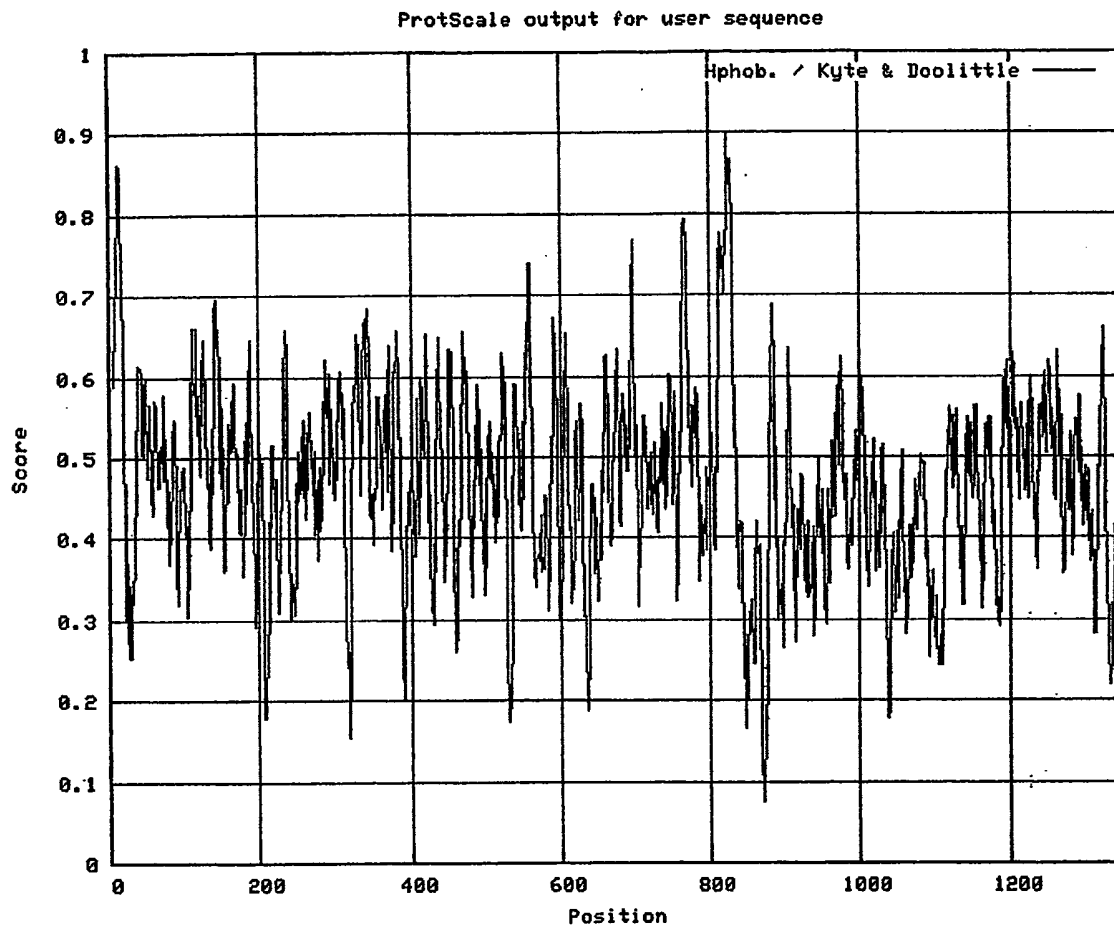


Figure 6d: 109P1D4 variant 4
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

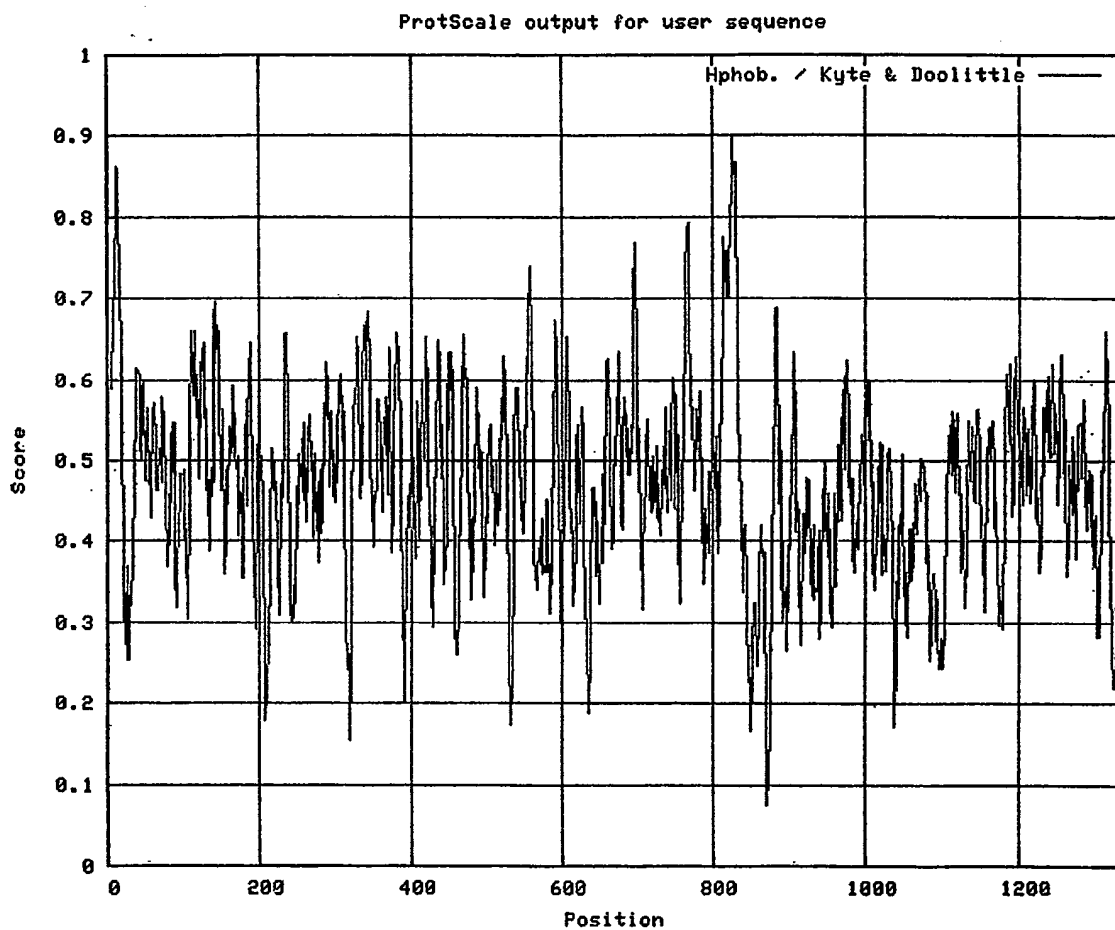


Figure 6e: 109P1D4 variant 5
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

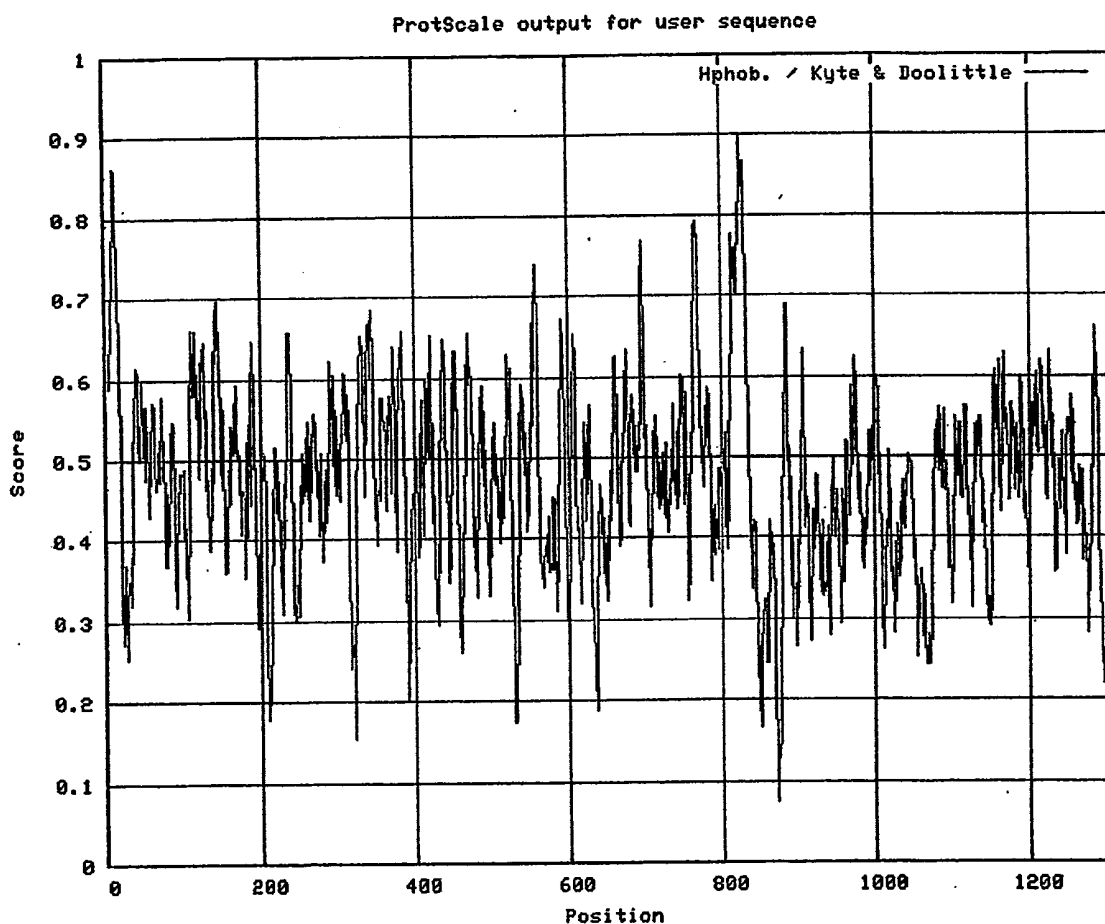


Figure 6f: 109P1D4 variant 6
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

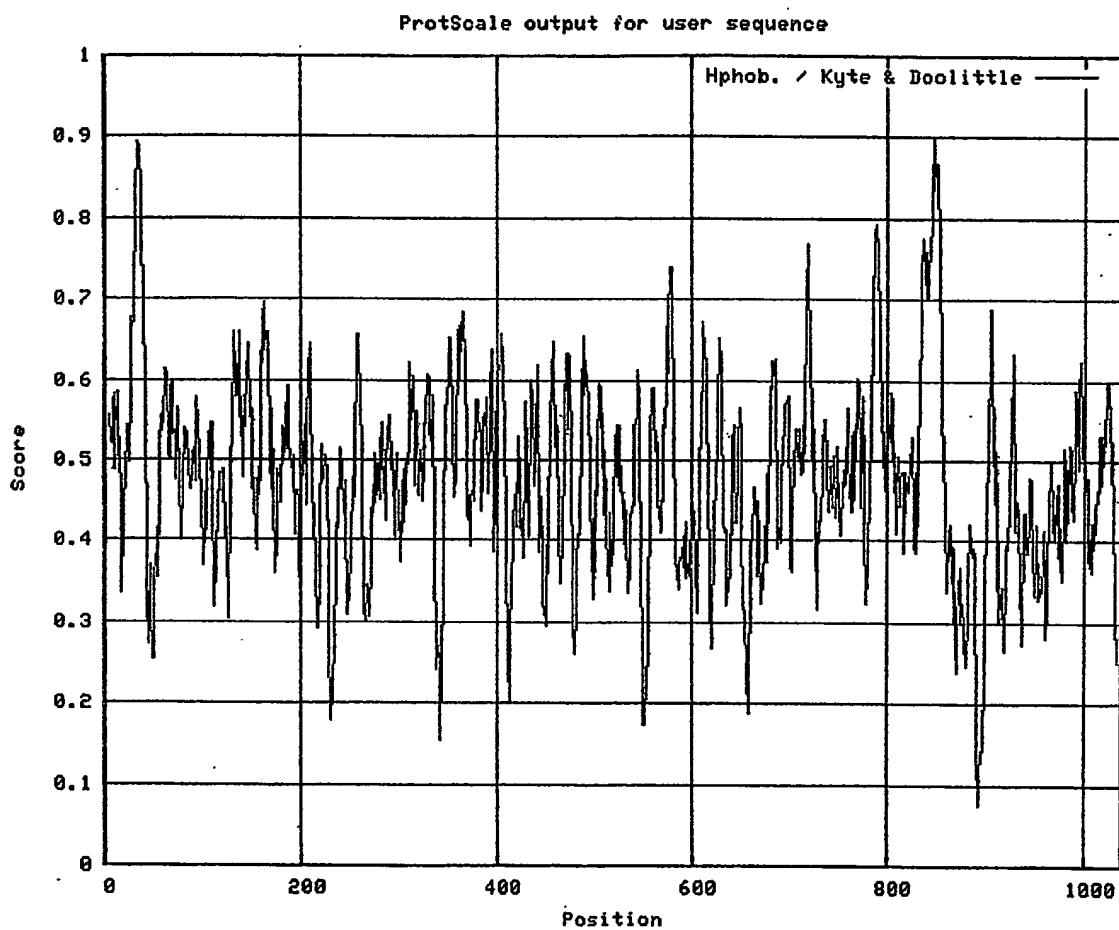


Figure 6g: 109P1D4 variant 7
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

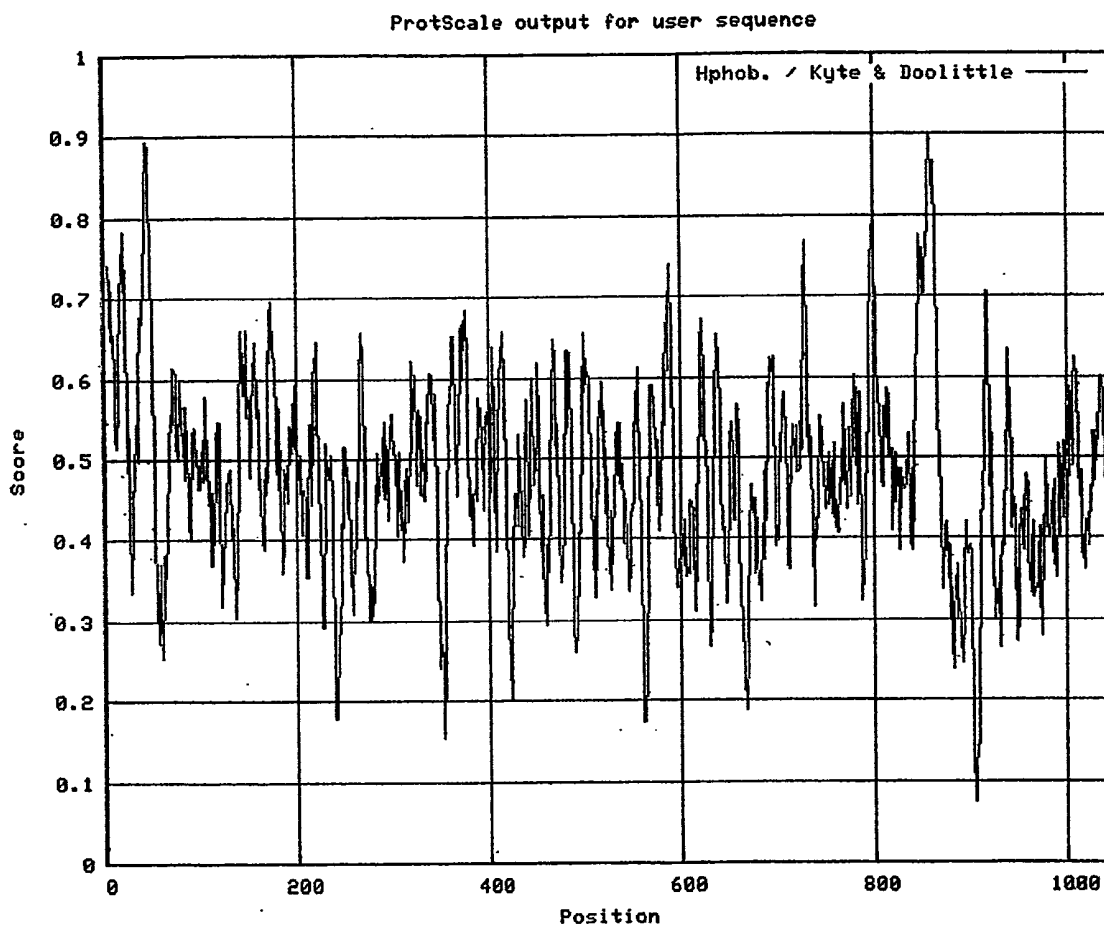


Figure 6h: 109P1D4 variant 8
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

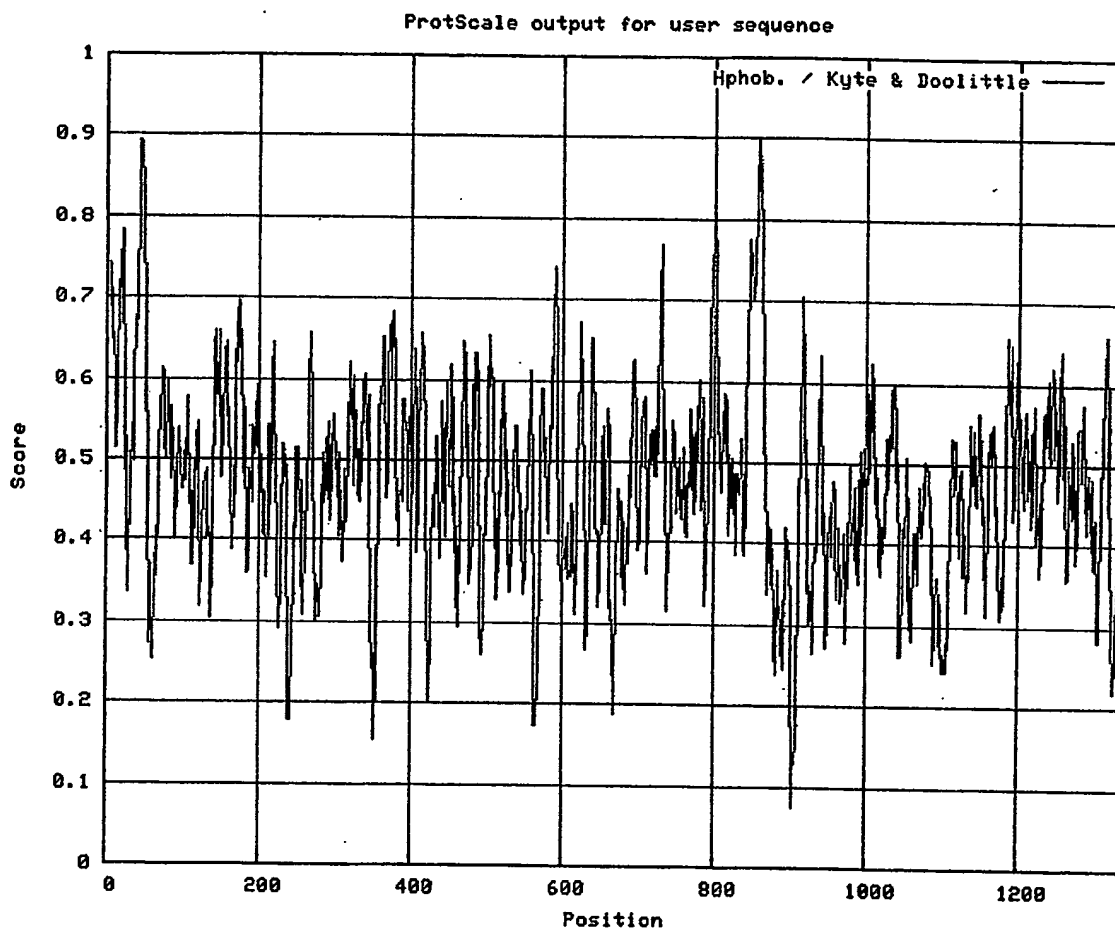


Figure 6i: 109P1D4 variant 9
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

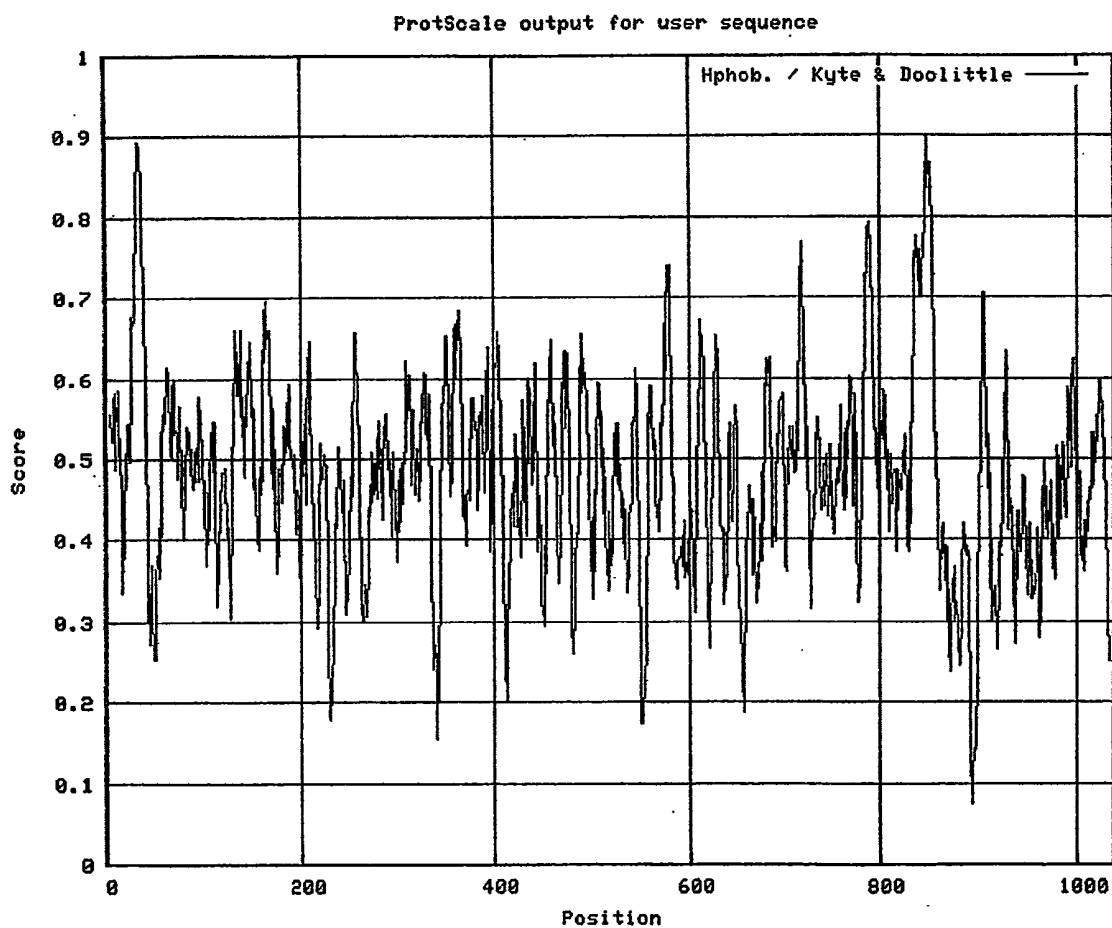


Figure 7a: 109P1D4 variant 1 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

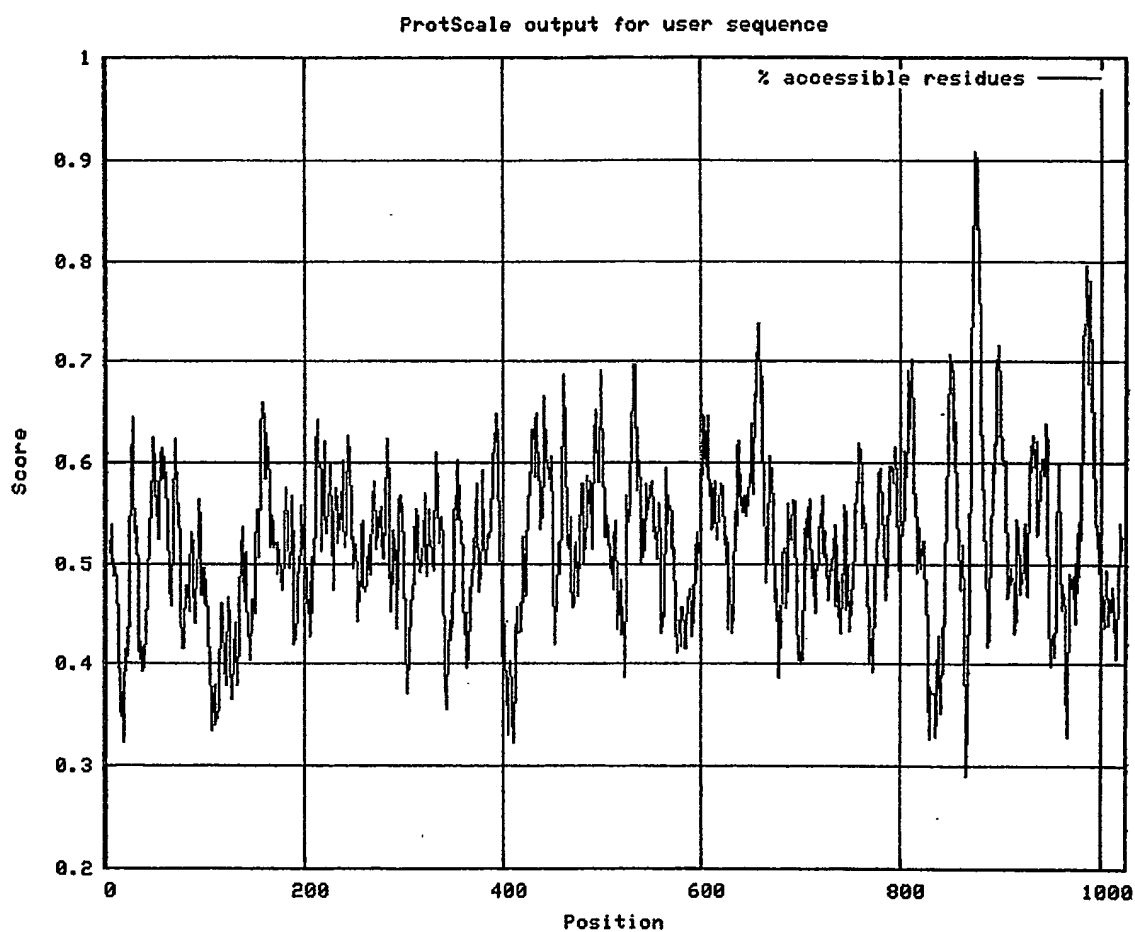


Figure 7b: 109P1D4 variant 2 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

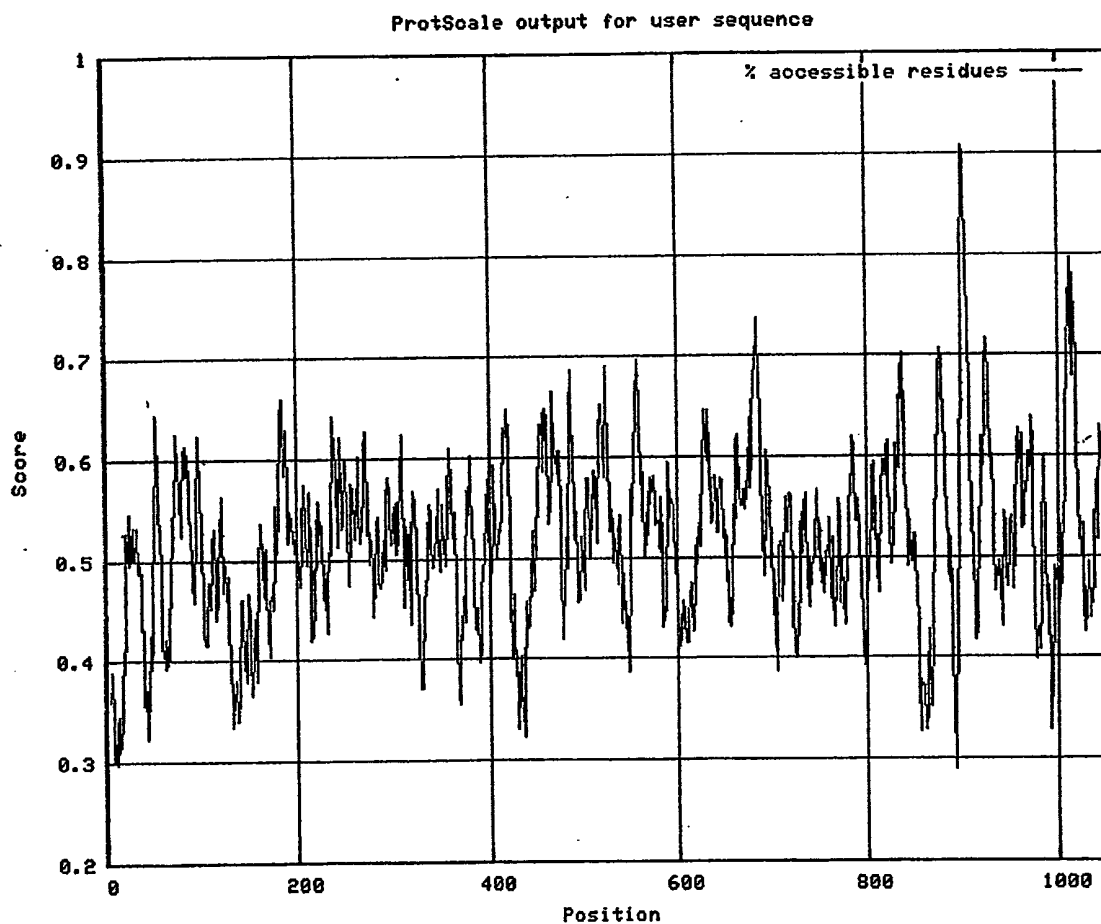


Figure 7c: 109P1D4 variant 3 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

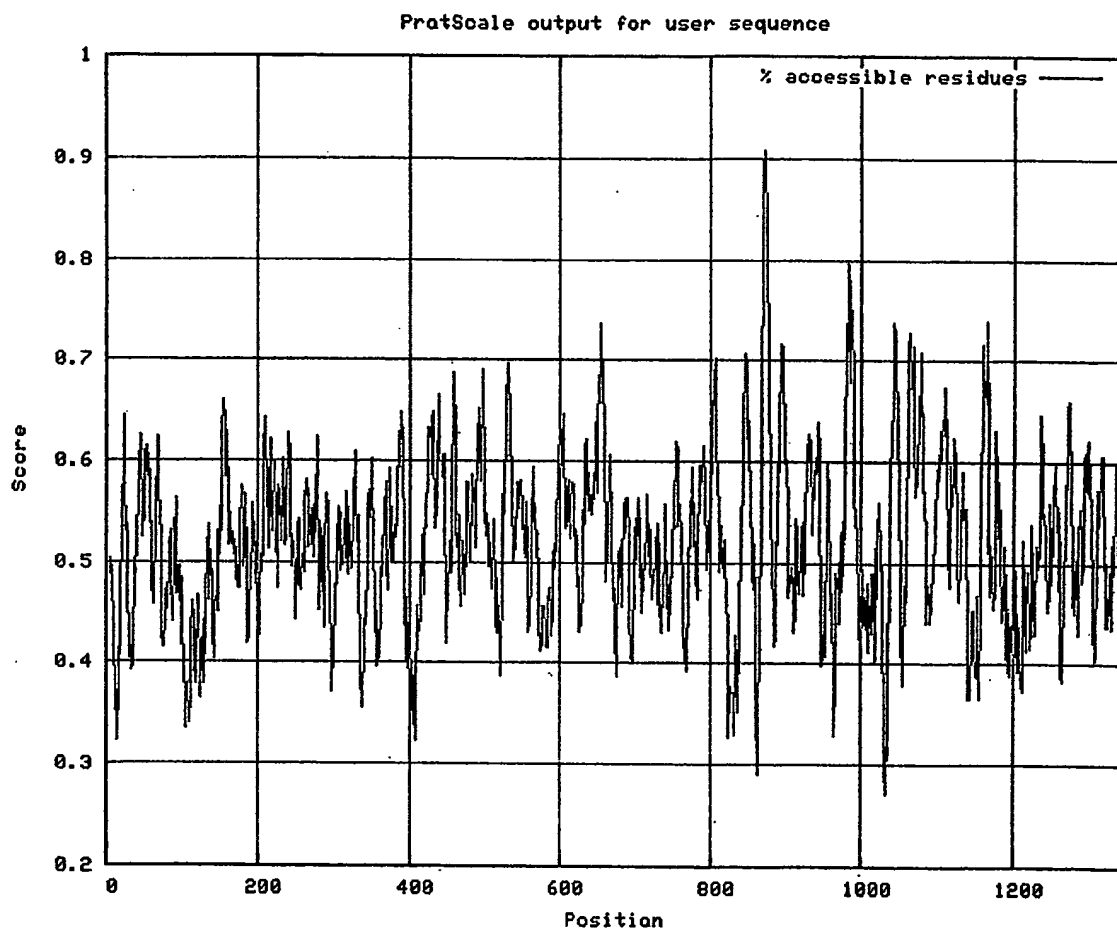


Figure 7d: 109P1D4 variant 4 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

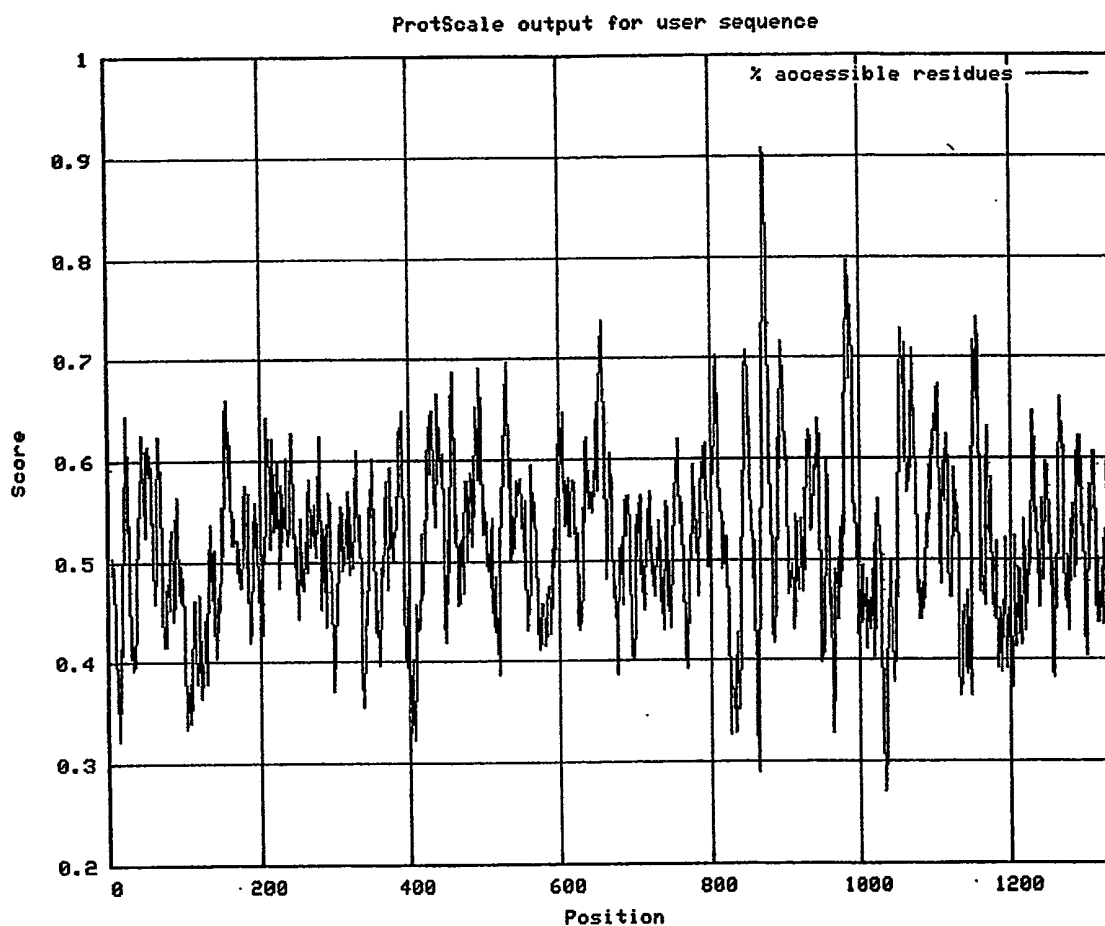


Figure 7e: 109P1D4 variant 5 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

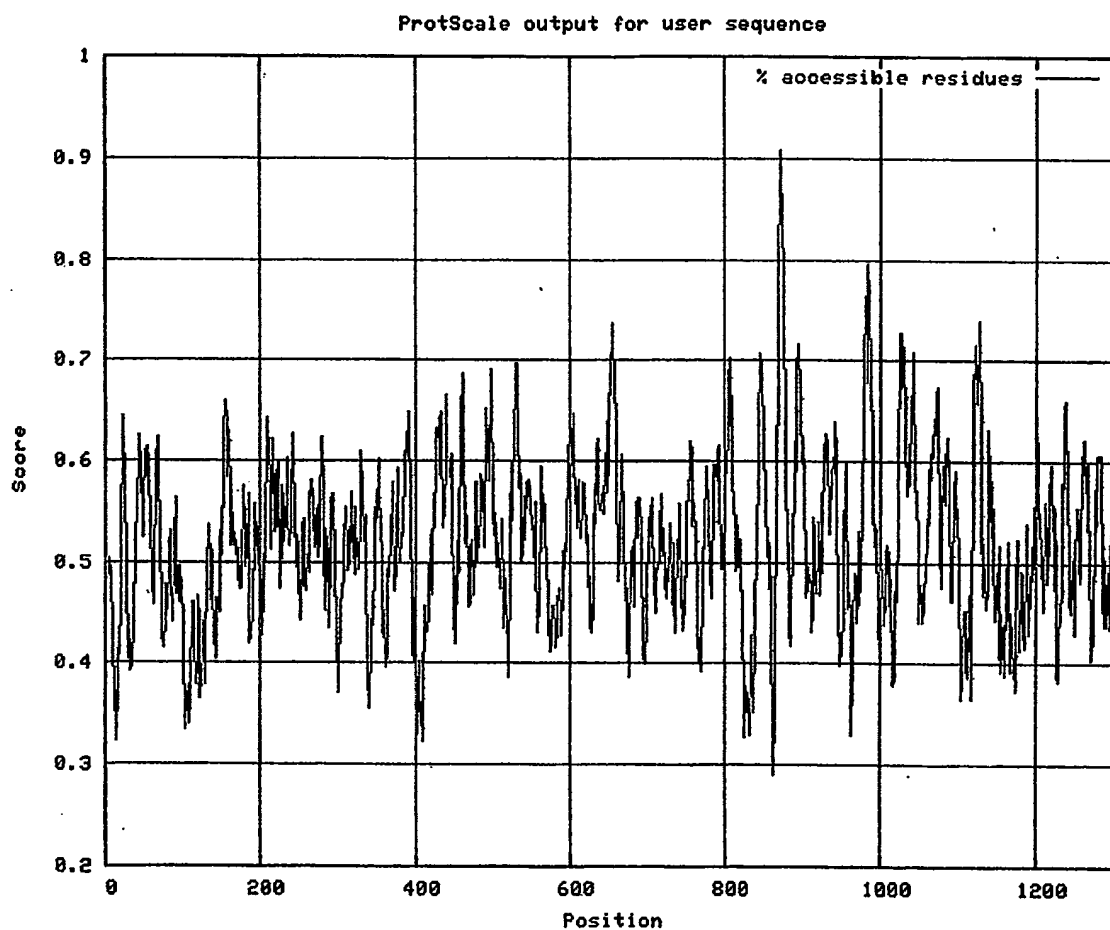


Figure 7f: 109P1D4 variant 6 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

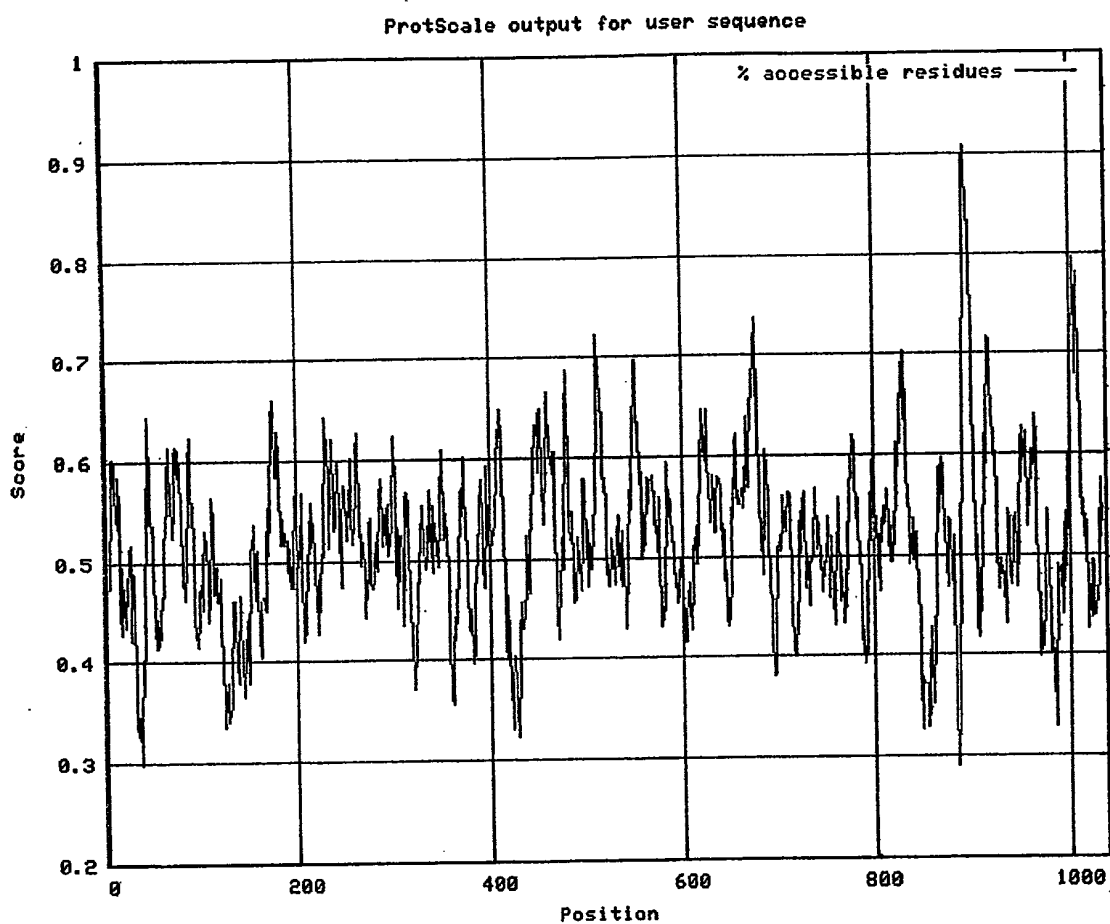


Figure 7g: 109P1D4 variant 7 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

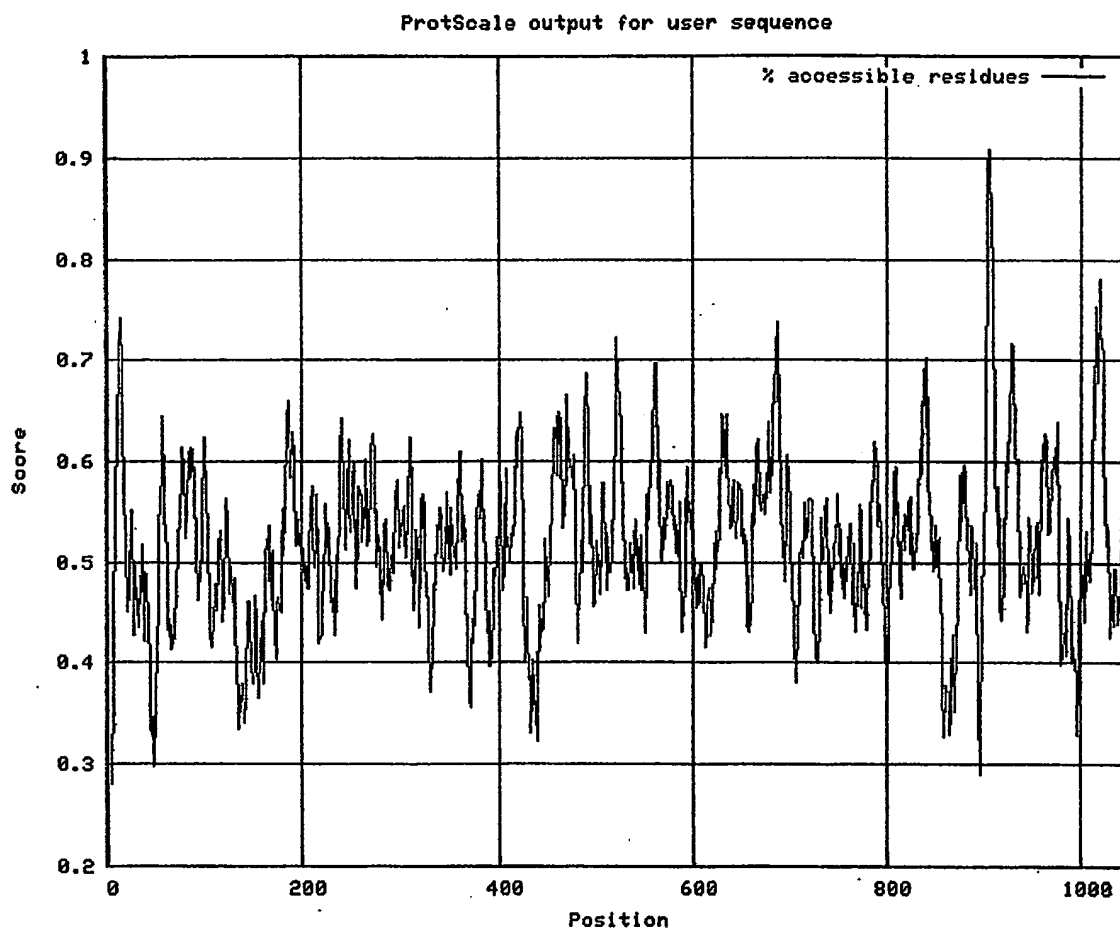


Figure 7h: 109P1D4 variant 8 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

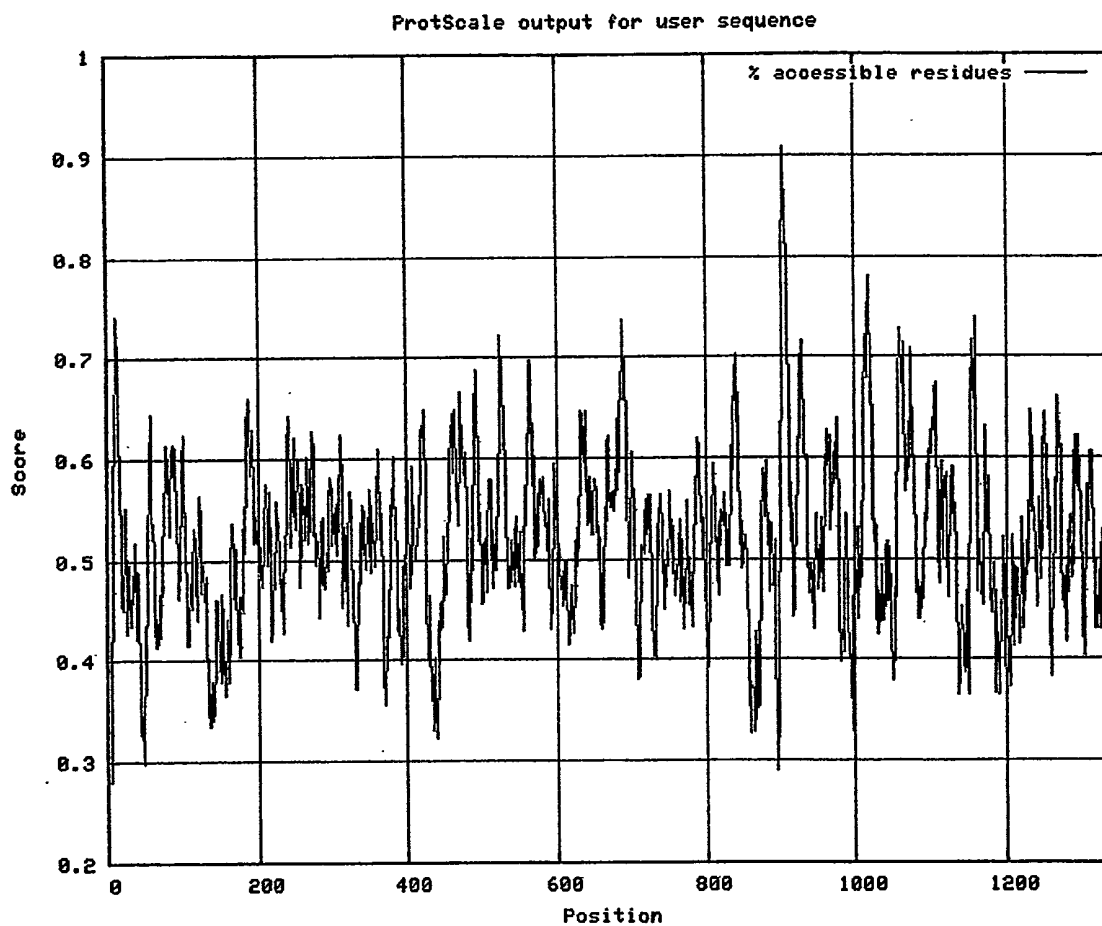


Figure 7i: 109P1D4 variant 9 %
Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

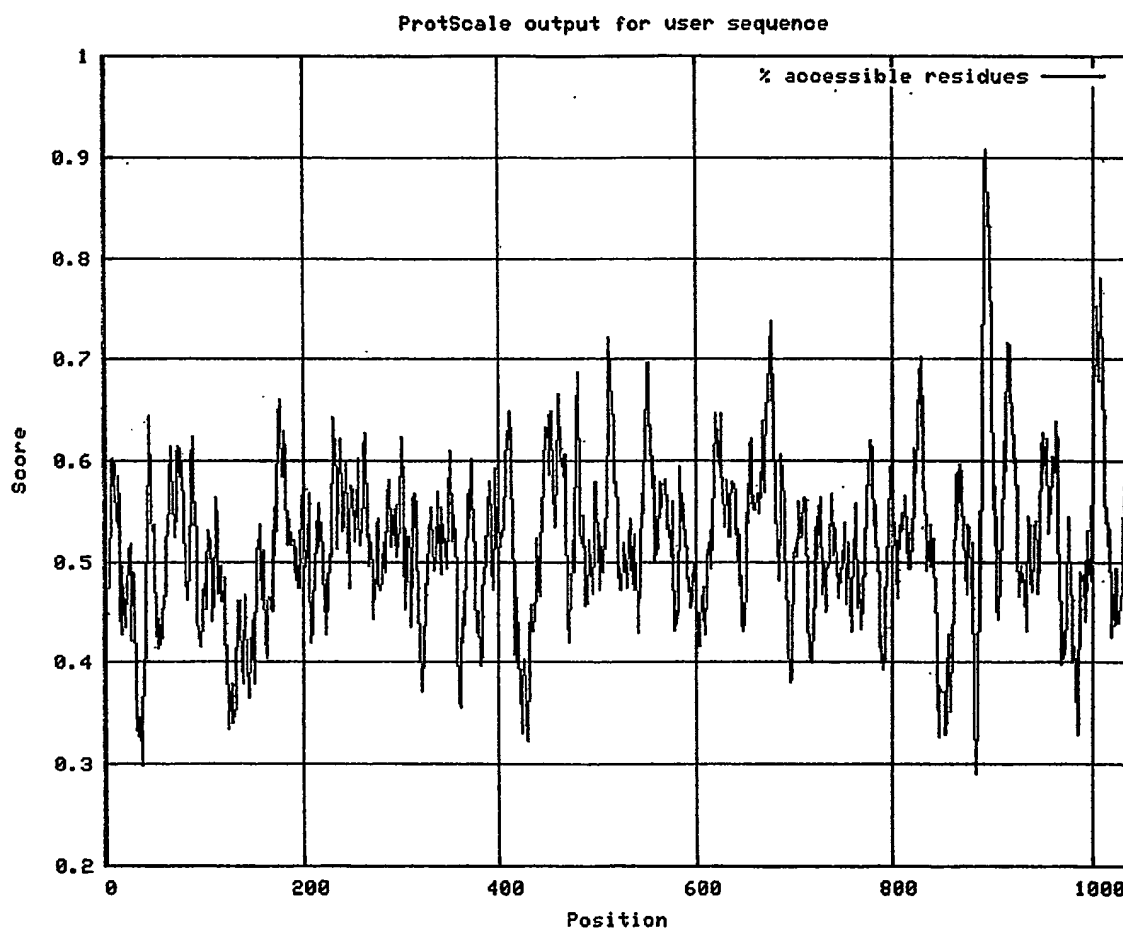


Figure 8a: 109P1D4 variant 1
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

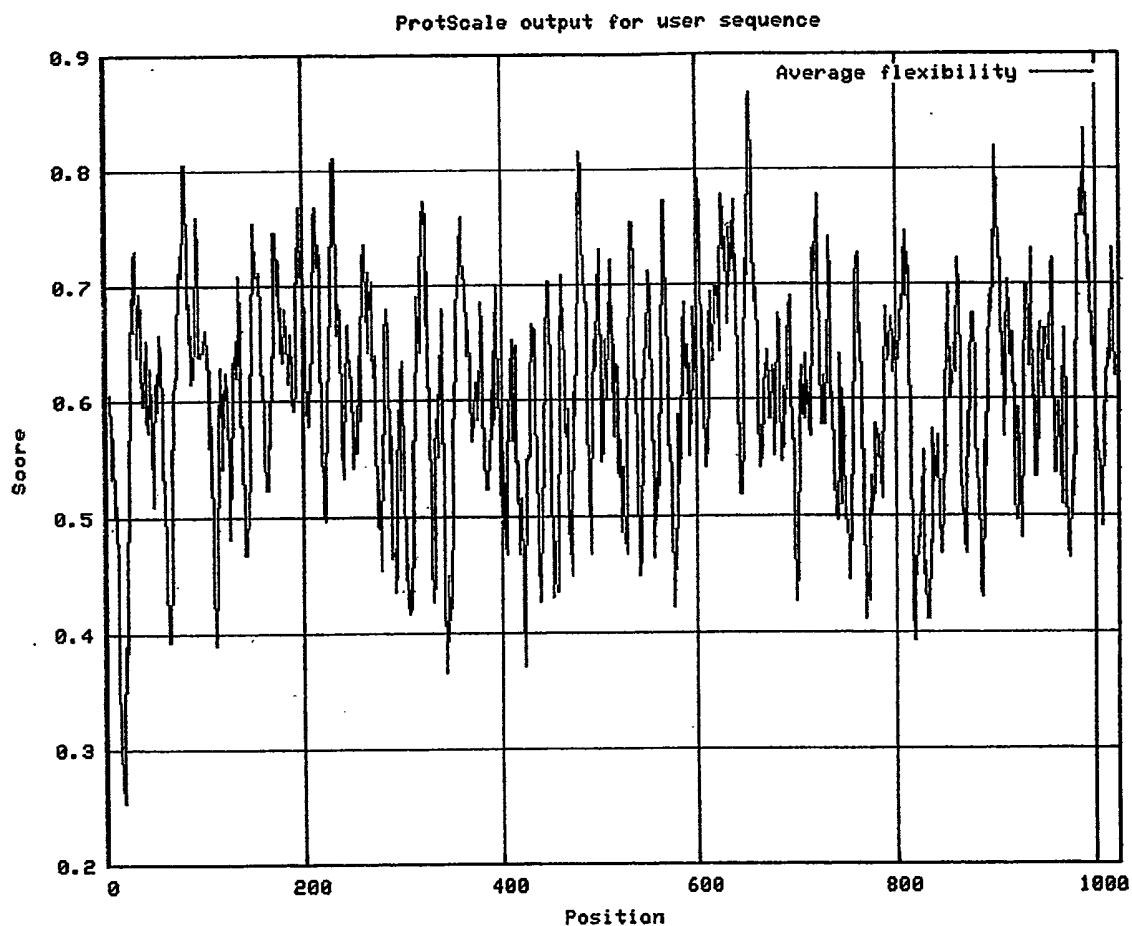


Figure 8b: 109P1D4 variant 2
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

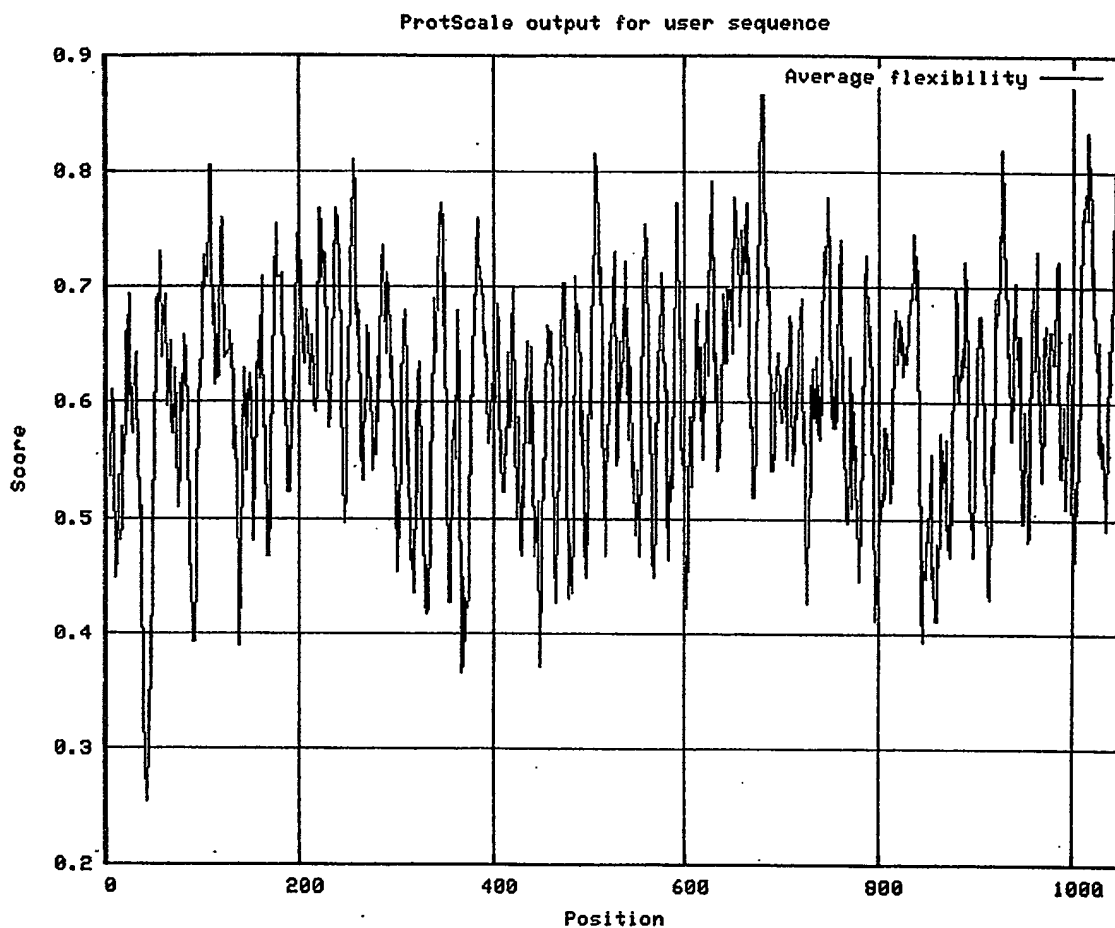


Figure 8c: 109P1D4 variant 3
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

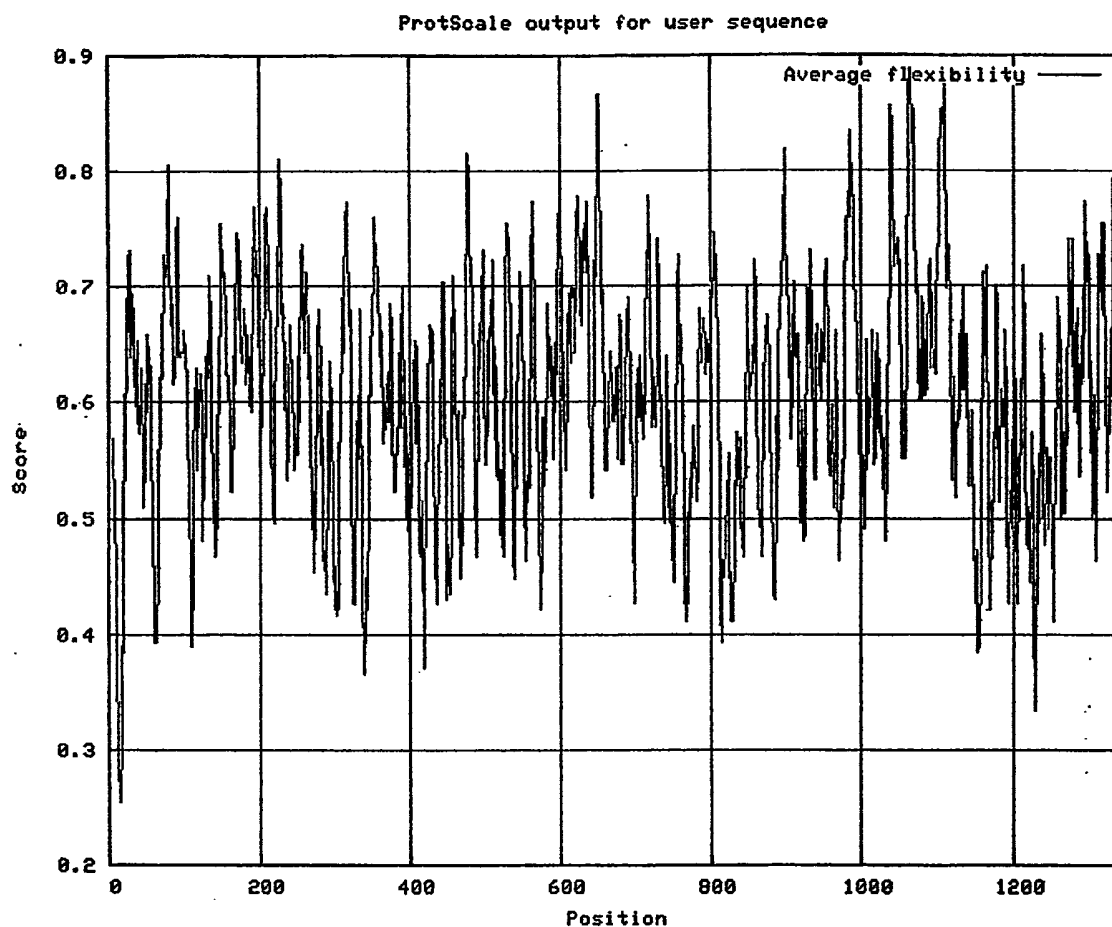


Figure 8d: 109P1D4 variant 4
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

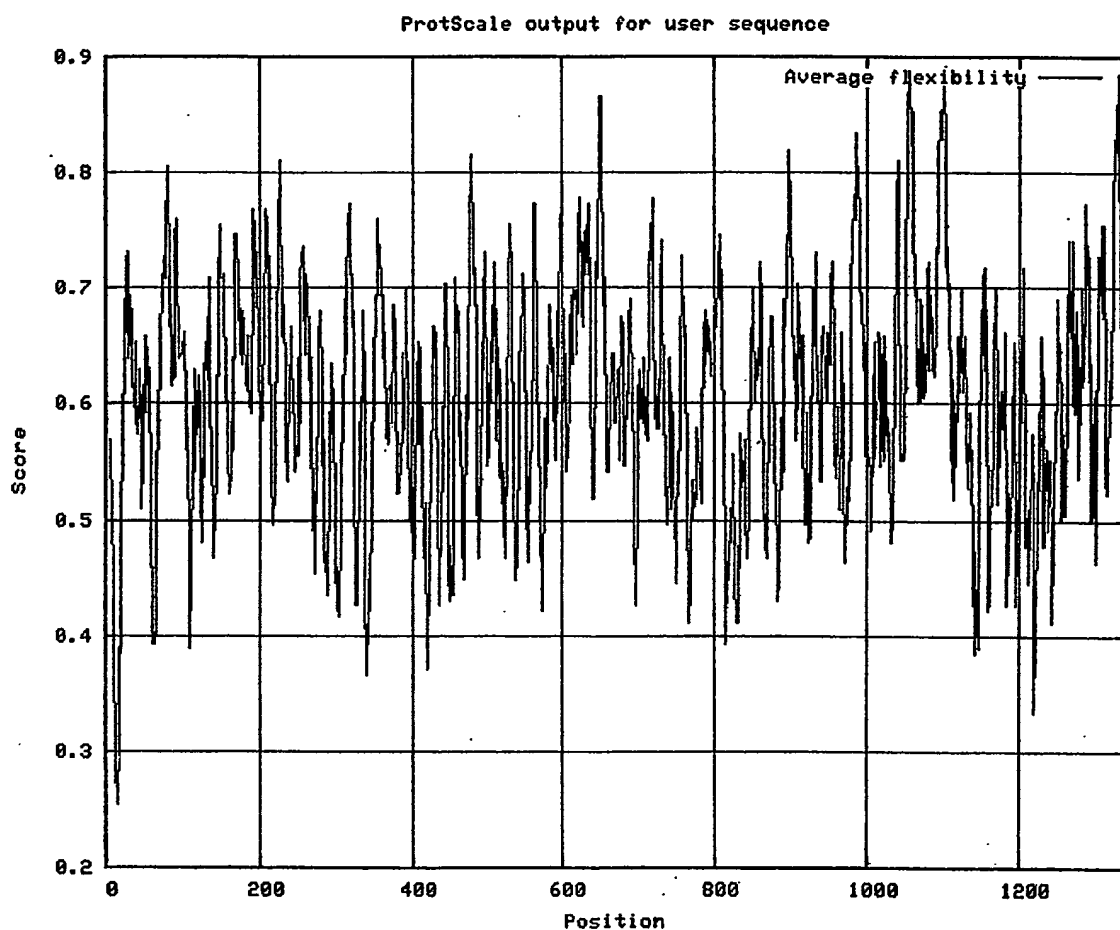


Figure 8e: 109P1D4 variant 5
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

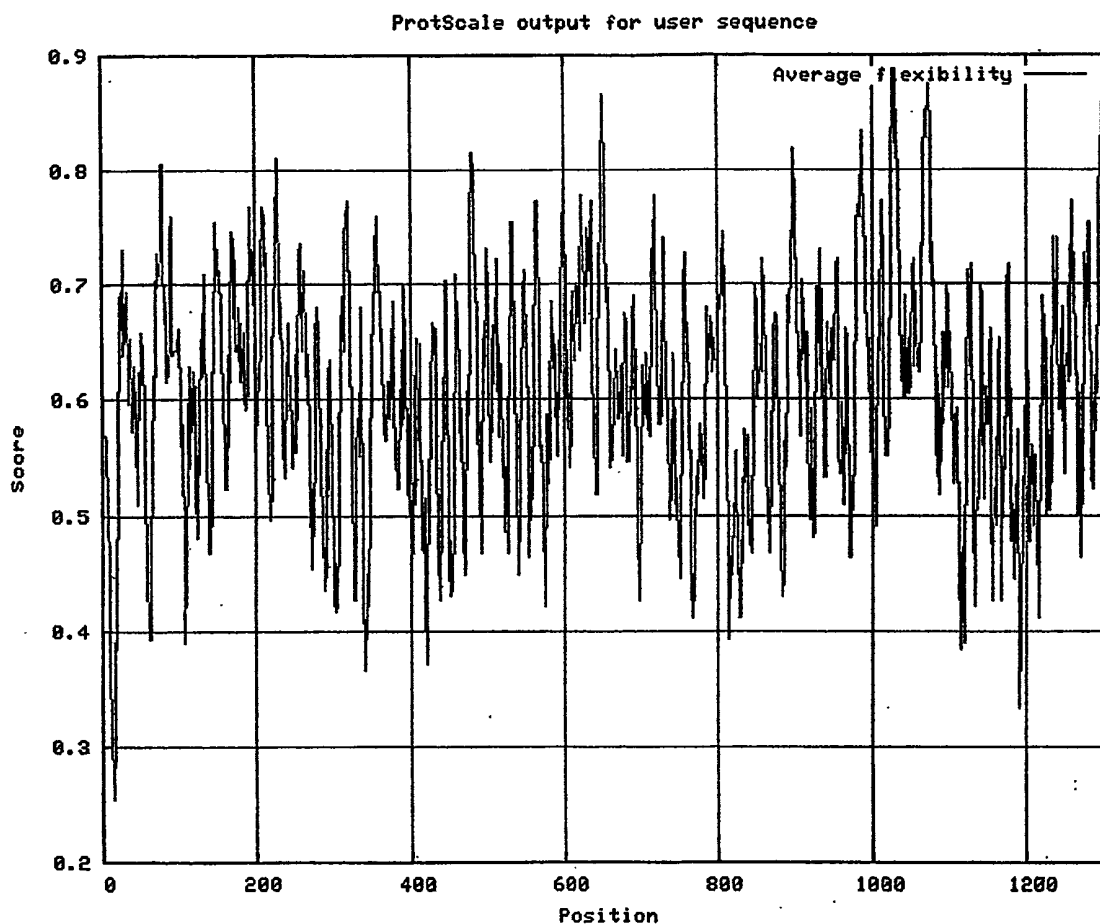


Figure 8f: 109P1D4 variant 6
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

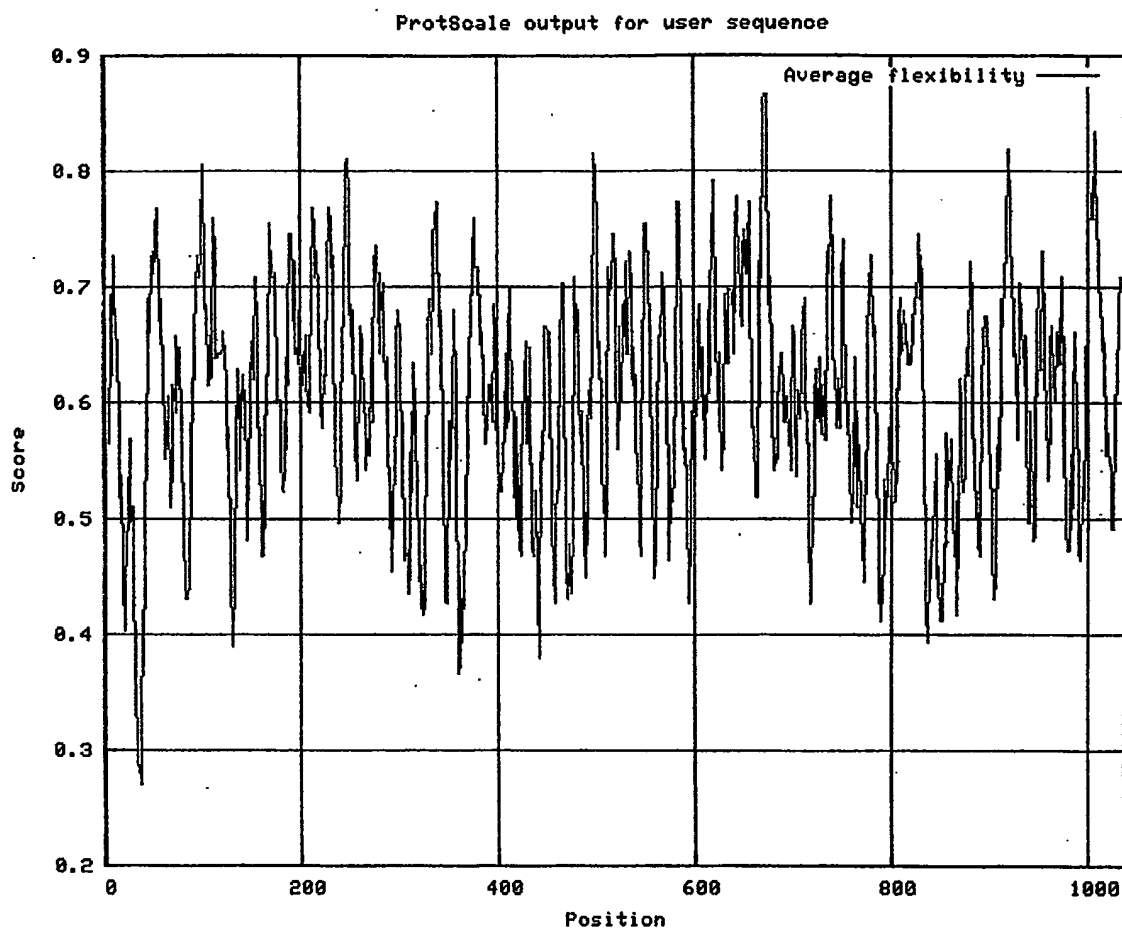


Figure 8g: 109P1D4 variant 7
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

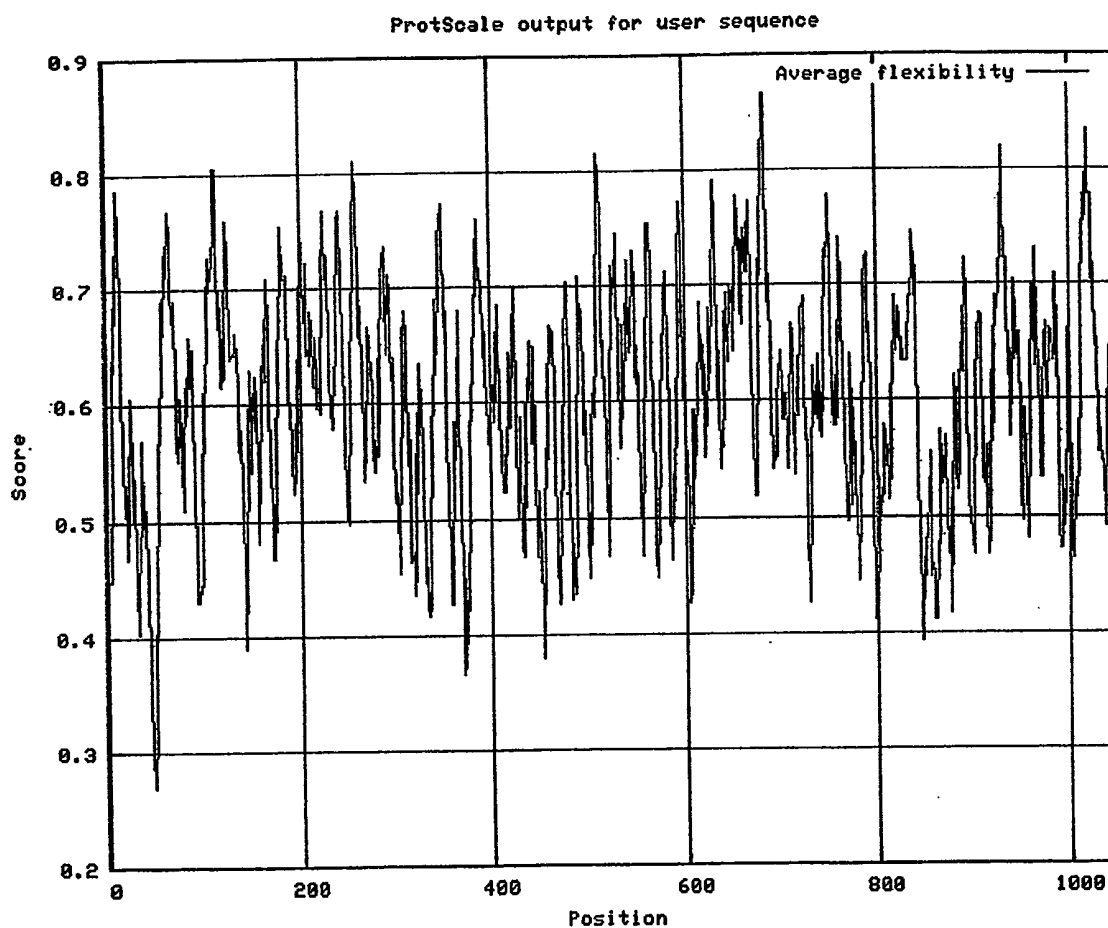


Figure 8h: 109P1D4 variant 8
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

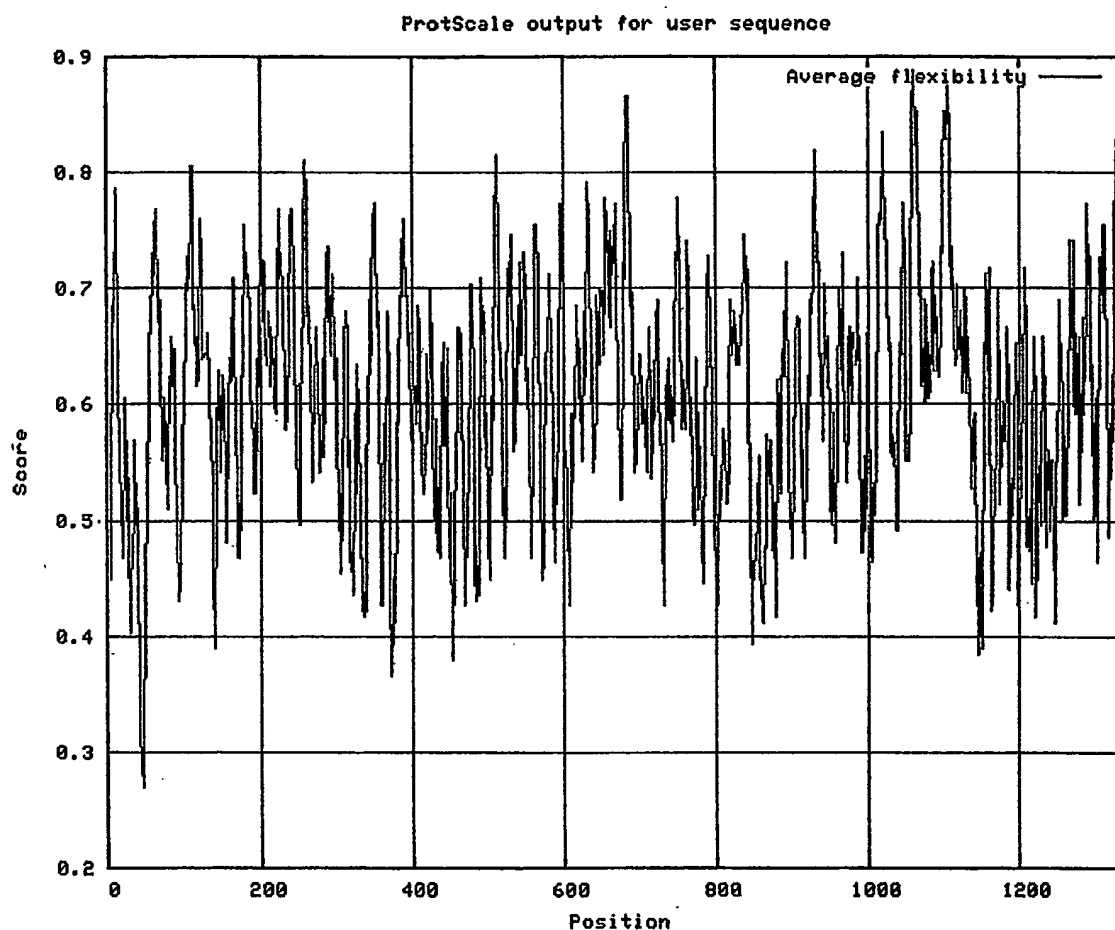


Figure 8i: 109P1D4 variant 9
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

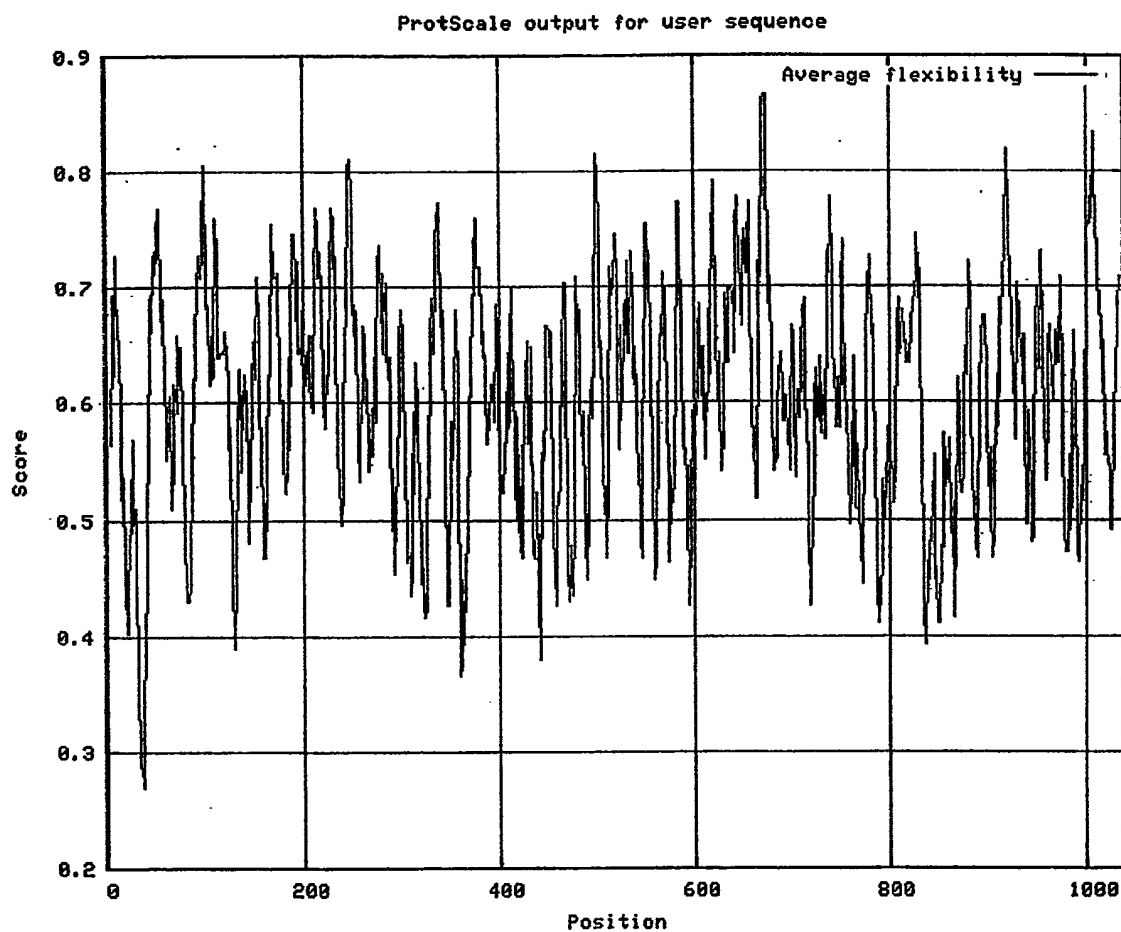


Figure 9a: 109P1D4 variant 1
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

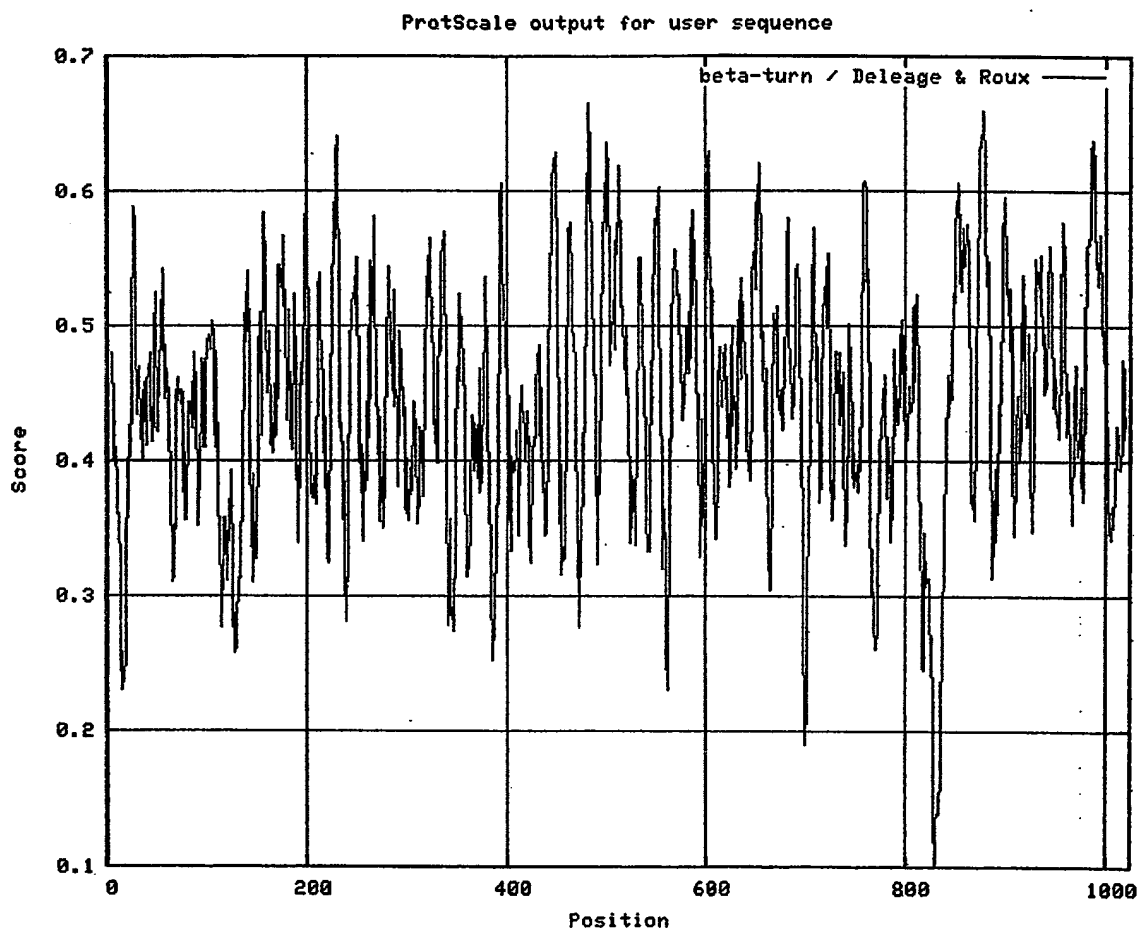


Figure 9b: 109P1D4 variant 2
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

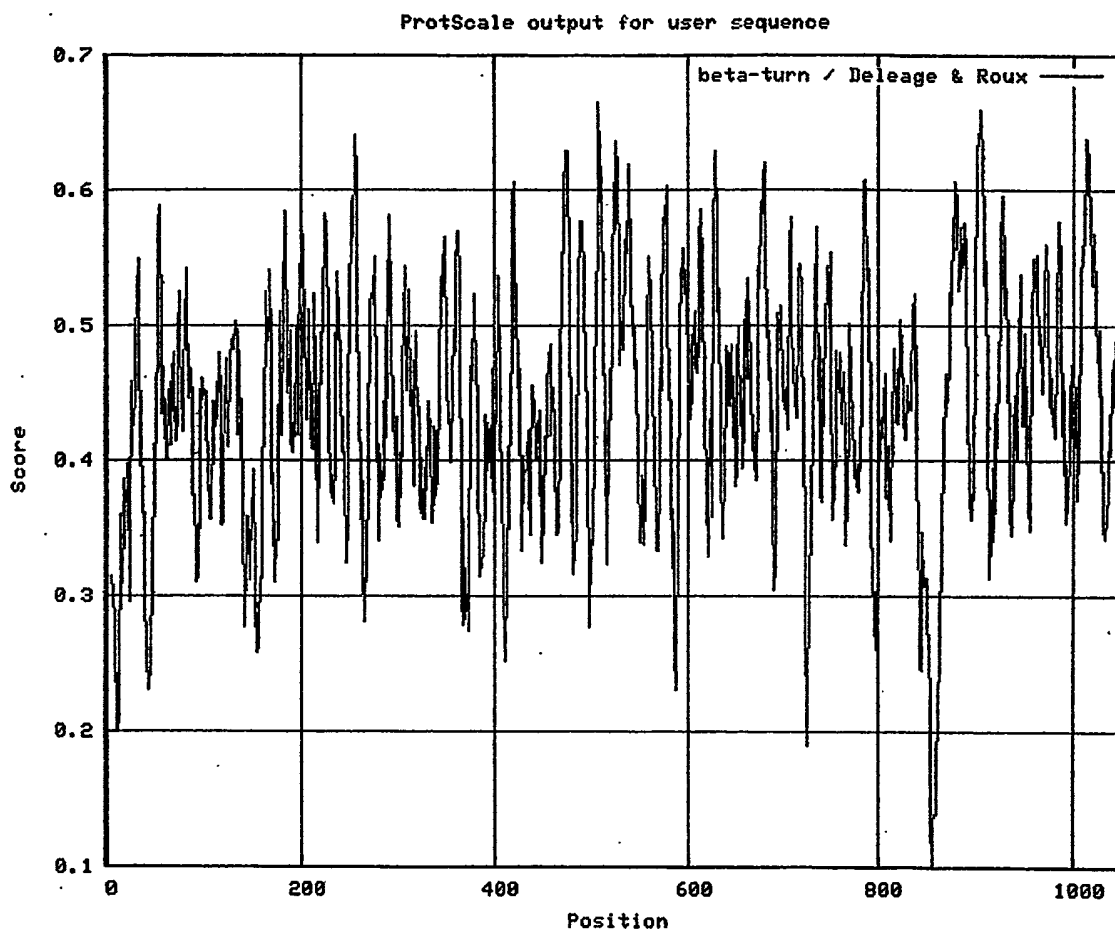


Figure 9c: 109P1D4 variant
3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

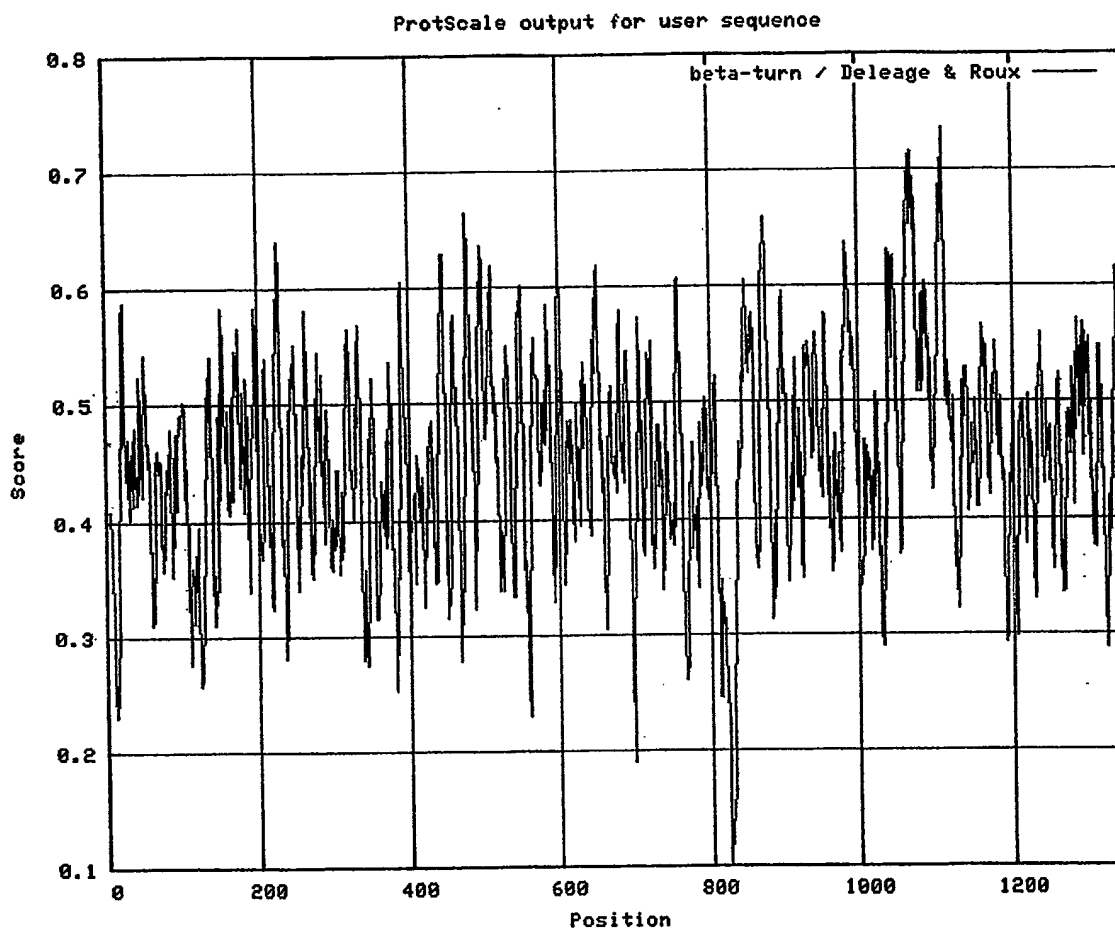


Figure 9d: 109P1D4 variant 4
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

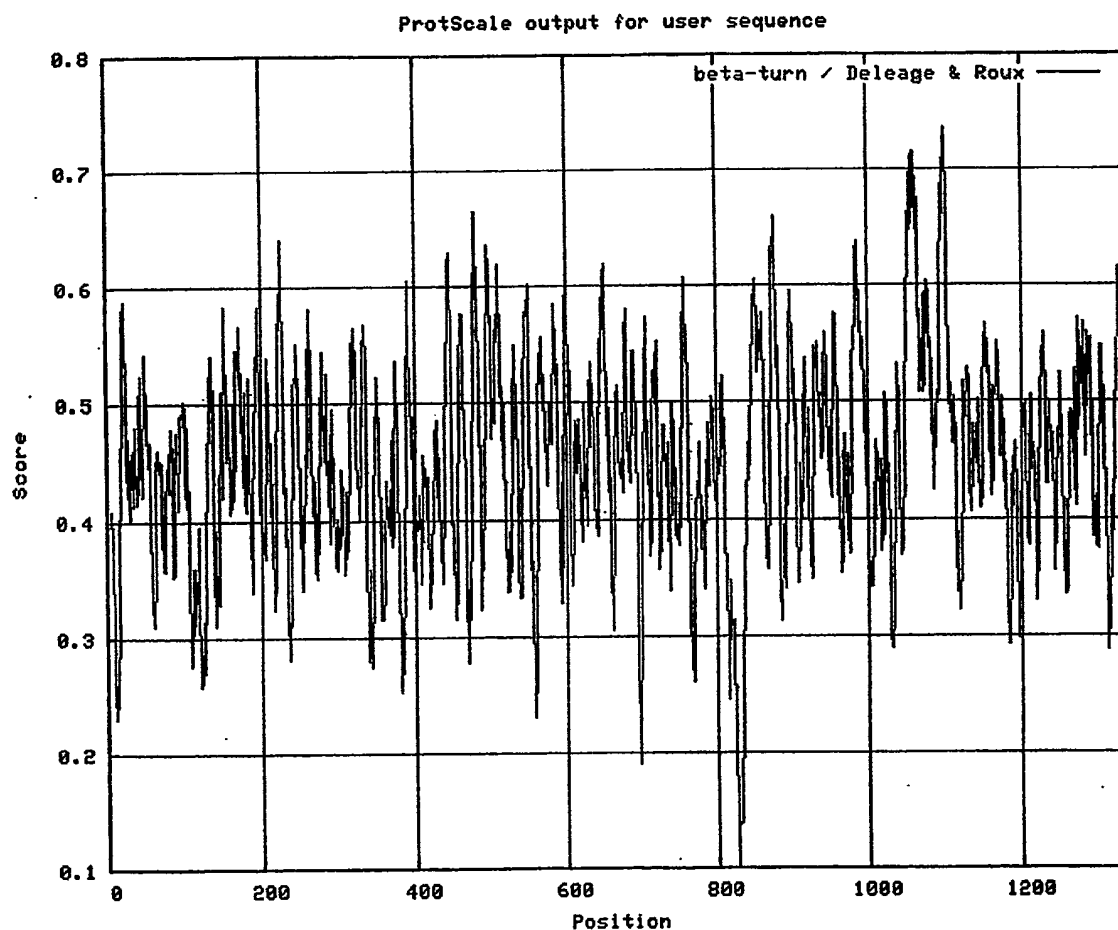


Figure 9e: 109P1D4 variant 5
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

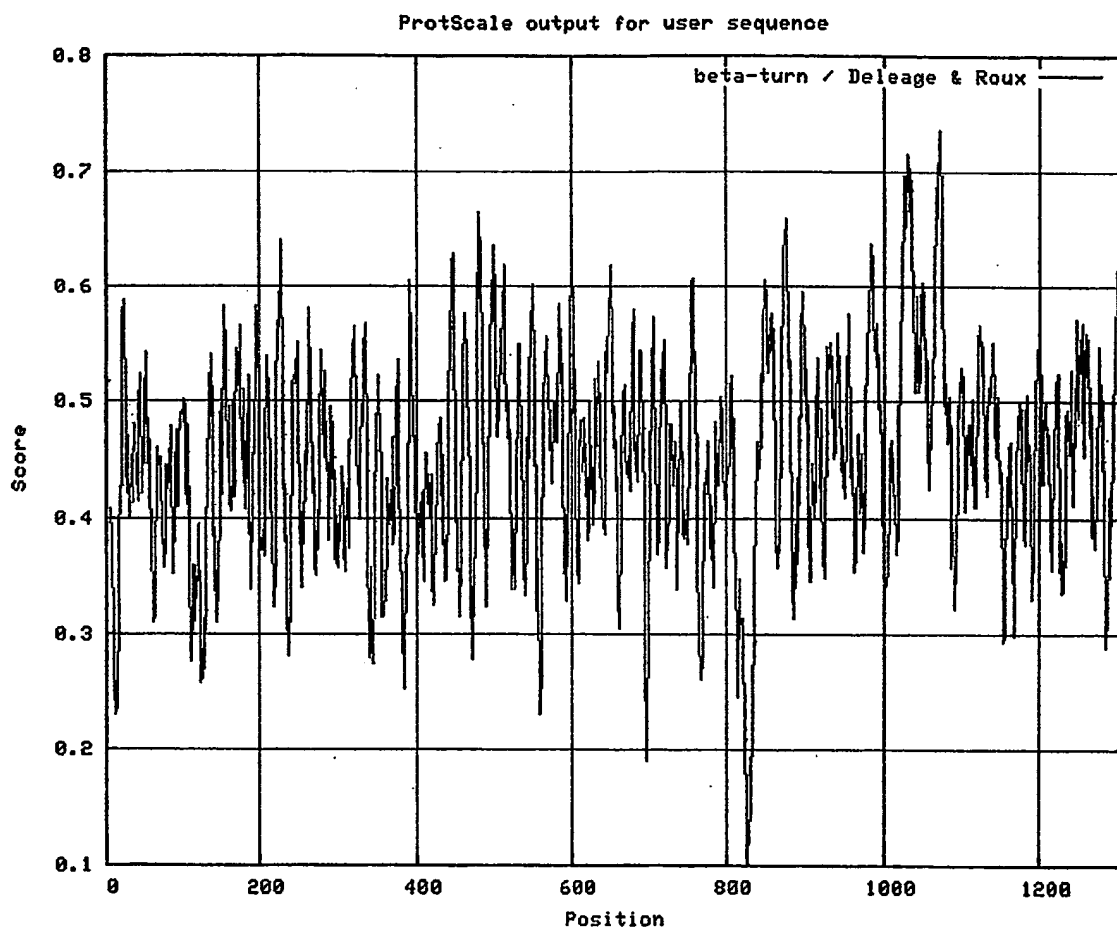


Figure 9f: 109P1D4 variant 6
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

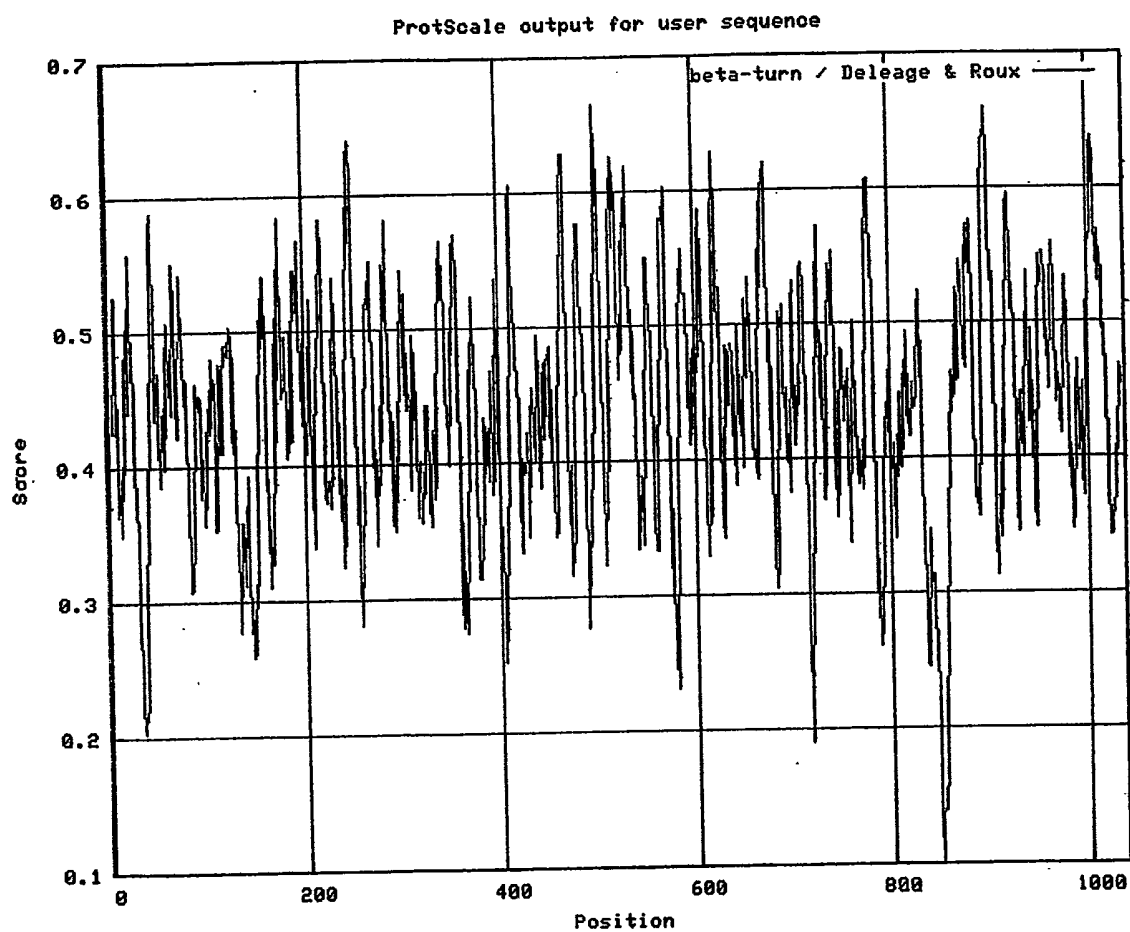


Figure 9g: 109P1D4 variant 7
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

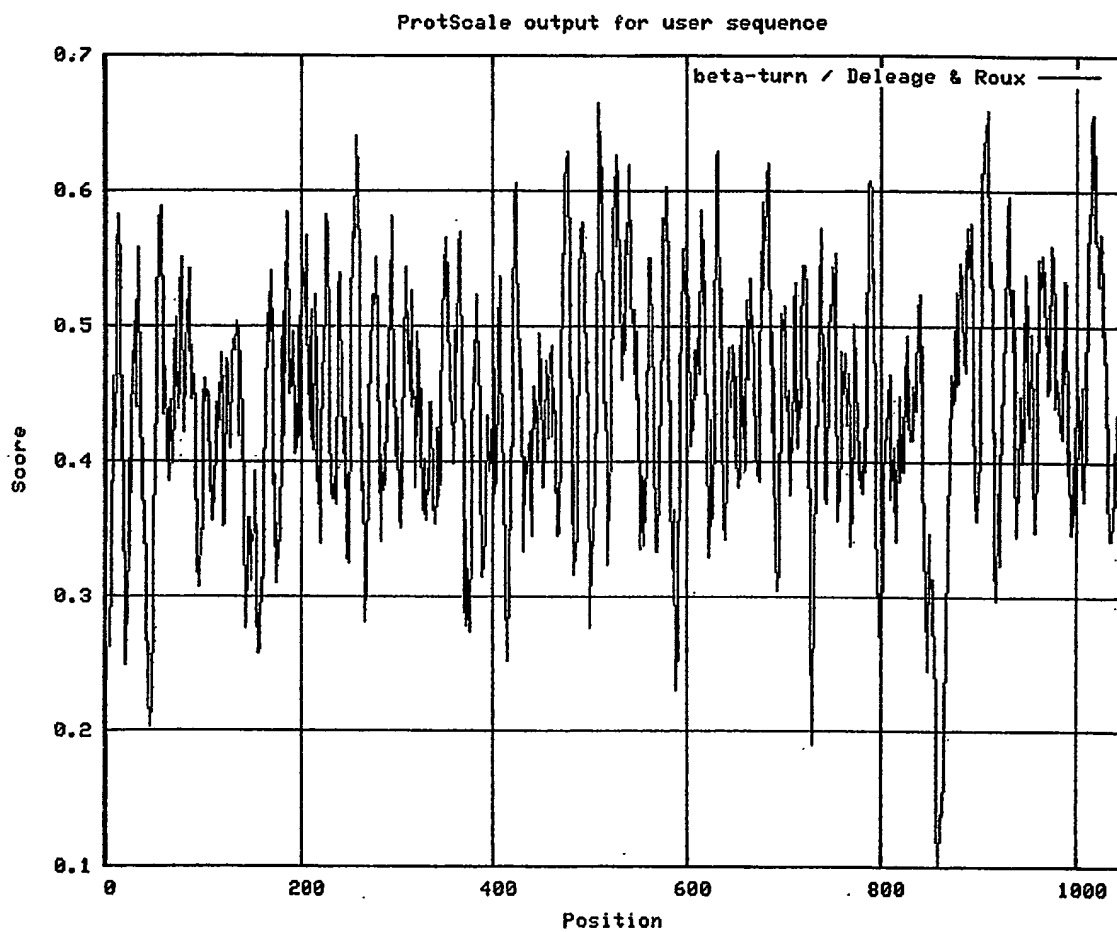


Figure 9h: 109P1D4 variant 8
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

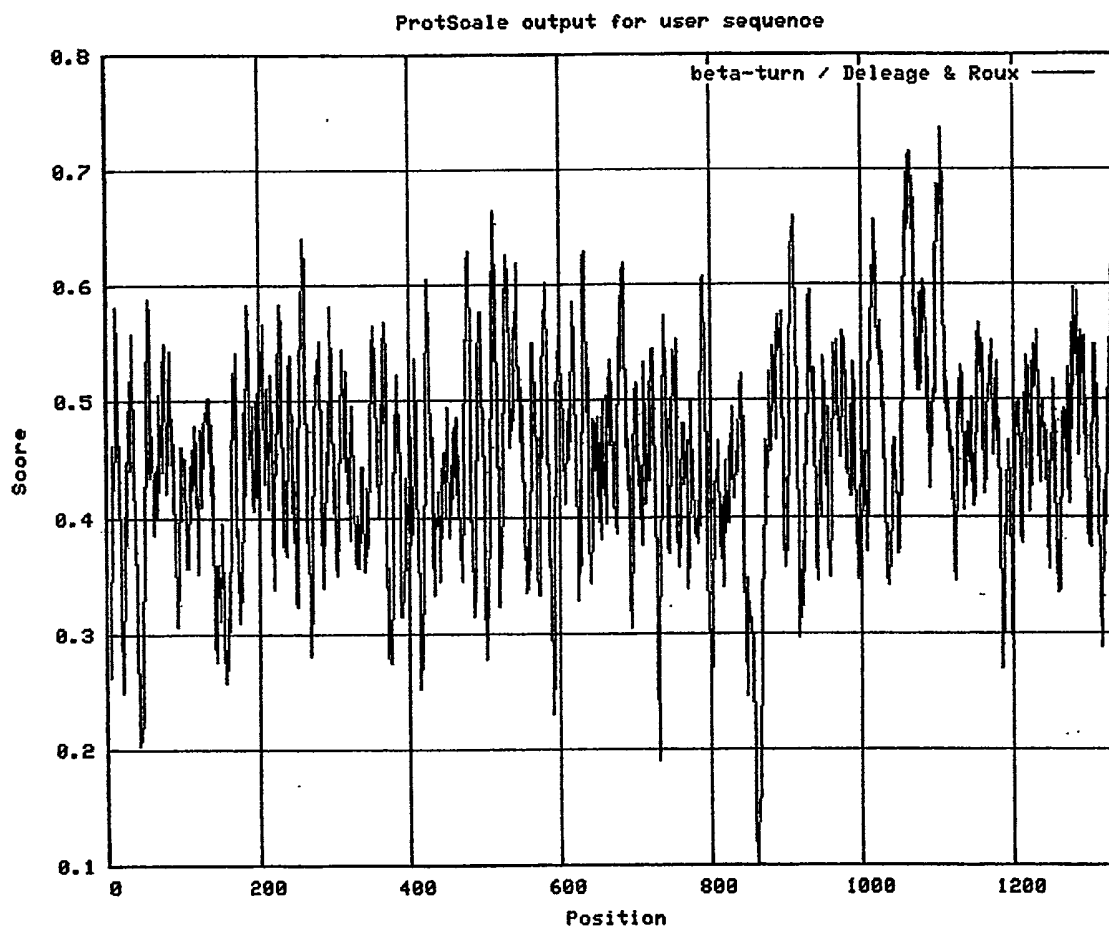


Figure 9i: 109P1D4 variant 9
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

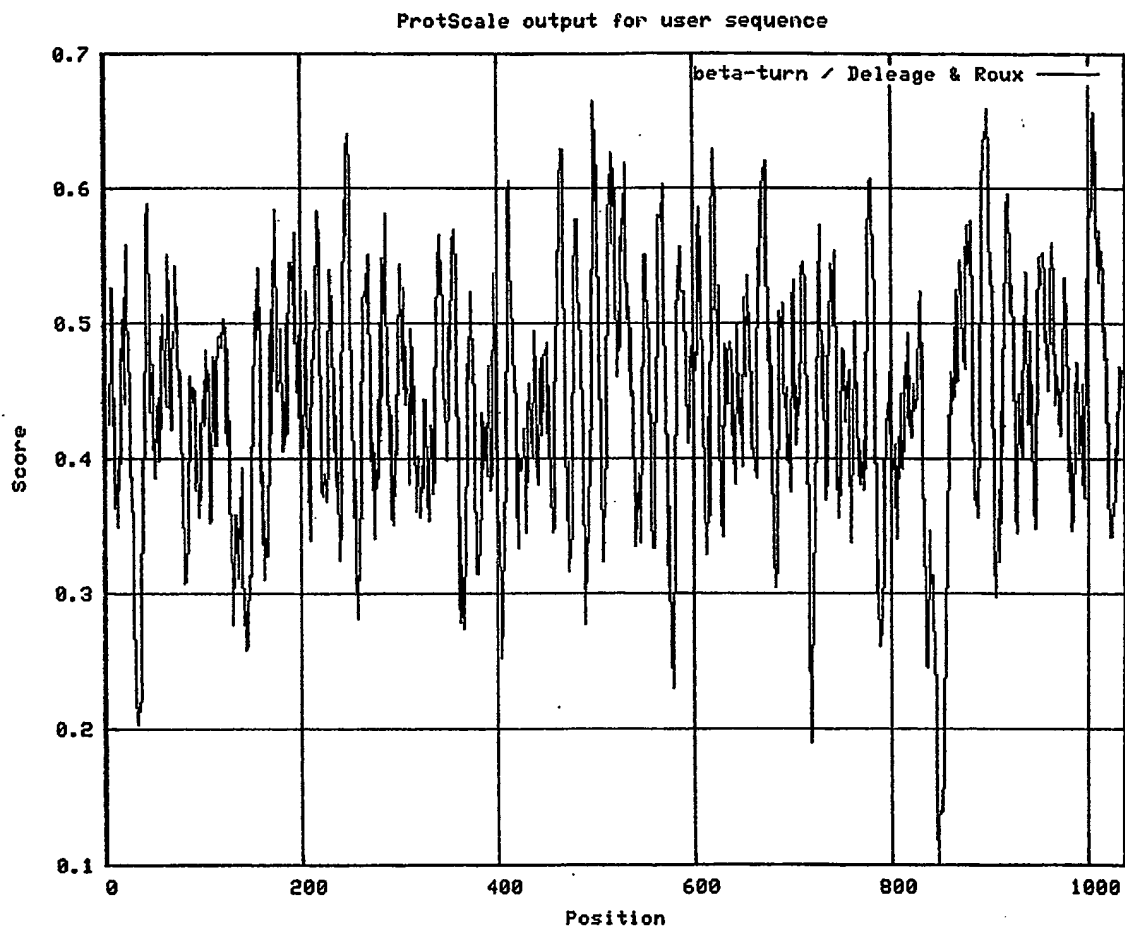


Figure 10

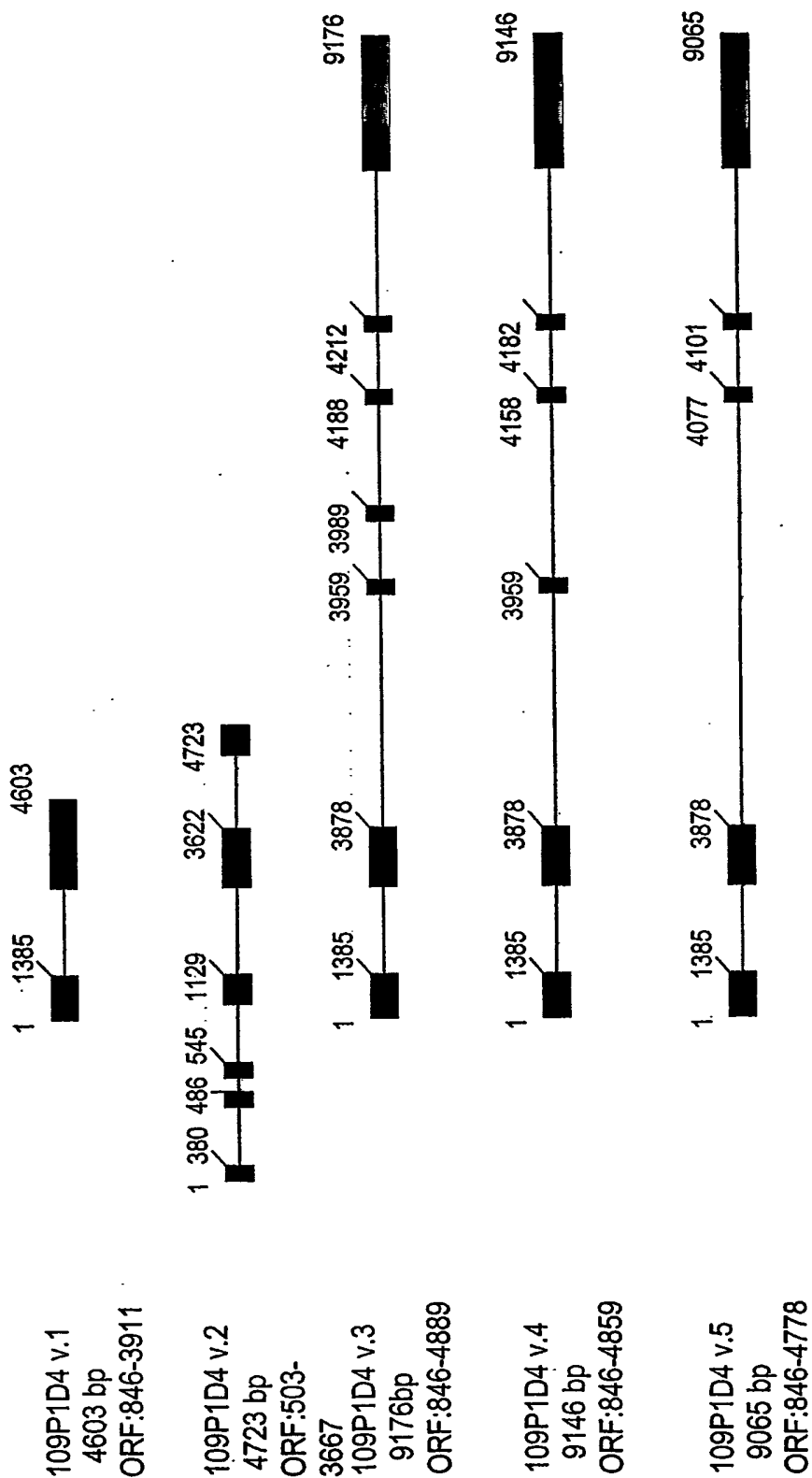


Figure 10 (con'd)

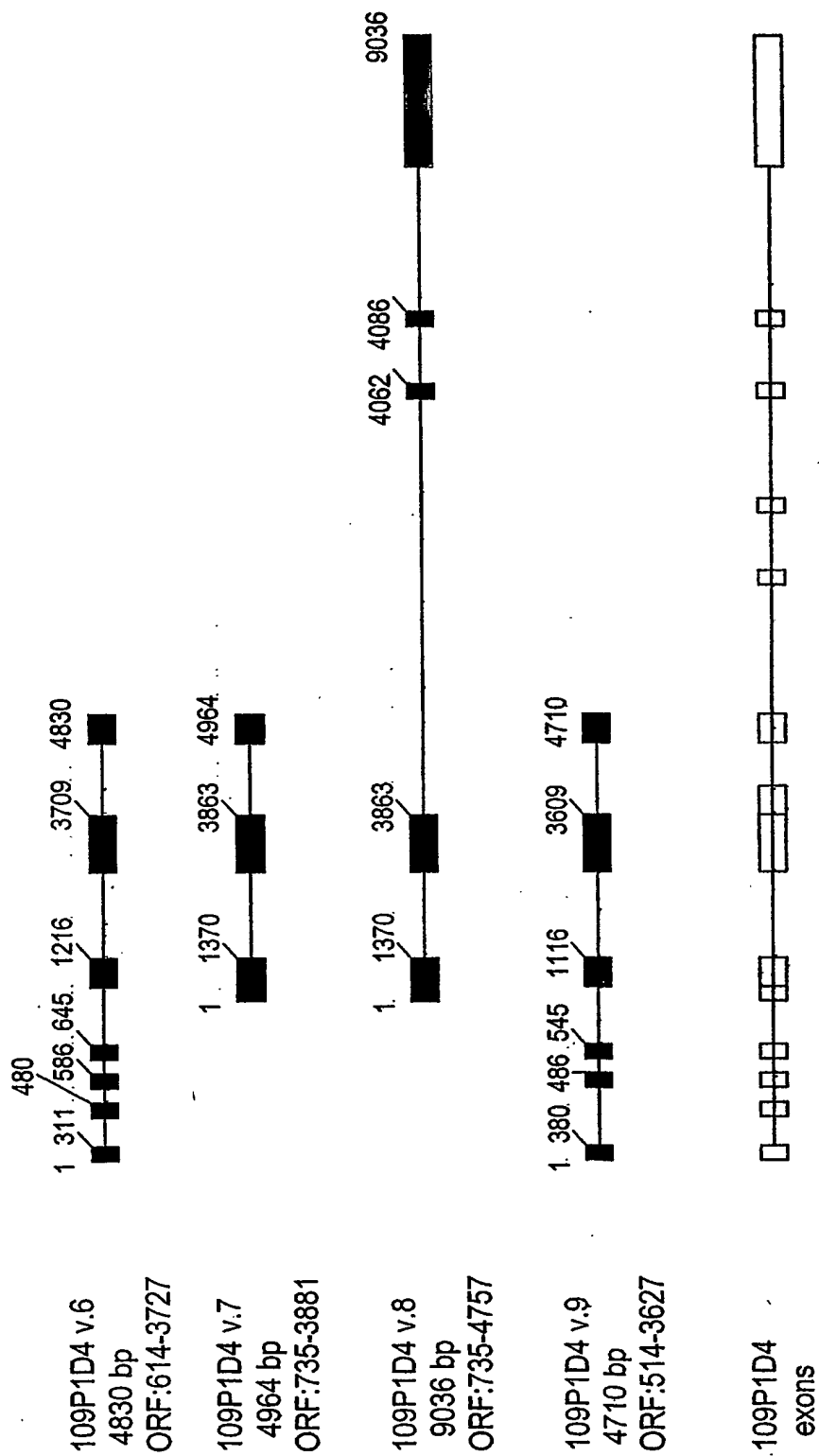


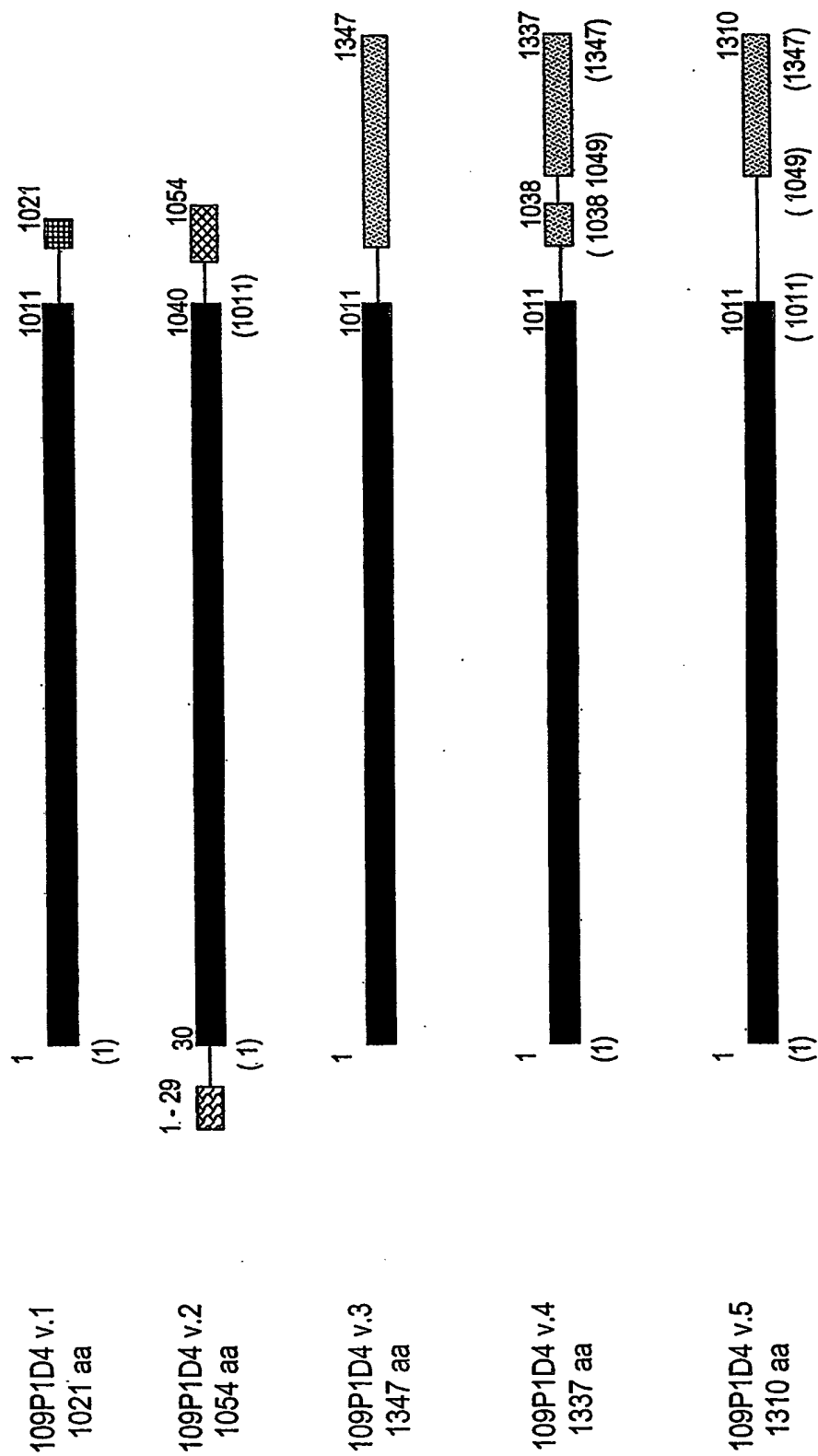
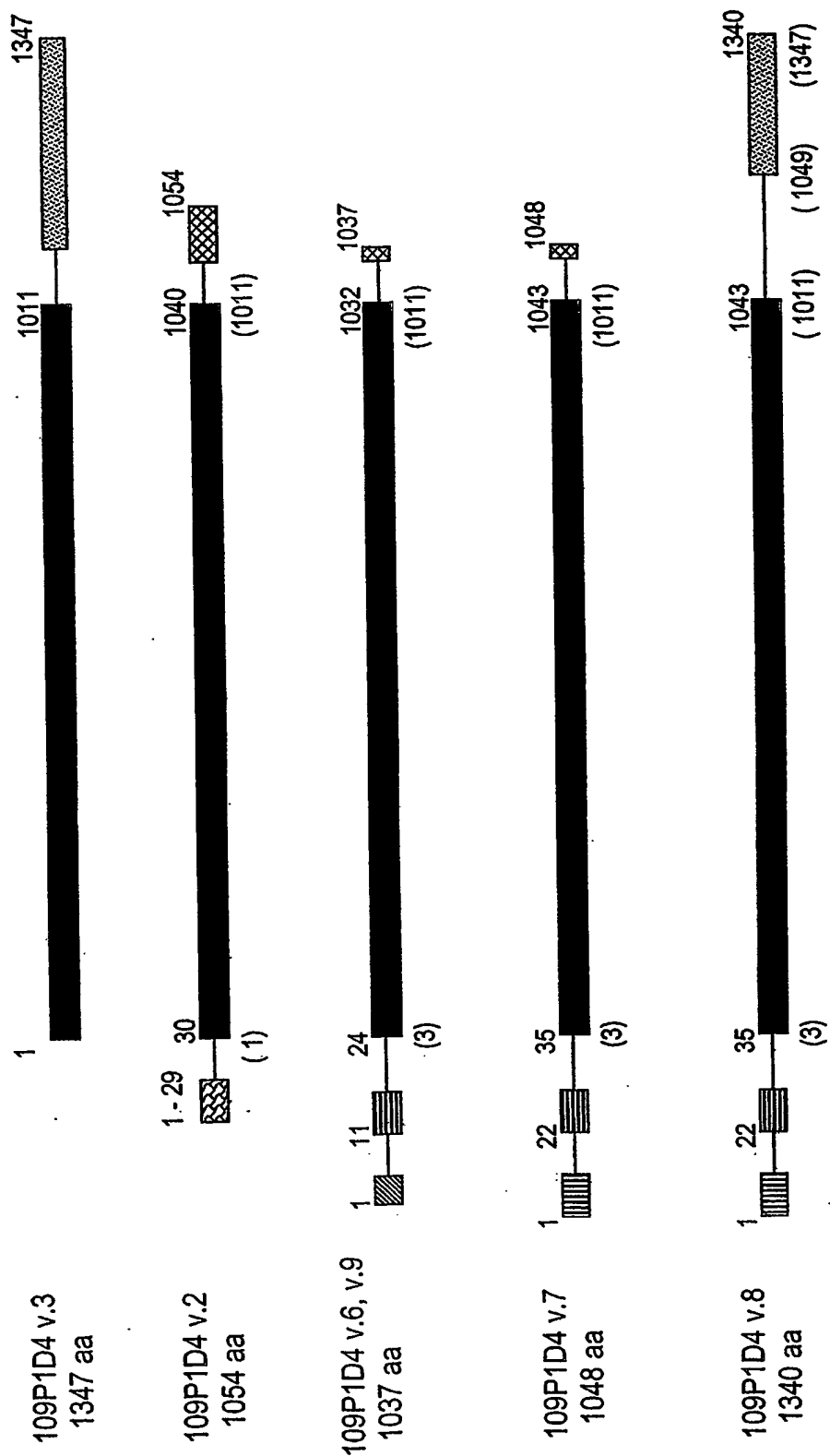
Figure 11

Figure 11(con'd)



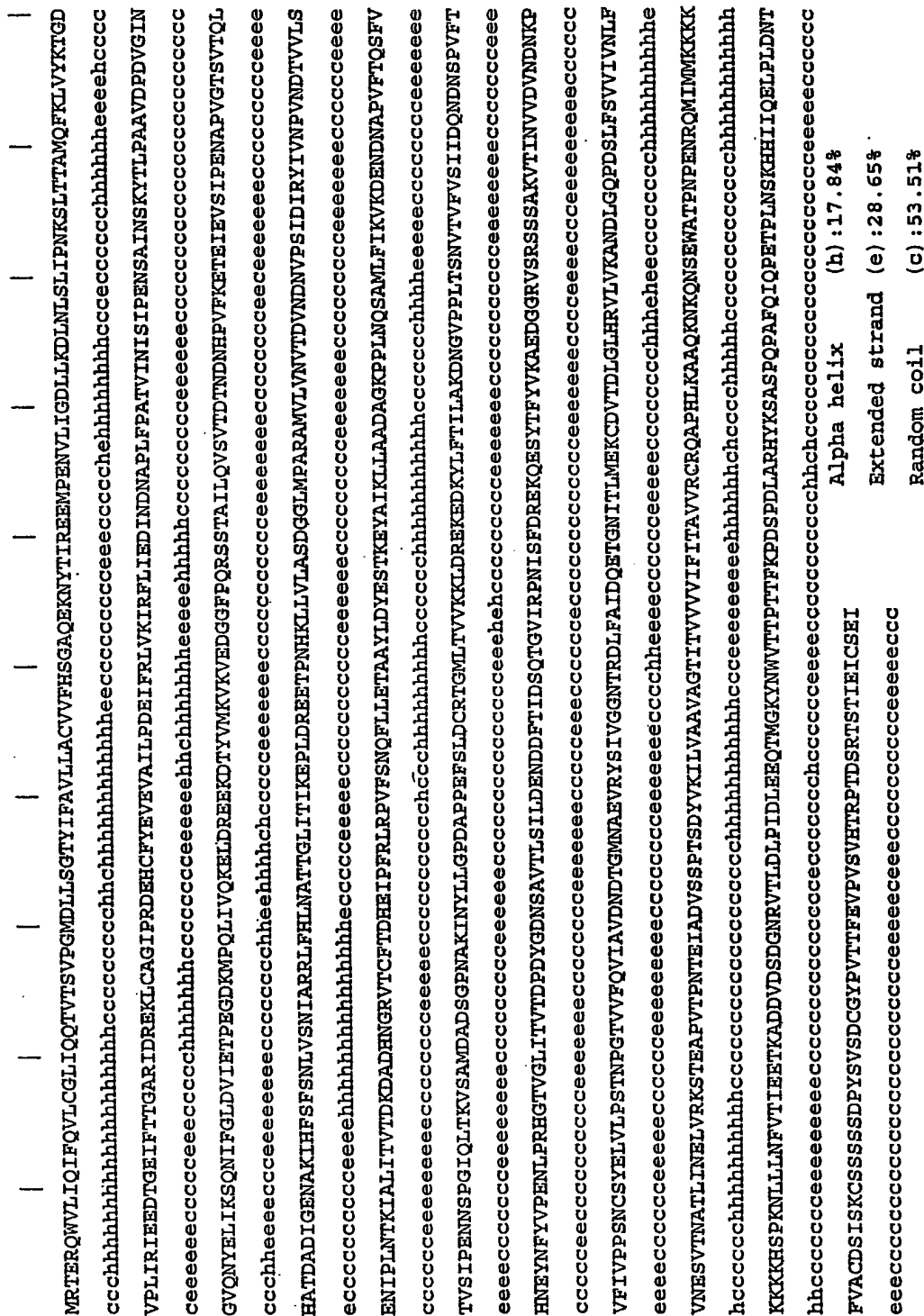
Year	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
Population (millions)	5.3	6.1	6.9	7.7	8.5	9.3	10.1	10.9	11.7	12.5	13.3	14.1
GDP (trillions of dollars)	1.5	2.5	4.0	6.0	9.0	13.0	18.0	24.0	31.0	39.0	47.0	55.0
Per capita GDP (dollars)	2,830	4,100	5,800	7,800	10,600	14,100	18,000	22,000	26,800	31,700	35,400	39,000

[illegible]

Alpha helix · (h):16.65%

Extended strand (e): 29.48%

Random coil (c): 53.87%



109P1D4 variant 3 Secondary Structure

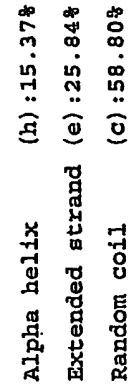


Fig. 13C continued 109P1D4 variant 3 Secondary Structure continued

810 820 830 840 850 860 870 880 890 900
| | | | | | | | | |
ADVSSPTSDYKILVAAGTITVVVIFITAVVRCRQAPHLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNFVTIETKADDVDSG
ccccccchhhhhhhhhcc
NRVTLDLPIDLEEQTMGKYNWVTTPTTFKPDSPDLARHYKASAPQAFQIQPETPLNKGHHIIQELPLDNTFVACDSISKSSSSDPYSVSDCGYPVTT
ccccccccchcc
FEVPVSVHTRPPMKEVVRSCTPMKESTTMEIWIHPQQRKSEGVAKSQRRVTFHLPEGSQESSDGLGDHDAAGSLTSTSHGLPLGYPQEEYFDRATP
eeeeeeeecc
SNRTEGDGNSDPSTFIPGLKKAABITVQPTVEASDNCCTOECLIIYGHSDACWMPASLDHSSSSQASALCHSPPLSQASTQHHSPRVTQTIALCHSPP
cc
VTQTIALCHSPPPIQVSALHSPPLVQATALHSPPSQAASALCYSPPLAQAAAIHSSPLPQVIALHRSQAQSSVSLQQGWVQAGDGLCSVDQGVQGSA
cc
TSQFYTMSERLHPSDDSIKVIPLTFTFPRQQARPSRGDSPIMEEHL
chhhhhcc

Alpha helix (h):15.37%

Extended strand (e):25.84%

Random coil (c):58.80%

Fig. 13D continued 109P1D4 variant 4 Secondary Structure continued

```

      810      820      830      840      850      860      870      880      890      900
      |      |      |      |      |      |      |      |      |      |
ADVSSPTSDYVKILVAAGTITVVVVFITAVVRCRQAPHLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLLNFTTLEETKADDVDSDG
ccccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
NRVTLDLPIDLEQTMGKYNWTTTTFKPDSPDLARHYKASAPQAFQIQPETPLNSKHIIQELPLDNTFVACDSISKSSSSDPYSVSDCGYFVTI
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
FEVPVSVHTRPPMKEVVRSCTPMKESTTMEIWIHPQSQRRVTFHLPEGQESSDGLGDHDAAGSLTSTSHGLPLGYPOEYFDRATPSNRTEGDGNS
eeeeeeeecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
DPESTFIPGLKKAABITVQPTVEASDNCCTQECCLIYGHSDACWMPASLDHSSSSQAQASALCHSPPLSQASTQHHSRPTQTIALCHSPVVTQTIALCHS
ccccchhchcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
PPPIQVSALHSPPLVQATALHSPSPAQASALCYSPPLAQAAIASHSSPLPQVIALHRSQAQSSVSLQQWVQAGDGLCSVDQGVQGSATSQFYTMSE
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
LHPSDDSIKVIPLTFTFRQARPSRGDSPIMEEHPL
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

Alpha helix (h):15.48%

Extended strand (e):25.88%

Random coil (c):58.64%

Fig. 13E 109P1D4 variant 5 Secondary Structure continued

```

810      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      ADVSSPTS DYKILVA AVAGTITVVVVFITAVVRCRQAPHLKAAQKNKQNSEWATPNPENRQIMMKKKKKKKHSPKNLLNLFVTIETKADDVDS DG
      cccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
      NRVTLDLPIDLEEQTMGKYNWVTTFTFKPDSPLARHYKASQPAPAFIQPETFLNSKHIIQELPLDNTFVACDSISKSSSSDPYSVSDCGYPVTI
      cccccccccchcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
      FEVPVSVHTRPSQRRVTFHLPEGSQESSSDGGLGDHAGSLTSTSHGLPLGYPOBEYFDRATPSNRTEGDGNSDPSTFIPGLKKAABITVQPTVEEASD
      eeeeecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
      NCTQECLIIYGHSDACWMPASLDHSSSSQAQASALCHSPPLSQASTQHSPRVTTQTIALCHSPPTQTIALCHSPPIQVSALHHSPLVQATALHHSPPS
      ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
      AQASALCYSPPPLAQAAAI SHSSPLPQVIALHRSQAQSSVSLQQGWVQADGLCSVDQVQGSATSQFTMSERLHPSDDSIKVIPLTFTTPRQQARPSRG
      cccccccccchhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
      .DSPIMEEHPL
      ccccccccccc

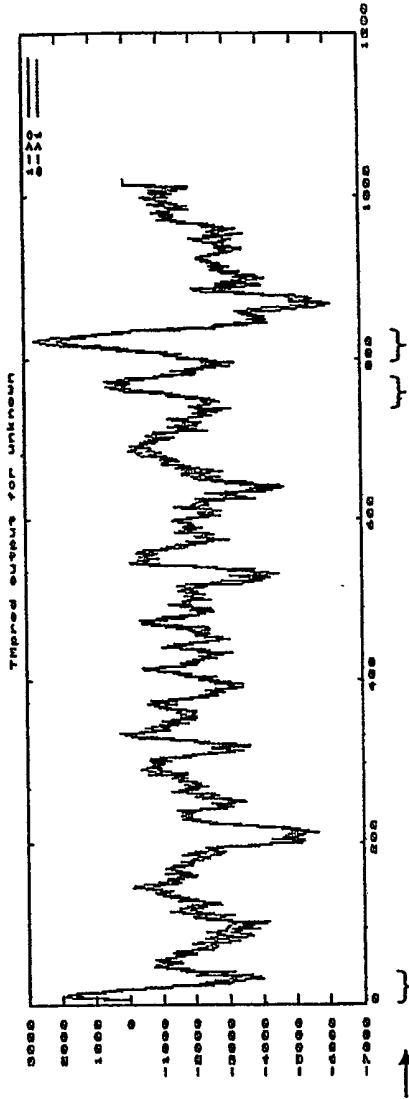
```

Alpha helix (h): 15.73%

Extended strand (e): 25.80%

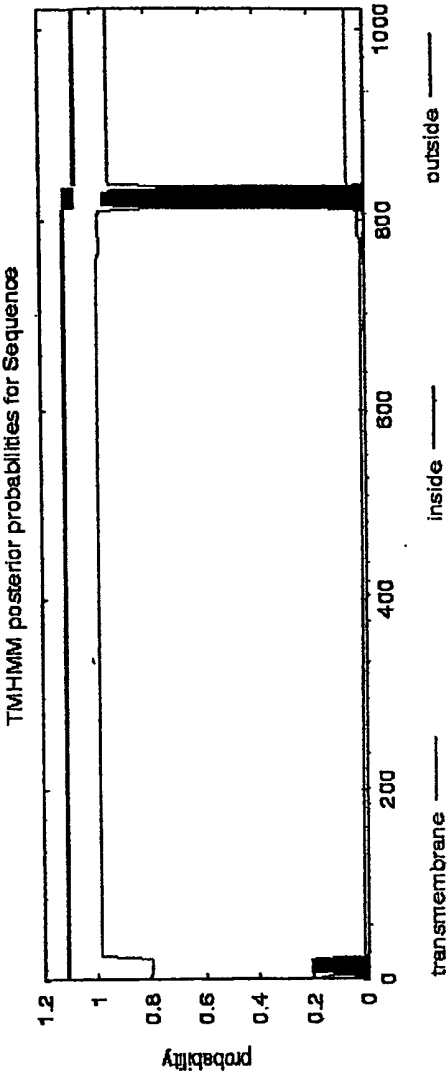
Random coil (c): 58.47%

Fig. 13J: Transmembrane prediction for 109P1D4 variant 1



3 transmembrane regions predicted

Predicted transmembrane regions



1 transmembrane region predicted

Fig. 13K: Transmembrane prediction for 109P1D4 variant 2

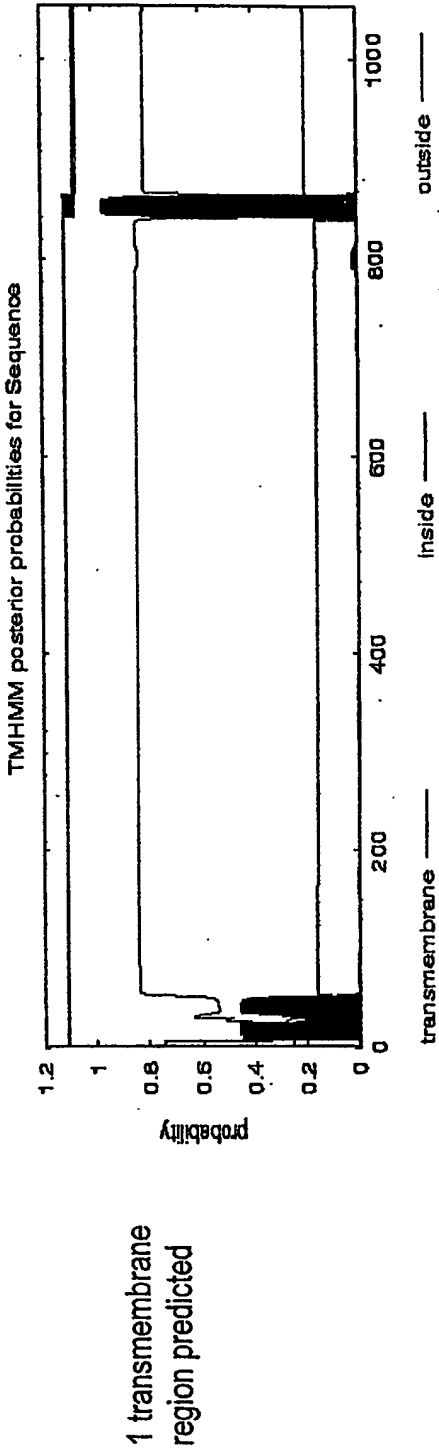
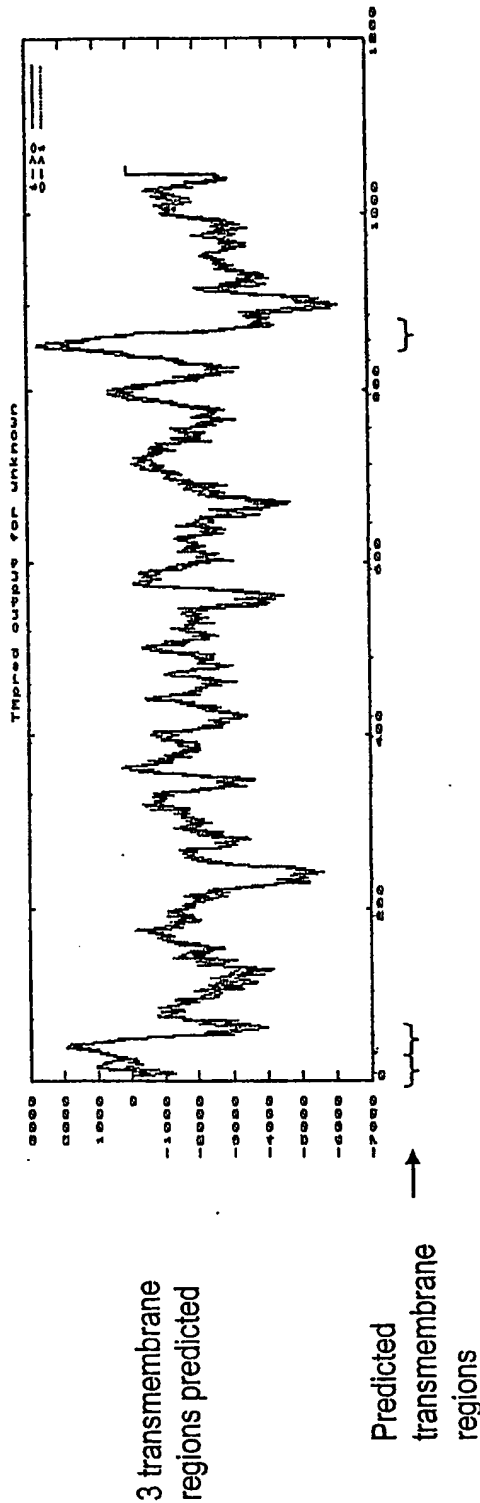
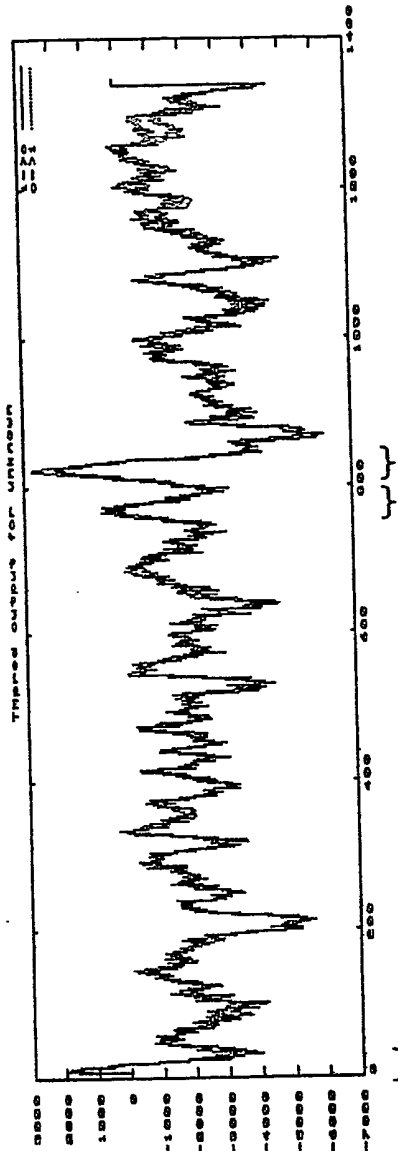
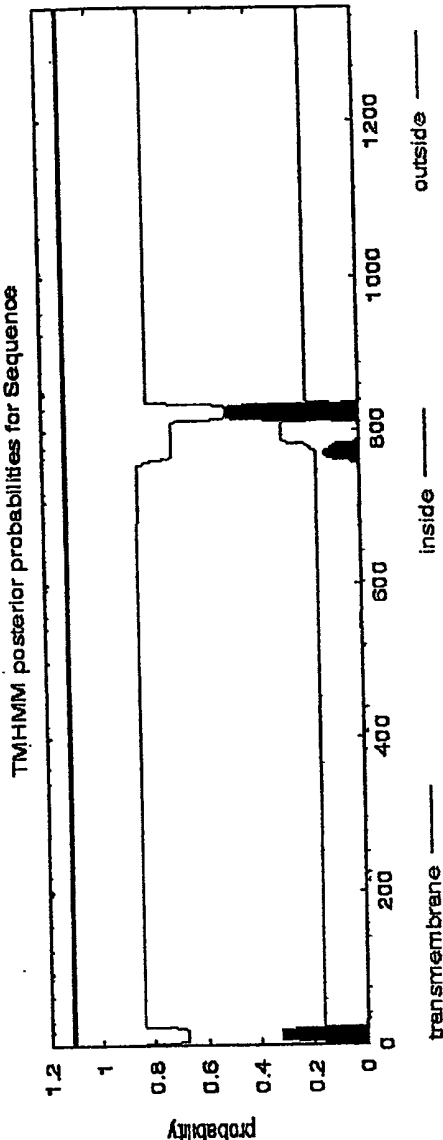


Fig. 13L: Transmembrane prediction for 109P1D4 variant 3



3 transmembrane regions predicted

Predicted transmembrane regions →



No transmembrane region predicted

Fig. 13M: Transmembrane prediction for 109P1D4 variant 4

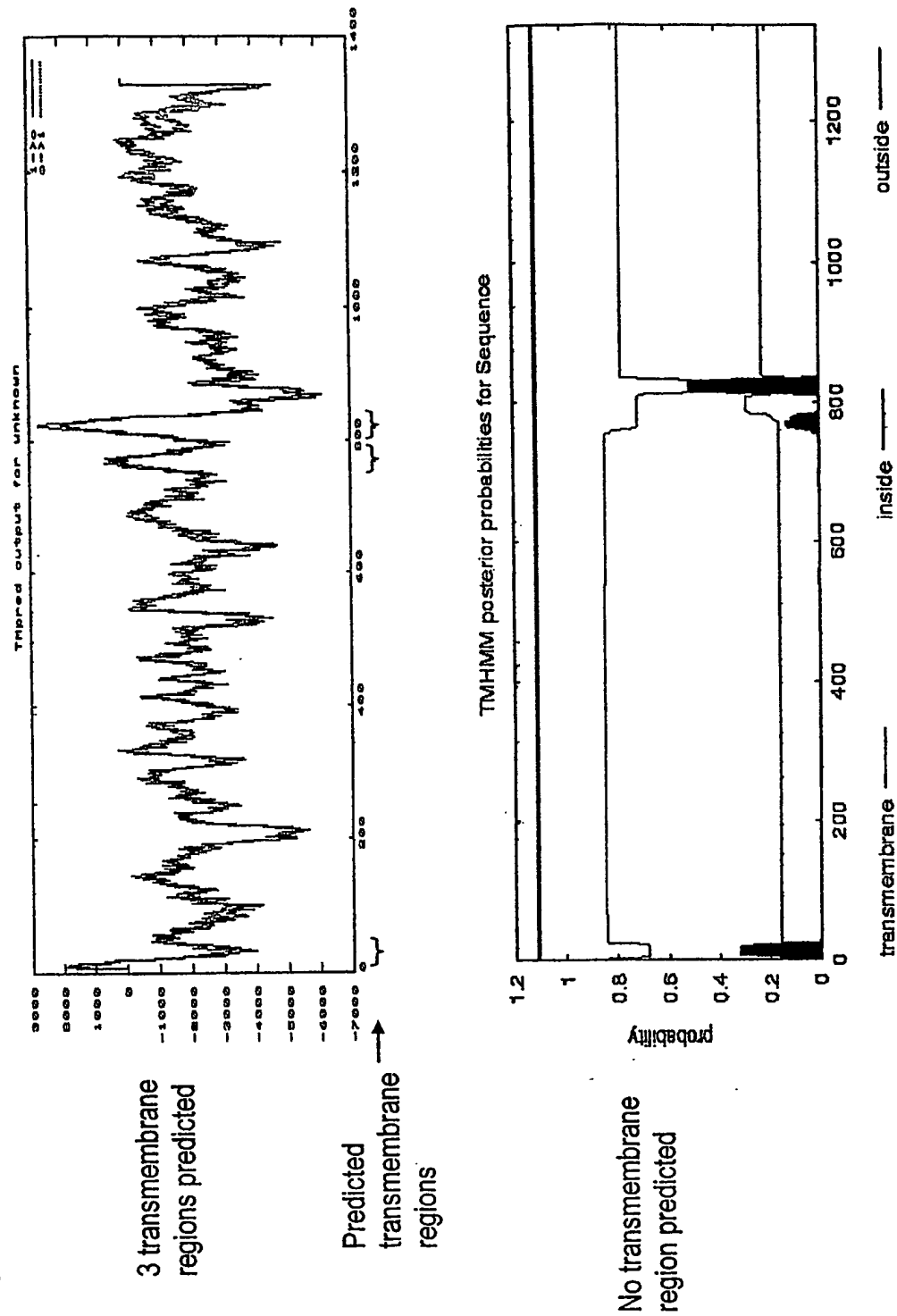


Fig. 13N: Transmembrane prediction for 109P1D4 variant 5

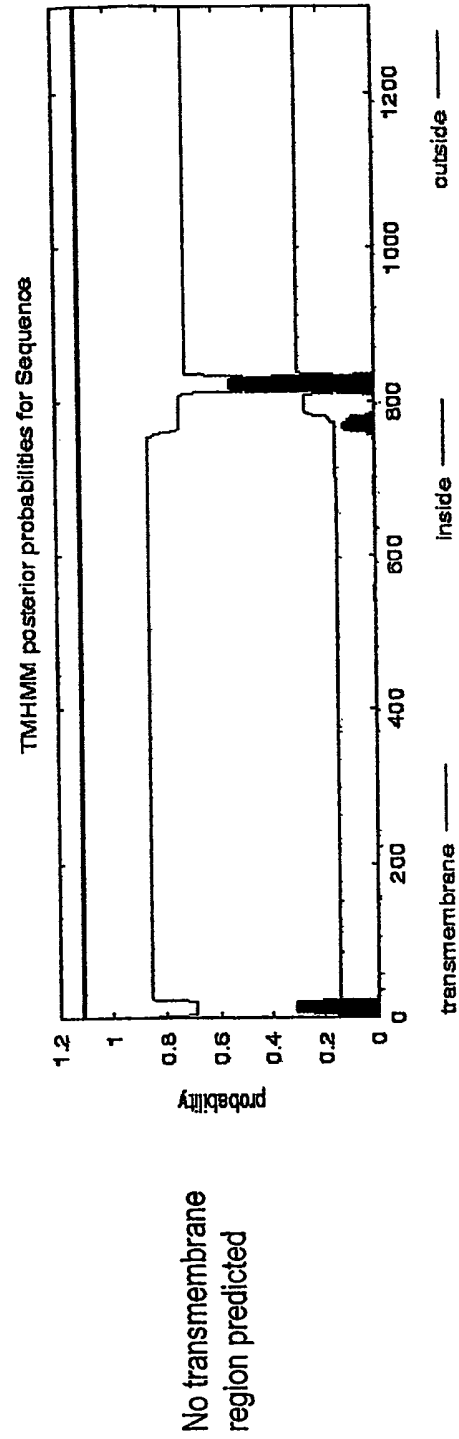
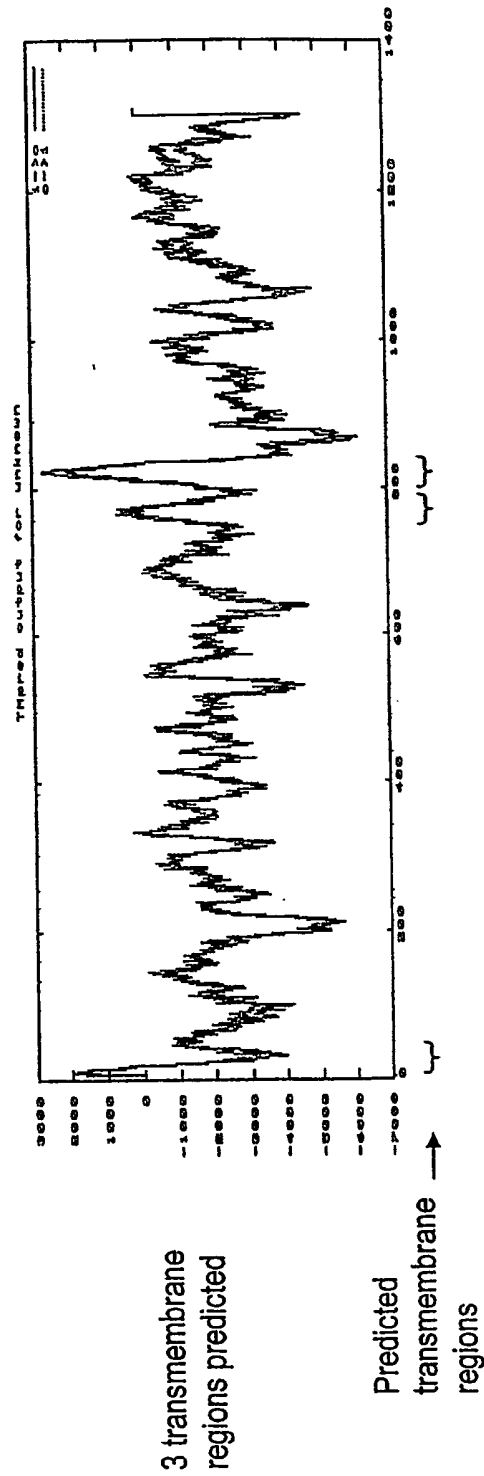


Fig. 130: Transmembrane prediction for 109P1D4 variant 6

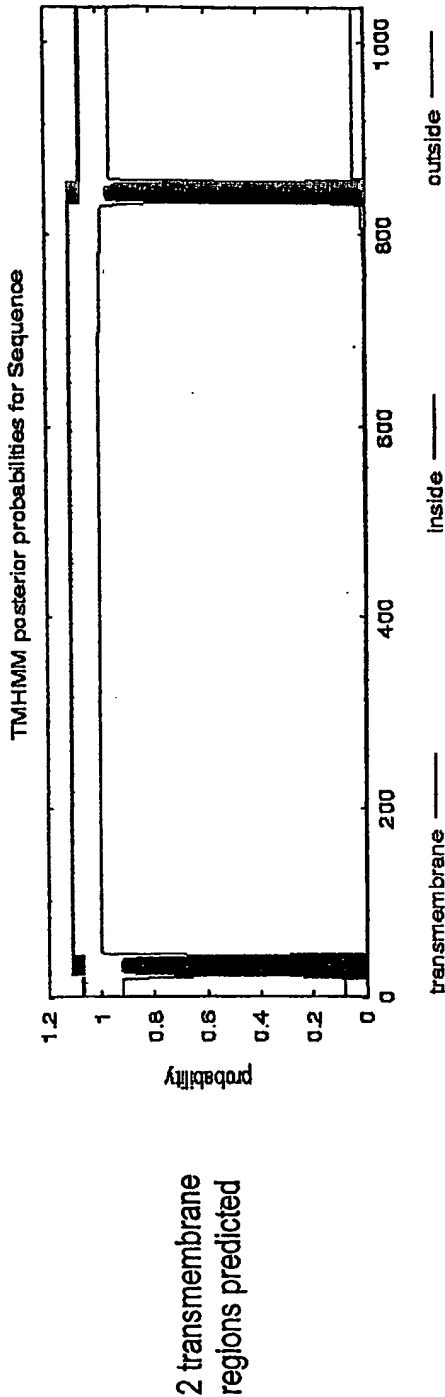
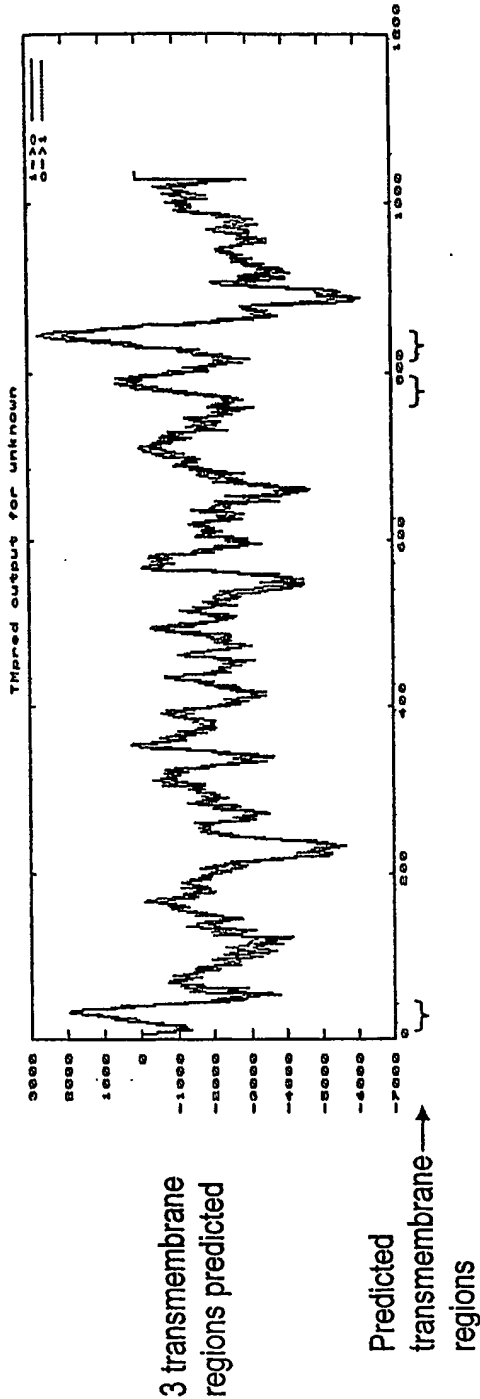


Fig. 13P: Transmembrane prediction for 109P1D4 variant 7

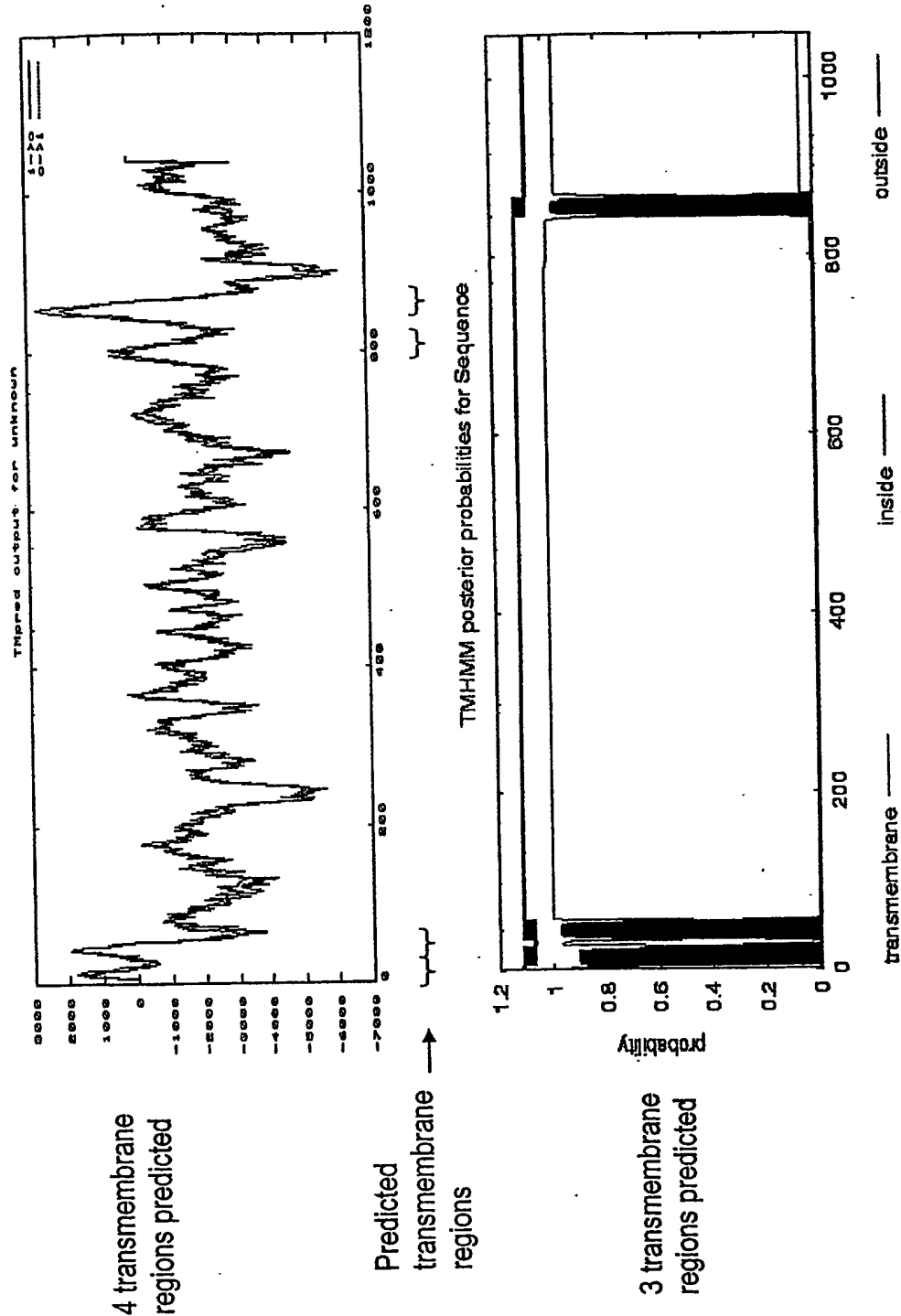


Fig. 13Q: Transmembrane prediction for 109P1D4 variant 8

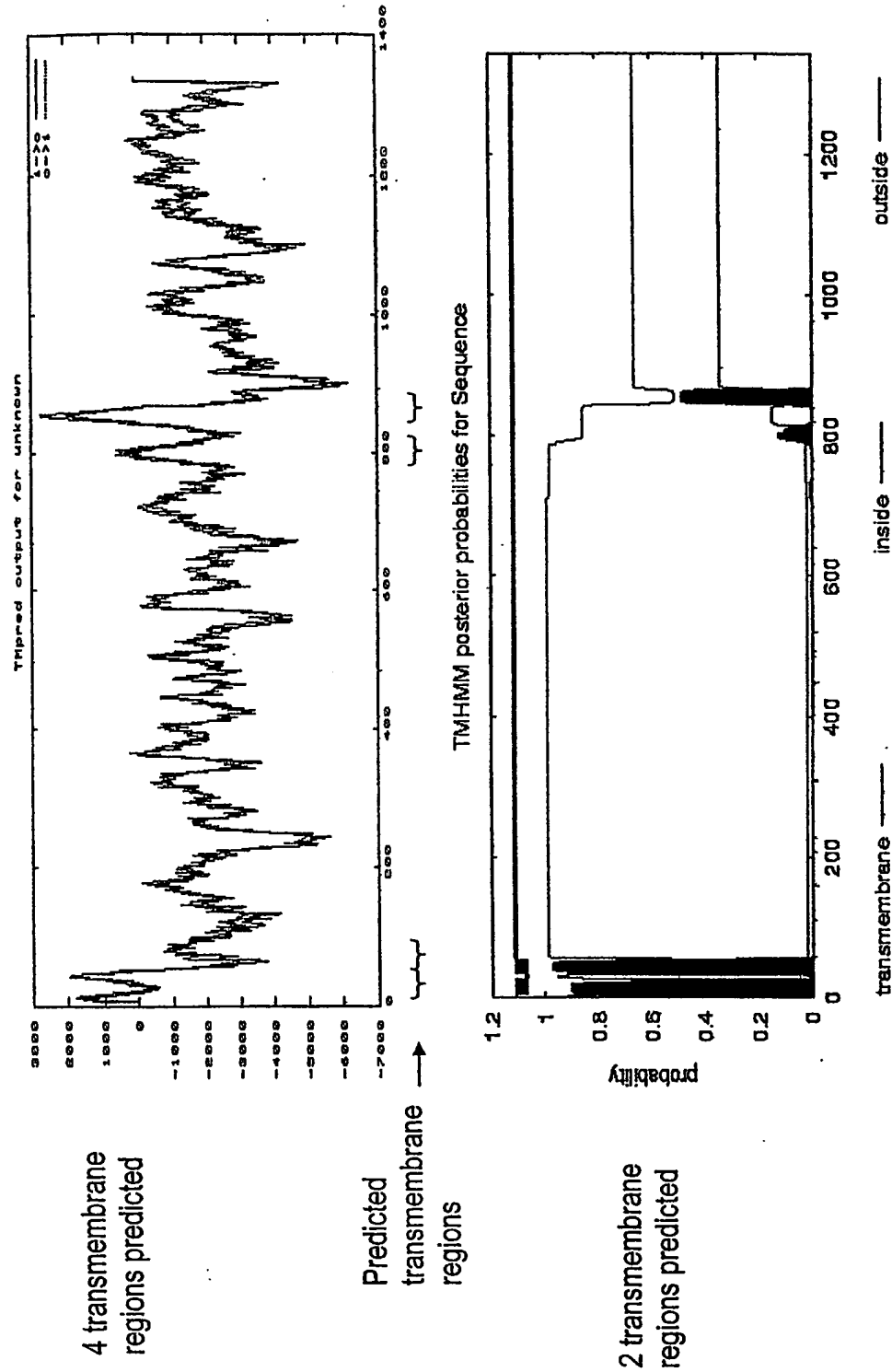


Fig. 13R: Transmembrane prediction for 109P1D4 variant 9

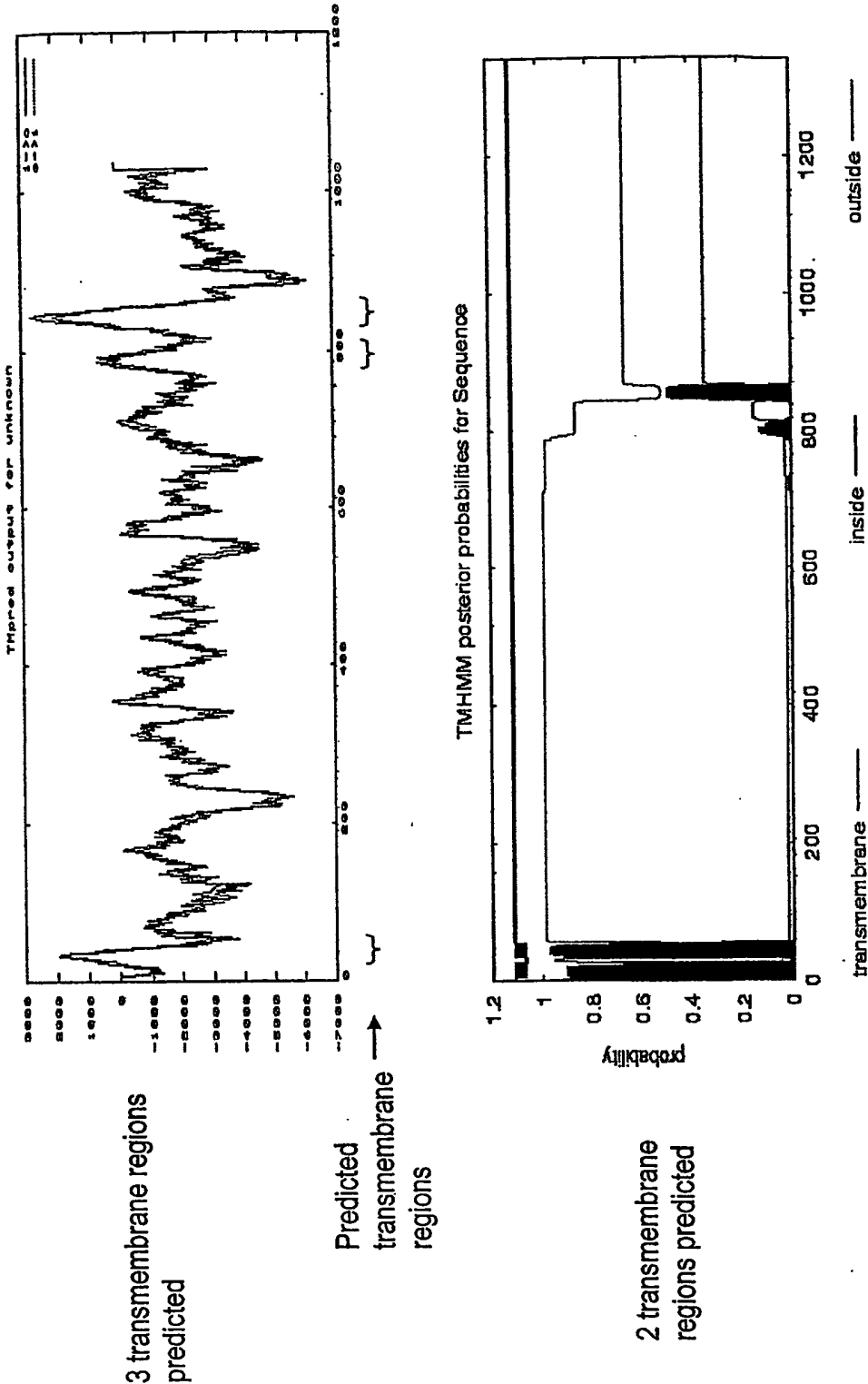


Figure 14: 109P1D4 Expression in Patient Lymphoma Specimens

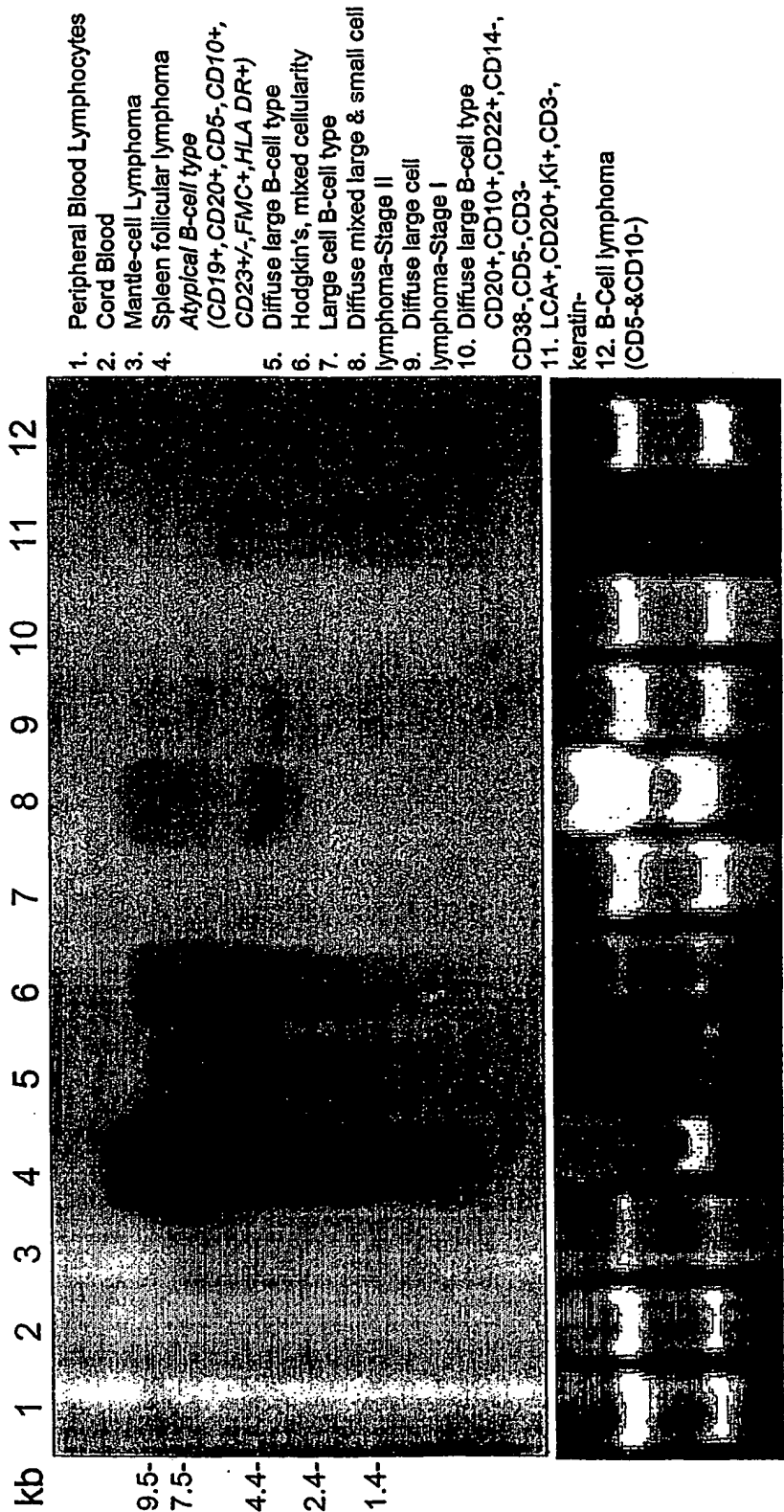


Figure 15 Expression of 109P1D4 by RT-PCR

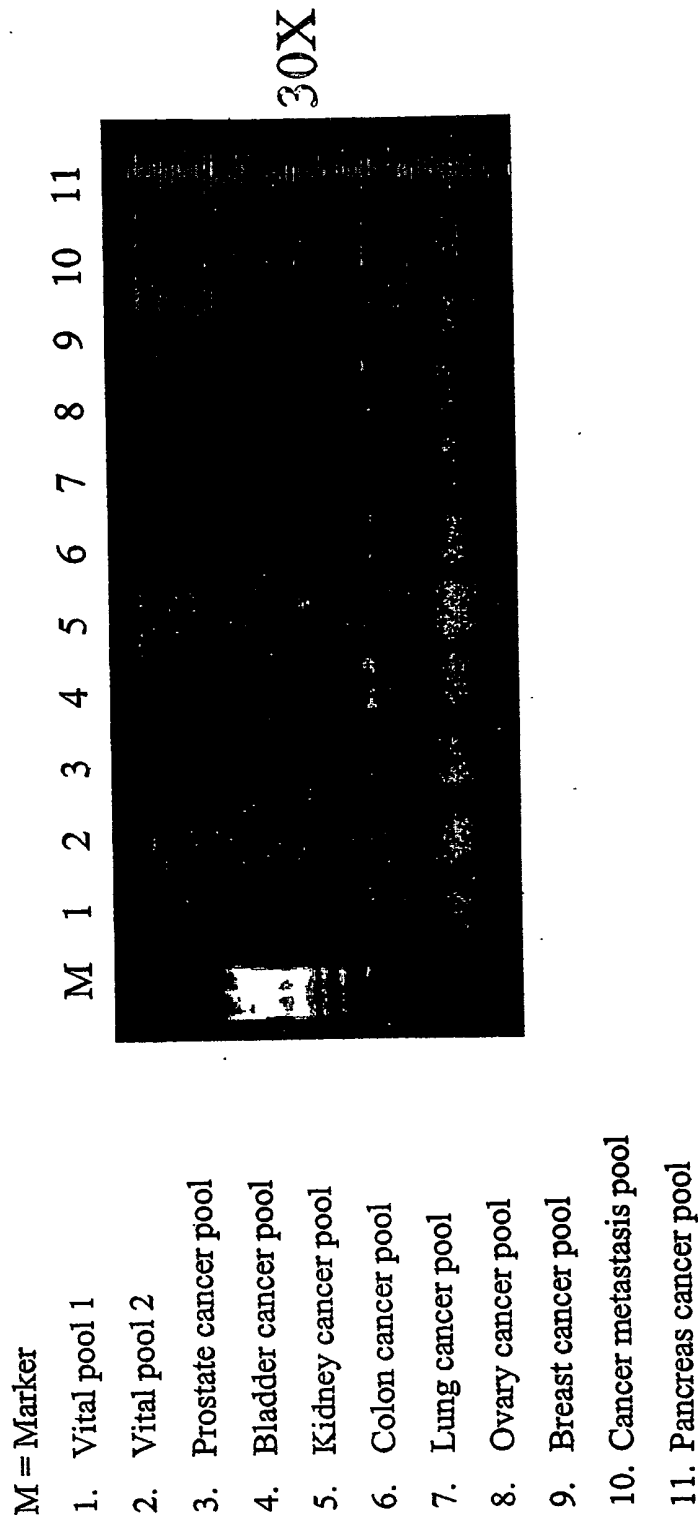


Figure 16 Expression of 109P1D4 in Normal Tissues by Northern Blot

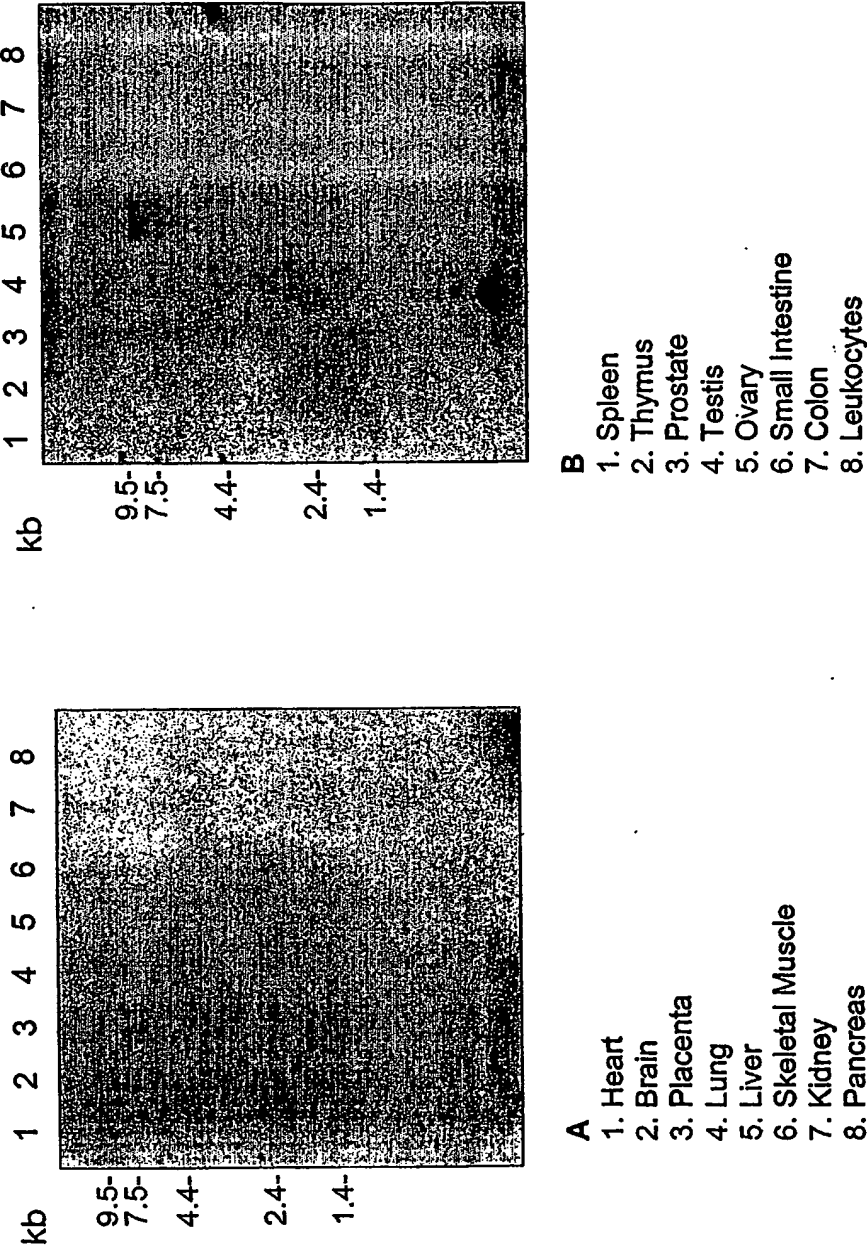


Figure 17 Expression of 109P1D4 in prostate and bone cancer cell lines

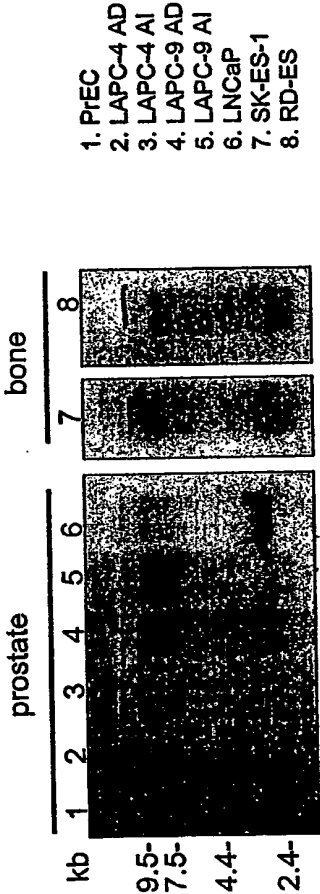


Figure 18A 109P1D4 Expression in Human Normal Tissues

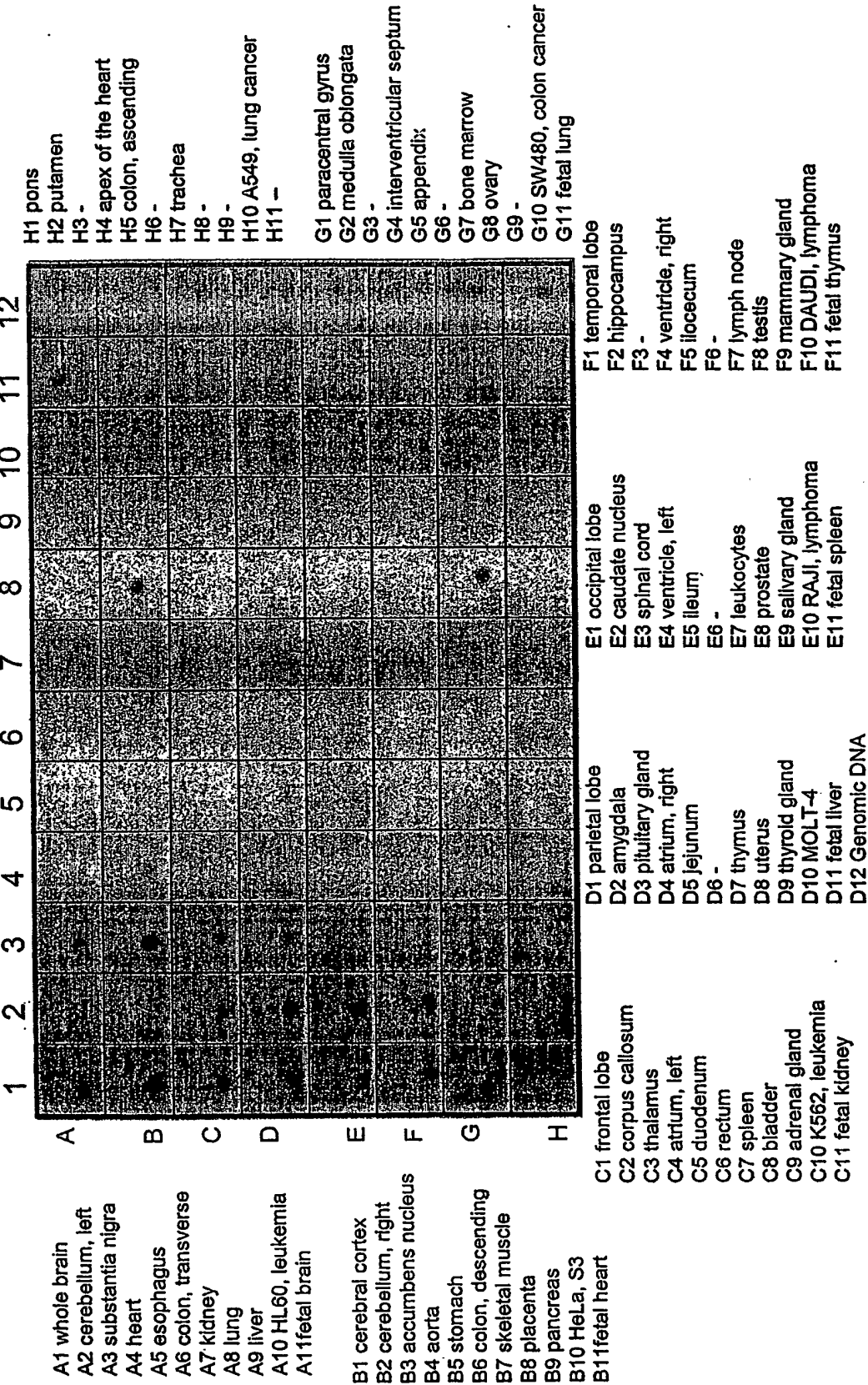
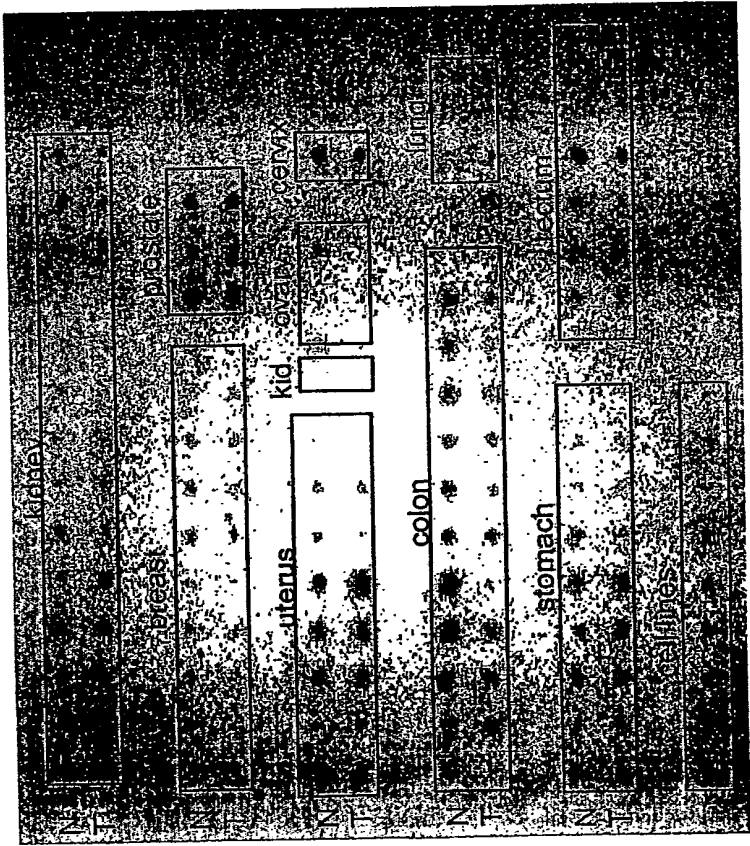


Figure 18B Expression of 109P1D4 in Human Patient
Cancer Specimens

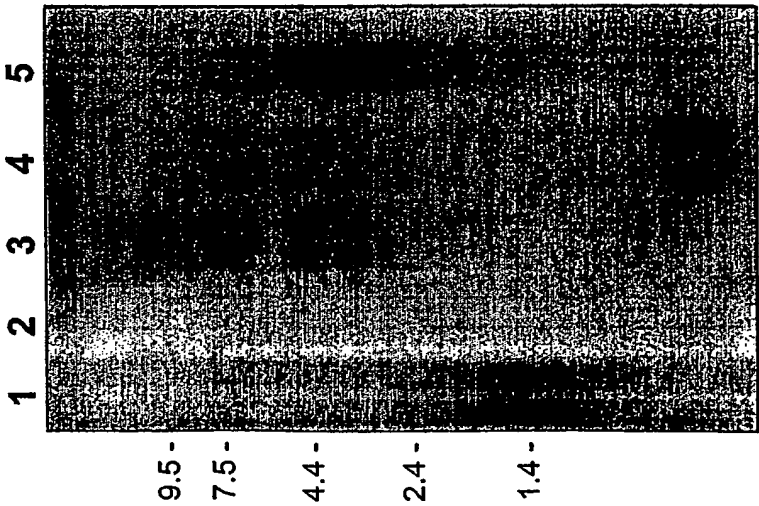


Cancer cell lines are:
(from left to right)

- HeLa (cervical carcinoma)
- Daudi (Burkitt's lymphoma)
- K562 (CML)
- HL-60 (PML)
- G361 (melanoma)
- A549 (lung carcinoma)
- MOLT-4 (lymphoblastic leuk.)
- SW480 (colorectal carcinoma)
- Raji (Burkitt's lymphoma)

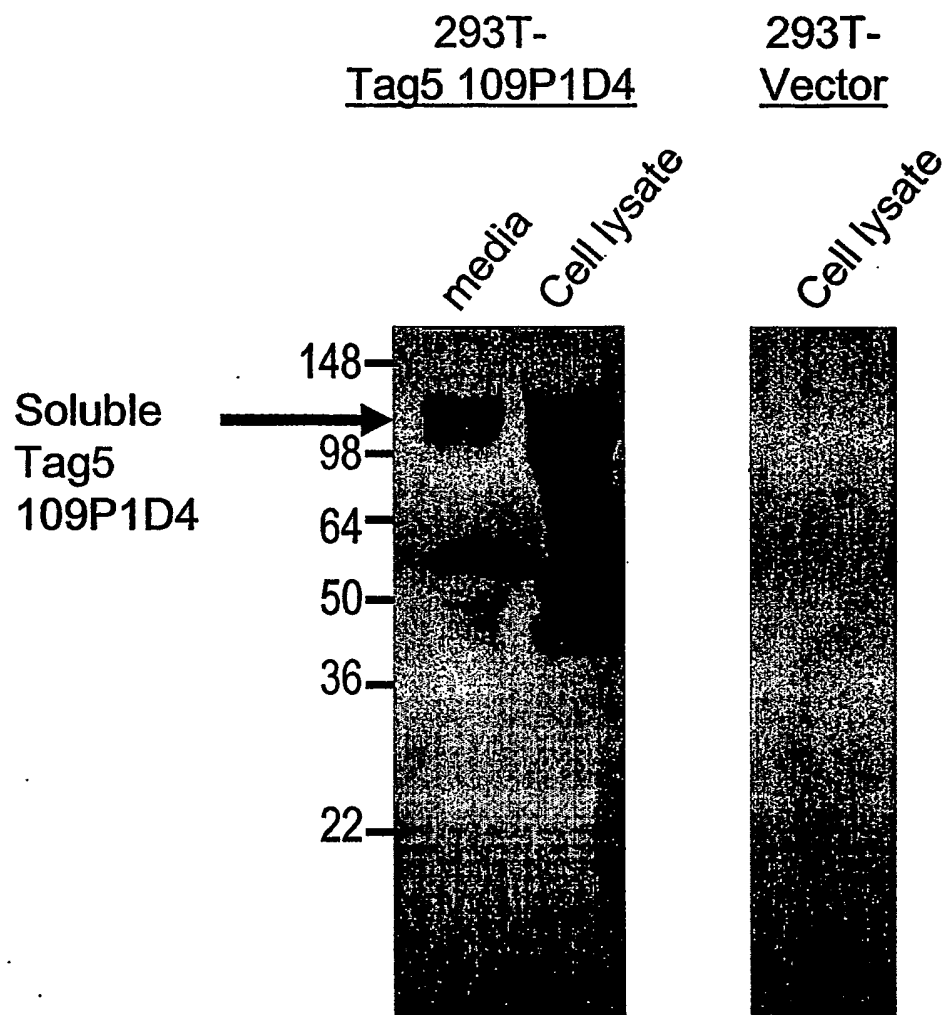
N = normal adjacent tissue RNA
T = tumor RNA

Figure 19 109P1D4 Expression in Lung Cancer Patient Specimens



1. Normal Lung
2. LAPC-9AD prostate cancer xenograft
3. RD-ES bone cancer cell line
4. Lung cancer patient specimen small cell carcinoma, stage I
5. Lung cancer patient specimen small cell carcinoma, stage I

**Figure 20: Expression of soluble secreted
Tag5 109P1D4 in 293T cells**



**Figure 21: Expression of 109P1D4
protein in 293T cells**

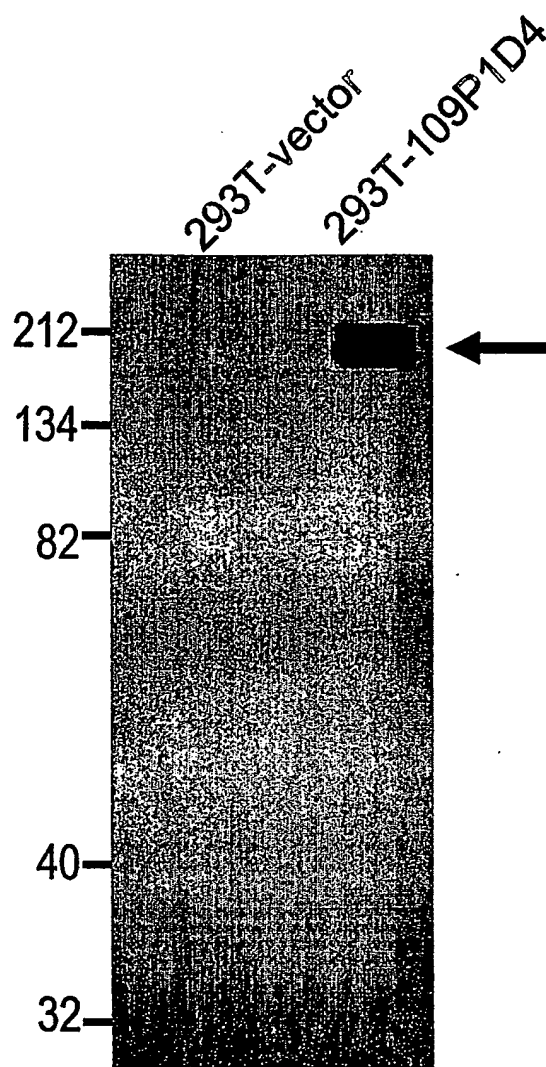


Figure 22: Tyrosine phosphorylation of 109P1D4 after pervanadate treatment

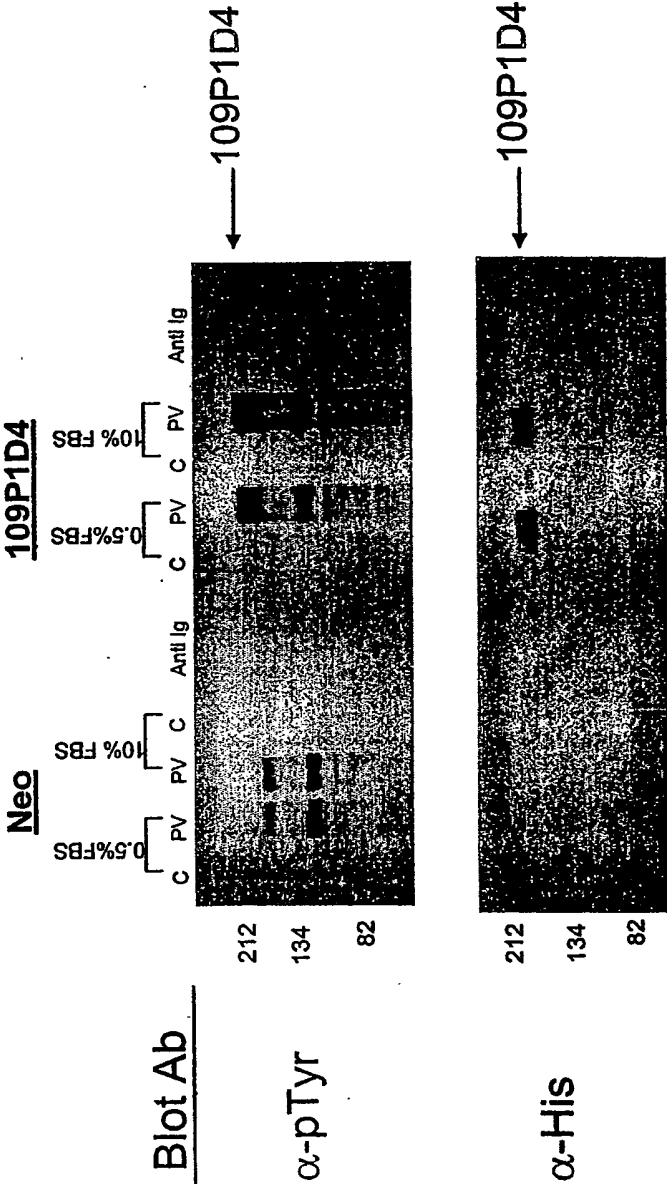
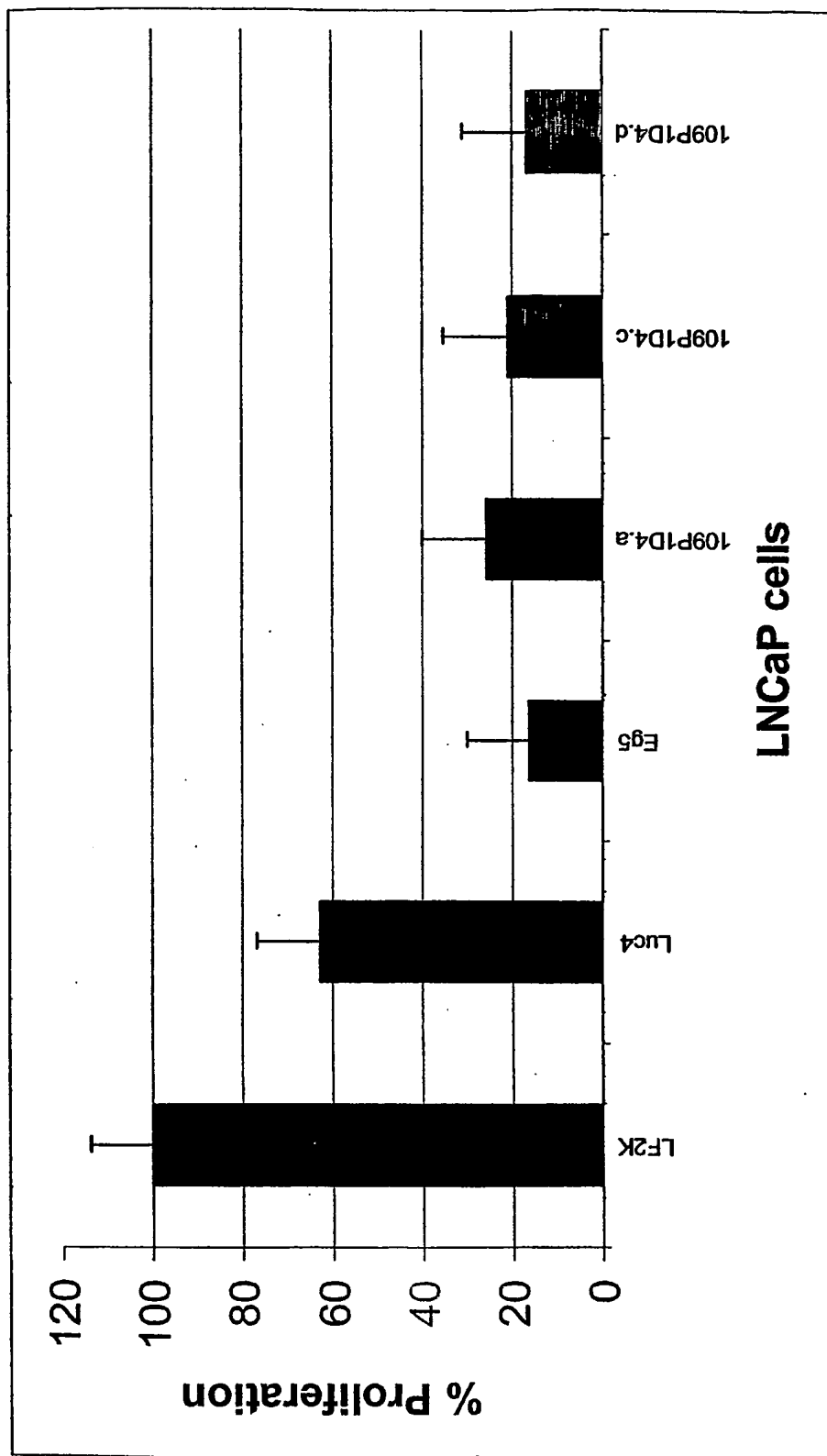


Figure 23. Effect of 109P1D4 RNAi on cell proliferation



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